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June 22, 2004, 16:44:25; Search time 43.583 Seconds (without alignments) 2301.458 Million cell updates/sec
                                                                                                                                                                                            US-09-886-349A-2
1802
1 MSNSRRRSLRWSWLLSVLAA......QTKSGGTRTGNVTLAEGPPA 355
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                    1586107 seqs, 282547505 residues
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                              Title:
Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

A Geneseq_29Jan04:*

1. geneseqp1980s:*
2. geneseqp1990s:*
4. geneseqp2001s:*
5. geneseqp2002s:*
6. geneseqp2003s:*
7. geneseqp2003bs:*
8. geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaw32367 Mycobacte	2	_	1670		310	Aau01890 M. tuberc	1 Myc	Aae17565 Mycobacte	Aay05000 Mycobacte	_	_		~		Aae29703 Mycobacte	17567	72	Ada26354 Mycobacte	Ada26356 Mycobacte	Ada26371 Mycobacte	70	Ada26368 Mycobacte	99	Ada26367 Mycobacta
SUMMARIES	QI	AAW32367	AAW32435	AAW64307	AAW81670	AAY38972	AAY39109	AAU01890	AAE29701	AAE17565	0	AA022137	AAG81110	AAY04830	AAE29702	AAE17566	AAE29703	AAE17567	53	ADA26354	ADA26356	ADA26371	ADA26370	ADA26368	ADA26366	ADA26367
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ALIGNMENTS

1586107

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

RESULT 1 AAM32367 XX XX AC AAM32367; AC AAM32367; XX XX XX XX XX XX XX XX XX Mycobacterium tuberculosis antigen TbRa35. XX XX Antigen, immunogen, vaccine; tuberculosis; non specific adjuct testing; M.tuberculosis. XX Antigen, immunogen; vaccine; tuberculosis; non specific adjuct XX XX Antigen, immunogen; vaccine; tuberculosis; non specific adjuct XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis.
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                                                                                                                                                                                                                        POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
                                                                                                                                                                                  QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA
                                                                                                                                                                                                                                                                    IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
 antibodies,
                                                                                       1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
                                                                     Gaps
                                                                                                                                                                                                                                                                                        GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                     tuberculosis; non specific adjuvant;
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                                                Length 355;
especially monoclonal antibodies or equivalent polyclonal also used for diagnosis
                                                                     Indels
                                                 Score 1802; DB 2;
Pred. No. 7.2e-126;
) Mismatches 0;
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DR;
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95US-00533634.
96US-00620874.
96US-00659683.
96US-00680574.
                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           jen; immunogen; vaccine;
testing; M.tuberculosis.
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                                                           Best Local Similarity 100.
Matches 355; Conservative
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4, Twardzik
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                               Sequence 355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium
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22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
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Vedvick TH,
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                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
                    A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications. The present sequence represents a M.tuberculosis antigen, TDRa35. The immunogenic protein, and fusion proteins containing one or more of the proteins one of the proteins energy search in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                       121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGQTV
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                                                                                                                                                                                                                                              1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAWVAQVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculosis; infection; diagnosis; antigen; TbRa35
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                                                                                                                                                                                         100.0%; Score 1802; DB 2;
100.0%; Pred. No. 7.2e-126;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen TbRa35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis; strain H37Ra.
3; Page 114-116; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky YAW, Dillon DC, Ca
3, Twardzik DR, Lodes MJ;
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97US-00818111.
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(first entry)
                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 355; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORI-) CORIXA CORP.
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                                                                                                                                                                   Sequence 355 AA;
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Vedvick TS,
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09-NOV-1998
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                                                                                                                                       prevention)
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Example 3; Page 110-111; 230pp; English
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3, Twardzik DR, Lodes MJ;
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                                                     96US-00730510.
97US-00818112.
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hes 355; Conservative
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N-PSDB; AAV64463.
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                 07-OCT-1997;
                                                                      13-MAR-1997;
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Vedvick TS,
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                                                                                                                                             This polypeptide comprises Mycobacterium tuberculosis soluble antigen TbRa35. It is encoded by a DNA sequence (see AAV44355) isolated from a M. tuberculosis strain H37Ra expression library with rabbit anti-sera raised
                                                                                                                                                                                              against M. tuberculosis supermatant. No significant homology was found between TDRa35 and Genebank database sequences. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291 W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, or an immunogenic portion of an M. polypeptides, recombinant expression vectors and transferred or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a parient using the above polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS
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                                   polypeptides and DNA - used
tuberculosis infection and
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100.0%; Pred. No. 7.2e-126;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis immunogenic polypeptide TbRa35
                                 New isolated Mycobacterium tuberculosis prevelop products for the detection of M. diagnosis of tuberculosis.
                                                                                                          Example 3; Page 115-116; 250pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
N-PSDB; AAV44355
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium
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Query Match

181 241 241

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used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGGFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
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                                                                                                                                                                                                              and DNA -- infection
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Houghton
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                                                                                                                                                                                                              Immunogenic Mycobacterium tuberculosis polypeptide(s) develop products for the detection of M. tuberculosis diagnosis, treatment and prevention of tuberculosis.
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100.0%; Pred. No. 7.2e-126;
ive 0; Mismatches 0;
Campos-Neto
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120 120 180 180 240

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Campos-Neto A, Houghton J, Hendrickson RC;

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New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
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                                                                                                                                                                                                                         lon DC, Ca
Lodes MJ,
                                                                                                            99WO-US003268
                                                                                                                                          98US-00025197
                                                                                                                                                        98US-00072967
             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 355; Conservative
                                                                                                                                                                                                                         Skeiky YAW,
                                                                                                                                                                                                                                                                        WPI; 1999-527409/44.
                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                       N-PSDB; AAZ19265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 355 AA;
                                                                                                                                            18-FEB-1998;
                                                                                                            17-FEB-1999;
                                                                                                                                                          05-MAY-1998;
                                              WO9942076-A2
                                                                                                                                                                                                                                         TS,
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                                                                                                                                                                                                                         Reed SG,
Vedvick 1
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                                                                                                                                                                                                                                                                                                                                     This invention describes novel recombinant antigens and their encoding mucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
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                                                                                                                                                                                                                                                                           New polypeptide comprising antigenic portions of M. tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 355;
                                                                                                                                                                             Houghton
RC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 1802; DB 2;
; Pred. No. 7.2e-126;
0; Mismatches 0;
                                                                                                                                                                             Campos-Neto A,
J, Hendrickson
                                                                                                                                                                                                                                                                                                          Example 3; Page 151-153; 323pp; English.
                                                                                                                                                                         Dillon DC, Cal
DR, Lodes MJ,
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ilarity 100.0%;
Conservative 0
                                                               99WO-US003265,
                                                                                            98US-00024753
98US-00072596
                                                                                                                                                                           Skeiky YAW, Dil
3, Twardzik DR,
                                                                                                                                                                                                                           WPI; 1999-527416/44.
N-PSDB; AAZ19053.
                                                                                                                                            (CORI-) CORIXA CORP
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Best Local Similarity
Matches 355; Conserv
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WO9942118-A2
                                                               17-FEB-1999;
                                                                                                               05-MAY-1998;
                                                                                                                                                                           Reed SG, Sk
Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1999
                                26-AUG-1999
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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. And the vaccines and fusion protein containing M. tuberculosis Ag's. M. DAR encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or tuberculosis to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ1949 to AAX19460 and AAX39083 to AAX19425 are used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QASDSLIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1802; DB 2;
100.0%; Pred. No. 7.2e-126;
tive 0; Mismatches 0;
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ID AAU0
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RESULT 6 AAY39109

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AAE29701

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The sequence represents Mycobacterium tuberculosis TbRa35 (also known as Mtb32A), an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                       Lodes ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA
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                                                                                                                                                                                                                                                                                                                                                     Dillon
                                                                                TbRa35; Mtb32A; antigen; vaccine; tuberculosis; AIDS; acquired immunodeficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1802; DB 4;
100.0%; Pred. No. 7.2e-126;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 153-154; 168pp; English.
                                                tuberculosis antigen TbRa35 (Mtb32A)
                                                                                                                                                                                                                                                                                                                                                     Houghton RL,
                                                                                                                                                                                                                                   10-OCT-2000; 2000WO-US028095,
                                                                                                                                                                                                                                                                   99US-0158338P
99US-0158425P
                                                                                                                                 Mycobacterium tuberculosis.
                 (first entry)
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-290576/30
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                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS03781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 355 AA;
                                                                                                                                                                                                                                                                                                                                                     Reed
                                                                                                                                                                 WO200124820-A1.
                                                                                                                                                                                                                                                                   07-OCT-1999;
                                                                                                                                                                                                                                                                                   07-OCT-1999;
                 29-AUG-2001
                                                                                                                                                                                                 .2-APR-2001
                                                                                                                                                                                                                                                                                                                                                  Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynuclectide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to eliciting immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. Luberculosis MTB32A antigenic protien. MTB32A is also referred to as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDRTODVAVLOLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGOGGTPRAVPGRVVALGOTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                        Vaccine, immunity; diagnostic agent; gene therapy; MTB32A antigen;
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                                                                                                        Mycobacterium tuberculosis MTB32A antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1802; DB 5; 100.0%; Pred. No. 7.2e-126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 78-79; 155pp; English.
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AAE29701 standard; protein; 355
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                                                                                                                                                                                                                                                                                                                                      13-MAR-2001; 2001US-0275837P.
                                                                                                                                                                                                                                                                                                  13-MAR-2002; 2002WO-US008223
                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-759844/82.
                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
-- Tocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 355 AA;
                                                                                                                                                                                                                             WO200272792-A2
                                                                    27-JAN-2003
                                                                                                                                                                                                                                                               19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355;
                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky Y,
                                   AAE29701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
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MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with increase the expensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. The diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species MTB32A (MTB32A (RAB2EL)) protein
IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTB39 antigen and MTB32A antigen from useful for eliciting immune response in a subject.
                   GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                 GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                          serological sensitivity; immune response; vaccine; MTB32A; Ra32FL protein.
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100.0%; Score 1802; DB 5;
Best Local Similarity 100.0%; Pred. No. 7.2e-126;
Matches 355; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      (Ra35FL) protein.
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                                                                                                                                                                                                          AAE17565 standard; protein; 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alderson M;
                                                                                                                                                                                                                                                                                                                      Mycobacterium species MTB32A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-2001; 2001WO-US019959
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01-FEB-2001; 2001US-0265737P
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                            Fusion protein; antigen;
tuberculosis; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition comprising Mycobacterium species,
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N-PSDB; AAD28335.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium sp
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Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
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1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
                                            PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGGTYGDVVG
                                                                                                  QASDSLTGAESTLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA
                            POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGOTYGVDVVG
                                                                                  YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
                                                                                                                                                                                           241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
                                                                                                                                       QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA
                                                                                                                                                                                                                                                                   GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium species protein sequence 50D.
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97FR-00011325.
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Goguet De La Salmoniere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-181045/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium sp.
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DB 2; Length 355;

99.4%; Score 1792;

Query Match

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Gaps

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Indels

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polymucleotide sequence of Ral2, a 14 kDa C-terminal fragment of serine protease antigen MTB32A of Mycobacterium tuberculosis, and a heterologous polymucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum
                                                                                                                                                                                                         1.80
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                                                                                                                                                                                                                                                                                                  IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
                                                                                  1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVG
                                                                                                                                  PQVVIINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVVVG
                                                                                                                                                                                                YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGQTV
                                                                                                                                                                                                                                                               QASDSLTGARETLNGLIQFDAAIQPGDSGGPVVNGLGGVVGMNTAASDNFQLSQGGQGFA
                                                                                                                 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
                                                                                                                                                                            YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPWVAMGNSGGQGGTPRAVPGRWALGQTV
                                                                                                                                                                                                                                        QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA
                                                                                                                                                                                                                                                                                                                              241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
                                                     1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
                           Gaps
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antibodies to.M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another can be used in vivo as a DNA vaccine. This sequence ran adjuvant and Mycobacterium tuberculosis MTB32A protein
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   between nucleotide or polypeptide sequences, and comparing the sequences.
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                                                                                                                                                                                                                                                 Score 1792; DB 4; Length 355;
Pred. No. 4e-125;
0; Mismatches 2; Indels
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                           Disclosure; Page 157; 207pp; English
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11-SEP-1997;
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                                                                                                                                                              Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
                                                                                                                                                                                                                                                                                                                                      Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QASDSLTGAEETILNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis mature Ra35 antigenic protein.
   Guigueno A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1792; DB 2;
Pred. No. 4.3e-125;
   Pelicic V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%; Score 1792; 99.4%; Pred. No. 4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by GAG"
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Lim E,
Y;
                                                                                                                                                                                                                                                                                        Claim 32; Fig 50F; 309pp; French
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis
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Gicquel B, Portnoie D,
Goguet De La Salmoniere
                                                                                  WPI; 1999-181045/15.
N-PSDB; AAX34252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 379 AA;
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Mycobacterium sp. MTB32A (Ra35FL) mature protein

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MJS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis mature Ra35 (N-terminus of MTB32A; RA35FL) antigenic protein New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis. Disclosure; Page 79-80; 155pp; English. Guderian J; 13-MAR-2002; 2002WO-US008223 13-MAR-2001; 2001US-0275837P Skeiky Y, Brannon M, WPI; 2002-759844/82. N-PSDB; AAD47077. (CORI-) CORIXA CORP Sequence 330 AA; 19-SEP-2002

212 272 307 152 128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187 247 GVVDNNGNGARVORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 332 92 67 8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGFTAFLGL 93 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP 33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT Query Match

90.7%; Score 1634; DB 5; Length 330;
Best Local Similarity 99.4%; Pred. No. 2.1e-113;
Matches 321; Conservative 0; Mismatches 2; Indels 308 VIWQIKSGGIRIGNVILAEGPPA 330 333 VNWQTKSGGTRIGNVTLAEGPPA 355 153 213 248 g g a ò QQ 유 ò ò $\dot{\circ}$

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92 67

AAE17566 standard; protein; 330 AA

(first entry)

22-APR-2002

AAE17566

RESULT 15 AAE17566 ID AAE1 XX AC AAE1 XX DT 22-A

The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infection the serological sensitivity of sera from individuals infected with the tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, considered with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymorlectides are useful as diagnostic tools in partients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the infection or monitoring of disease progression, as immal. Sequences of the invention are also used as vaccines. MTB32A, fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species MTB32A (MTB32A) mature protein 93 NNHVIAGAIDINAFSVGSGQIYGVDVVGYDRIQDVAVLQLRGAGGLPSAAIGGGVAVGED 152 Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject 33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT serological sensitivity; immune response; vaccine; MTB32A; Ra32FL protein. . 0 Length 330; Indels /note= "Encoded by GCG" 199. .330 /note= "Ra35 C-terminal peptide, Ra12" Score 1634; DB 5; 1 Pred. No. 2.1e-113; 0; Mismatches 2; /note= "Ra35 N-terminal peptide" Location/Qualifiers 8. .202 /note= "Encoded by Claim 70; Fig 6; 136pp; English. Alderson M; Query Match
Best Local Similarity 99.4%;
Matches 321; Conservative 20-JUN-2000; 2000US-00597796. 01-FEB-2001; 2001US-0265737P. 20-JUN-2001; 2001WO-US019959 Fusion protein; antigen; tuberculosis; infection; WPI; 2002-147798/19. N-PSDB; AAD28336. Reed S, CORI-) CORIXA CORP Misc-difference 182 Misc-difference Sequence 330 AA; WO200198460-A2. Mycobacterium 27-DEC-2001 Skeiky Y, Region Region 임 ò ò

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Db 68 NNHVIAGATDINAFSVGSGCTGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGCGVAVGEP 127

Oy 153 VVAMGNSGGCGCTPRAVPGRVVALGGTVQASDSLTGAEETLAGLIQFDAAIQPGDSGGPV 212

Db 128 VVAMGNSGGCGCTPRAVPGRVVALGGTVQASDSLTGAEETLAGLIQFDAAIQPGDSGGPV 187

OY 213 VNGLGQVVGANTAASDNFQLSCGGCFAIPIGQAMAIAGQIRSGGGSFTVHIGPTAFLGL 272

Db 188 VNGLGQVVGANTAASDNFQLSCGGGFAIPIGQAMAIAGQIRSGGGSFTVHIGPTAFLGL 247

OY 273 GVVDNNGAGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 332

OY 333 VNWQTKSGGTRTGNVTLAEGPPA 355

Db 308 VTWQTKSGGTRTGNVTLAEGPPA 355

Db 308 VTWQTKSGGTRTGNVTLAEGPPA 330

Search completed: June 22, 2004, 17:15:23

Job time: 44.583 secs
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RESULT 1
US-08-818-112-79
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Sequence 79, Appl
Sequence 79, Appl
Sequence 26, Appl
Sequence 2, Appl
Sequence 67, Appl
Sequence 819, Appl
Sequence 819, Appl
Sequence 819, Appl
Sequence 818, Appl
Sequence 825, Appl
Sequence 825, Appl
Sequence 352, Appl
Sequence 352, Appl
Sequence 352, Appl
Sequence 352, Appl
Sequence 354, Appl
Sequence 835, Appl
                                                                                                                                                    June 22, 2004, 17:07:54; Search time 12.6725 Seconds (without alignments) 1446.225 Million cell updates/sec
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                                                                                                                                                                                                                                                                                     1802
1 MSNSRRRSLRWSWLLSVLAA......QTKSGGTRTGNVTLAEGPPA 355
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6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-05-556-79
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US-09-223-049-26
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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Gaps
                                                                                                            GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
APPLICANT: Seattle
STREET: 6300 Columbia Center, 701 Fifth Avenue
CONTRY: Seattle
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 98104-77092
CONTRY: USA
INFORMATION DATE: PC-DOPS/MS-DOS
SOFTWARE: PLOPPY disk
COMPUTER: IBM PC compatible
STATE: Washington
CONTRY: BED PE Floppy disk
COMPUTER: IBM PC compatible
STATE: PREDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: BAP Compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
CONTRY: A27
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 31,393
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100.0%; Score 1802; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.1e-151;
Matches 355; Conservative 0; Mismatches 0;
Sequence 79, Application US/08818112 Patent No. 6290969 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
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180 240 300

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121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                          181 QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
                                   1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
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                                                                                                                                                                       61 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
                                                                                                                                                                                                                                                                                                   121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
                                                                                                                                                                                                                                                                                                                                                                                  QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLLASSIFICATION:
ATTORNEY/AGRATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 79, Application US/09056556;
Patent No. 6350456;
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TILLE OF INVENTION: COMPOUNDS AND M.
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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US-09-056-556-79
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                                                                       PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
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   MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTONNEY/AGENT INPORMATION:
NAME: MAKY, DAVIG J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INVERMATION:
math EDDATOR (2007) A 100 A 100
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 80, Application US/08818111; Patent No. 633885.
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
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INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (206) 622-4900
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STATE:
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                                                                                                                                                                                        181 QASDSLIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA 240
                                                                                                                                                                                                                   241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
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1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDFSAMVAQVA 60
                                                                                                               YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
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APPLICANT: Reed, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Lodes, Michael R.
APPLICANT: Lodes, Michael R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1802; DB 4;
100.0%; Pred. No. 2.1e-151;
iive 0; Mismatches 0;
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6300 Columbia Center, 701 Fifth Avenue
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NAME: MAKI, David J.
REGISTATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-691
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 80, Application US/09072596; Patent No. 6458366; GENERAL INFORMATION: APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A.W.
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amino acid
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Best Local Similarity 100.
Matches 355; Conservative
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ZIP: 98104-7092
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STATE: Washing
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US-09-072-596-80
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                                        1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAWVAQVA 60
1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA 60
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Houghton, Romand C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Houghton, Romand C.
APPLICANT: Hondrickson, Ronald C.
APPLICANT: HONDRICON: 355
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ZIP: 98104-7092
COMPUTER: ELDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, 1
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5. 6592877
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INFORMATION FOR SEQ ID NO: 79
SEQUENCE CHARACTERISTICS:
TENGTH: 355 amir.
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ADDRESSEE: SEED and
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Washington
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US-09-223-040-2
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US-09-287-849-2
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APPLICANT: Bullon, Davin C.
APPLICANT: Campos-NetO, Antonio
APPLICANT: Corisa Corporation
TITLE OF INVENTION: Endson Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
CURRENT APPLICATION NUMBER: US 08/09/287, 849
CURRENT FILING DATE: 1999-04-07
FRIOR FILING DATE: 1997-10-01
FRIOR PAPLICATION NUMBER: US 09/025,197
FRIOR APPLICATION NUMBER: US 09/025,197
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-12-30
FRIOR FILING DATE: 1998-13-30
FRIOR FILING DATE: 1998-13-30
FRIOR FILING DATE: 1998-13-30
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                                                                                                                                                                                                                                                                                                                                                                                    121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA 240
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                                                                                                                                                                                        1 MSNSRRRSIRWSWILSVIAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA 60
                                                                                                                               1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
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                                                                   Gaps
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          Length 355;
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                                                               Indels
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Best Local Similarity 97.5%; Pred. No. 1.1e-78;
Matches 195; Conservative 0; Mismatches 5; Indels
   ; Score 1802; DB 4;
; Pred. No. 2.1e-151;
0; Mismatches 0;
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Patent No. 6627198
GENERAL INFORMATION:
Query Match
Best Local Similarity 100.0%;
Matches 355; Conservative 0
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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AAGDIAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPN

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APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009010US
CURRENT APPLICATION NUMBER: US/09/223,040
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
FILE REFERENCE: 014058-009020US
                                                                                                                     207
                                                                                                                                                                     517 AVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGD 576
GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGV 147
                                                       457 GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGV 516
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Best Local Similarity 97.5%; Pred. No. 1.5e-78;
Matches 195; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                208 SGGPVVNGLGQVVGMNTAAS 227
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Patent No. 6627198
GENERAL INFORMATION:
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Patent No. 6338852
GENERAL INFORMATION:
                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEPAK: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.0
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STATE: Washington
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ZIP: 98104-7092
       CLASSIFICATION:
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US-08-818-112-66
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US-08-818-111-67
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
ADRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 54.6%; Score 983; DB 4; Length 729;
Best Local Similarity 97.5%; Pred. No. 1.5e-78;
Matches 195; Conservative 0; Mismatches 5; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patcettin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,112

FILING DATE: 13-MAR-1997
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR PLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SCO ID NOWS: 46
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Patent No. 6290969
GENERAL INFORMATION:
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US-08-818-112-66
                                                                                                                                                                                                                                                                                                                                SOFTWARE: Pat
SEQ ID NO 2
LENGTH: 729
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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61 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTR 120
                                                                           224 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 283
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                                         Gaps
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APPLICANT: Read, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Netc, Antonia
APPLICANT: Campos-Netc, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardick, Thomas S.
APPLICANT: Twardick, Thomas S.
APPLICANT: Twardick, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
    Length 132;
37.5%; Score 676; DB 3; Length 13
100.0%; Pred. No. 2e-52;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
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61 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVMWQTKSGGTR 120
61 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTR 120
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0
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APPLICANT: Dillon, Davin C.
APPLICANT: Campos Netc, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twendrick, Thommas S.
APPLICANT: Twendrick, Daniel R.
APPLICANT: Twendrick, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Compounds AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 37.5%; Score 676; DB 4; Length 132; Best Local Similarity 100.0%; Pred. No. 2e-52; Matches 132; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-702c
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROCESSION PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210121.417C9
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APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                    RESULT 12
US-09-072-596-67
; Sequence 67, Application US/09072596
; Patent No. 6488366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                  344 TGNVTLAEGPPA 355
                                                                                   121 TGNVTLAEGPPA 132
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
US-09-072-596-67
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US-09-072-967-66
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                                                                                                                                                                                                                                                  1 TAASDNFQLSQGGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTFLGLGVVDNNGNGAR 60
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                                                                                                                                                                         0; Gaps
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                         Query Match 37.5%; Score 676; DB 4; Length 132; Best Local Similarity 100.0%; Pred. No. 2e-52; Matches 132; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.5%; Score 676; DB 4; Length 132; Best Local Similarity 100.0%; Pred. No. 2e-52; Matches 132; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/056,556 FILIG DATE: 07-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/ACENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 132 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                  344 TGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single;
TOPOLOGY: linear
US-08-818-111-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
       amino acid
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ZIP: 98104-7092
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CITY: Seattle
STATE: Washingt
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US-09-056-556-66
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37.5%; bcc. 100.0%; Pred. No. ac. ... 0; Mismatches
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Patent No. 6620922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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CORGANISM: Homo sapien
US-09-636-215-819
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Matches 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTR 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                             APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Hendrickson, Raymond
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 676; DB 4; Length 132;
100.0%; Pred. No. 2e-52;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         SIALE: MEANINGTON.
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                              E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Makt, David J.
NEGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELEPHONE: (206) 692-490
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 819, Application US/09636215
Parent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Hitchan, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
66, Application US/09072967
3. 6592877
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Best Local Similarity 100.
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Washington
      Sequence 66, Applicat:
Patent No. 6592877
GENERAL INFORMATION:
APPLICANT: Reed, 9
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SEED
STREET: 6300 Co
CITY: Seattle
STATE: Washingt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-09-636-215-819
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61 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTR 120
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Helpler, William
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42171717
CURRENT APPLICATION WUMBER: 105/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
APPLICANT: Retter, March
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Webler, William
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: US/09/636,215
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 919
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 676; DB 4; Length 132;
Pred. No. 2e-52;
0; Mismatches 0; Indels
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-215-848
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	0;	283
	Gaps	NGNGAR
	0,	MQAA!
Length 132;	Indels	HIGPTAFLGLG
	, ;	VI.
37.5%; Score 676; DB 4; Length 132;); Mismatches	IGQAMAIAGQIRSGGGS
	ū	224 TAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGFTAFLGLGVVDNNGNGAR 283
tch 7	132;	224 TA
Query Match	Matches	ζ

²²⁴ TAASDNFQLSQGGGGFAIPIGQAMAIAGQIRSGGGSFTVHIGFTAFLGLGVVDNNGNGAR 283

QQ

²⁸⁴ VORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTR 343

³⁴⁴ TGNVTLAEGPPA 355 ||||||||||| 121 TGNVTLAEGPPA 132 \$ 90 \$ 90

Search completed: June 22, 2004, 17:27:28 Job time: 13.6725 secs

Sequence 14, Appl Sequence 15, Appli Sequence 17, Appli Sequence 18, Appli Sequence 13, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 21, Appli 21, Appl

US-09-886-349A-20 US-10-359-460-26 US-09-886-349A-16 US-10-359-460-2 US-10-359-460-2 US-10-359-459-2 US-10-369-983-21 US-10-369-983-12 US-10-369-983-12 US-10-369-983-12 US-10-369-983-12 US-10-369-983-12 US-10-369-983-12 US-10-369-983-12 US-10-369-983-12

US-10-369-983-14 US-10-369-983-15 US-10-369-983-17 US-09-886-349A-8 US-10-986-732A-8 US-10-986-732A-8 US-10-287-849-26

US-09-759-143-818 US-09-759-143-848 US-09-780-669-819 US-09-822-827-819 US-09-822-827-848 US-09-822-827-848 US-09-895-793-819 US-09-895-818-818 US-09-895-818-818

ALIGNMENTS

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Sequence 80, Appli
Sequence 19, Appli
Sequence 161, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                         June 22, 2004, 17:23:10 ; Search time 32.8799 Seconds (without alignments) 3048.105 Million cell updates/sec
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                                                                                                                                               1 MSNSRRRSLRWSWLLSVLAA......QTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                         Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_PEP:*
| cgn2_6/ptodata/2/pubpaa/US06_NBW_PUB_PEP:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NBW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10NB_PUB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-193-002-80

US-10-098-732A-2

US-09-712-363-161

US-09-712-363-161

US-09-712-363-161

US-09-712-363-161

US-09-712-363-161

US-10-369-983-19

US-10-369-983-20

US-10-369-983-20

US-10-369-983-18
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                      1163542 seqs, 282313646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                       protein search, using sw model
                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                        US-09-886-349A-2
1802
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Match Length DB
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                                                                                                                                    Perfect score:
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                                                       OM protein
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                                                                                                                                                Sequence:
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No.
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US-09-380-3494-4
; Sequence 2, Application US/09886349A
; Publication No. US20040086523A1
; GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
; APPLICANT: Reed, Steven
; APPLICANT: Aderson, Mark
; APPLICANT: Corisa Corporation
; TITLE OF INVENTION: Fusion Froteins of Mycobacterium Tuberculosis
; TIE REFERENCE: 014058-009070US
; CURRENT APPLICATION NUMBER: US/09/886,349A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/597,796
; PRIOR APPLICATION NUMBER: US 60/265,737
; PRIOR PILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIN Ver: 2.1
; SEQ ID NO 2
; LENGTH: 355
; TURNED FOR THE SECOND SECO
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100.0%; Score 1802; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 355; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: MTB32A (Ra35FL)
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Sequence Sequence

Sequence

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Skeiky, Yasir A.W.
Skeiky, Yasir A.W.
Capaca Nation C.
Capaca Nation C.
Houghton, Raymond
Houghton, Raymond
Yedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendricksen, Romald C.
Hendricksen, Romald C.
And Diagnosis OF Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITYERS: Seatche COUNTRY: Seatche CONTRY: Seatche CONTRY: Washington CONTRY: Washington CONTRY: Washington COMPUTER READABLE FORM:
MADIUM TYPE: Ploppy disk COMPUTER: IBW PC compatible OPERATING SYSTEM: PC-DGS/MS-DGS SOFTWARE: Parentln Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: vUnknown>
PRIOR APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAK:, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-10-084-843-79
Sequence 79, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206)
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                                                                                  QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA 240
                                                                                                                        QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA 240
                                                                                                                                                                                                             241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
                           241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
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Best Local Similarity 100.0%; Pred. No. 1.6e-134; Length 355;
Matches 355; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE PORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Thomas S.
Lodes, Michael J.
Ledes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 80, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 80:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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  9
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                                                                                               61 PQVVININTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
                                                                                                                                                                                                                 1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
                                                              61 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
                                                                                                                                                                                YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
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241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
181 QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA 240
                                                                                                                                                                                                                                                     241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 161, Application US/09712363

Petent No. US200201645801

GRUERAL INFORMATION:

APPLICANT: Elsenberg, David

APPLICANT: Rotstein, Sergio H.

APPLICANT: Rotstein, Sergio H.

APPLICANT: Mostin David

TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND

TITLE OF INVENTION: DETERMINING THE FUNCTIONS BY COMPARATIVE ANALYSIS

FILE REFERENCE: 07419-032001

CURRENT APPLICATION NUMBER: DG/09/712,363

CURRENT APPLICATION NUMBER: PCT/US00/02246

PRIOR PILING DATE: 2000-01-13

PRIOR FILING DATE: 1299-01-29

PRIOR PLING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 60/119,531

PRIOR APPLICATION NUMBER: 60/119,264

PRIOR PLING DATE: 1999-01-29

PRIOR PLING DATE: 1999-05-14

PRIOR PLING DATE: 1999-11-12

PRIOR PLING DATE: 1990-11-12

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Pred, No. 9.6e-134;
0; Mismatches 2;
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Best Local Similarity 99.4%;
Matches 353; Conservative
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| Sequence 2, Application No. US20030175294A|
| Publication No. US20030175294A|
| GENERAL INFORMATION: Stair |
| APPLICANT: Stair |
| APPLICANT: Guderian, Jefffrey |
| APPLICANT: Guderian, Jeffrey |
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a |
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a |
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a |
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a |
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a |
| TITLE OF INVENTION UNDER: US/10/098, 732A |
| CURRENT FILING DATE: 2001-03-13 |
| NUMBER OF SEQ ID NOS: 80 |
| SEQ ID NO 2 |
| SEQ ID NO 2 |
| LENGTH: 355 |
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100.0%; Score 1802; DB 14; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 355; Conservative 0; Mismatches 0; Indels 0;
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100.0%; Score 1802; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 355; Conservative 0; Mismatches 0;
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                                                        TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
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US-10-098-732A-2
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US-10-098-732A-2
                                                                                                                         US-10-084-843-79
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                                                                                                                                           GDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                      GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                              JUDICATION OF US/0988349A

Sequence 4, Application US/09886349A

Publication No. US20040086523A1

SEQUENCE INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Alderson, Mark

APPLICANT: Corriva Corporation

ITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

FILE REFERENCE: 014058-009070US

CURRENT APPLICATION NUMBER: US/09/886,349A

CURRENT FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: US 09/597,796

PRIOR FILING DATE: 2001-06-20

PRIOR FILING DATE: 2001-06-10

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 330
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99.4%; Pred. No. 2.9e-121;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: MTB32A (Ra35 mature) US-09-886-349A-4
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Best Local Similarity 99.4
Matches 321; Conservative
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; Sequence 4, Application US/10098732A; Publication No. US20030175294A1
SENERAL INFORMATION: APPLICANT: SMelky, Yasir

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 VVAMGNSGGOGGTPRAVPGRVVALGOTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 VNGLGQVVGMNTAASDNPQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
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                   APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising
FILE REPERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR FILING DATE: 2001-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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| Sequence 19, Application US/10369983
| Sequence 19, Application US/10369983
| Publication No. US20030235593A1
| GENERAL INFORMATION:
| APPLICANT: Skeiky, Yasir
| APPLICANT: Reed, Steven
| APPLICANT: Reed, Steven
| APPLICANT: Corixa Corporation
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE TREFERENCE: 014058-009081US
| CURRENT FILING DATE: 2003-02-18
| PRIOR FILING DATE: 2002-02-15
| NUMBER: OF SEQ ID NOS: 22
| SOFTWARE: Patentin Ver. 2.1
| SEC ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence:Ra35 mature US-10-098-732A-4
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OTHER INFORMATION: Description of Artificial Sequence:wild-type
OTHER INFORMATION: mature MTB32A (Ra35)
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 330
Brannon, Mark
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273 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 332
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                                                                                                                                                                                    248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 6, Application US/10098732A | Sequence 6, Application US/10098732A | Sequence 6, Application No. US20030175294A1 | Sepublication No. US20030175294A1 | Sepublication No. US20030175294A1 | Sepublication No. US20030175294A1 | Sepublication No. USACONTION NO. USACONTIO
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                                                    188 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSFTVHIGFTGL
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               VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
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llarity 99.1%; Pred. No. 4.9e-121;
Conservative 1; Mismatches 2;
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US-10-369-983-20
Sequence 20, Application US/10369983
; Publication No. US20030235593A1
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ORGANISM: Artificial Sequence
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Best Local Simi
Matches 320;
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US-10-098-732A-6
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                                                                                                                                                                       92
                                                                                                                                                                                                                         67
                                                                                                                                                                                                                      8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV
                                                                                                                                                                    33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
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| Publication No. US20040086523A1
| Publication No. US20040086523A1
| GENERAL INPORMATION:
| APPLICANT: Skeiky, Yasir
| APPLICANT: Reed, Steven
| APPLICANT: Reed, Steven
| APPLICANT: Pusion Proteins of Mycobacterium Tuberculosis
| TILLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| FILE REFERENCE: 014058-009070US
| PRIOR APPLICATION NUMBER: US 60/265,737
| PRIOR FILING DATE: 2001-02-01
| NUMBER OF SEQ ID NOS: 50
| SOFTWARE: PatentIN Ver. 2.1
| SEQ ID NO 6
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; OTHER INFORMATION: Description of Artificial Sequence:Ra35FLMutSA
18-09-886-349A-6
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0
                                                    90.7%; Score 1634; DB 15; Length 330; 99.4%; Pred. No. 2.9e-121; ive 0; Mismatches 2; Indels 0;
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Pred. No. 4.9e-121;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 VNWQTKSGGTRTGNVTLAEGPPA 355
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Best Local Similarity 99.1%;
Matches 320; Conservative
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ORGANISM: Artificial Sequence
                                                                                                               Matches 321; Conservative
                                                                                   Similarity
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US-09-886-349A-6
US-10-369-983-19
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                                                                                   Best Local
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          APPLICANT: Skeiky. Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US 10/10/369, 983
CURRENT FILING DATE: 2002-02-18
PRIOR APPLICATION NUMBER: US 60/357,351.
PRIOR APPLICATION NUMBER: US 60/357,351.
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 20
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APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
TUTUE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 723
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OTHER INFORMATION: Description of Artificial Sequence:mutated
OTHER INFORMATION: MTB32AMutSA (Ra35 mutSA)
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ilarity 99.1%; Pred. No. 4.9e-121;
Conservative 1; Mismatches 2;
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Publication No. US20030235593A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 320; Conserv
SENERAL INFORMATION:
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Sequence 4, Application US/10369983

Publication No. US20030235593A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Read, Steven

APPLICANT: Read, Steven

APPLICANT: Corixa Corporation

TILE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis

FILE REPERENCE: 014058-009081US

CURRENT FILING DATE: 2003-02-18

FRICH APPLICATION NUMBER: US/10/369,983

CURRENT FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

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                                                                                                               Length 723;
; OTHER INFORMATION: Description of Artificial Sequence:mutated; CTHER INFORMATION: MTB32-MTB39F fusion protein (MTB32MutSA) US-10-369-983-2
                                                                                                                                                                        Indels
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99.1%; Pred. No. 2e-120;
tive 1; Mismatches 2; Indels
                                                                                                            Query Match 90.5%; Score 1631; DB 15; Best Local Similarity 99.1%; Pred. No. 1.3e-120; Matches 320; Conservative 1; Mismatches 2;
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.1'
Matches 320; Conservative
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US-10-369-983-4
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VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV 187
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                                                                                                              273 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS
                                                                      188 VNGLGQVVGMNTAASDNFQLSQGGGGAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
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APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corporation
TITLE OF INVENTION: Fuelon Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT PAPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
NUMBER OF FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOUTWARE: Patentin Ver. 2.1
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Sequence 16, Application US/1036983
Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
                                                                                                                                                                                                                                                                                   RESULT 14
US-10-369-983-18
Squence 18, Application US/10369983
Publication No. US20030235593A1
GGENERAL INFORMATION:
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ORGANISM: Artificial Seguence
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SPAVYL 769
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US-10-369-983-16
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LENGTH: 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 SGGPVVNGLGQVVGMNTAASDNFQLSQGGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 APAQAAPPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 AFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPI--NSATAMADALNGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Description of Artificial Sequence:fusion protein; OTHER INFORMATION: MTB114F (MTB72F-mTCC#2) US-10-369-983-16
       APPLICANT: Corixa Corporation
TITLE OP INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR PILING DATE: 2003-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SSEQ ID NO 16
LENGTH: 1154
                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                          Length 1154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           804 -----VGWLAATAALAKETATQARAABAFGTAFAMTVPPS 839
                                                                                                                                                                                                                                                                                                                                        55.0%; Score 992; DB 15;
63.8%; Pred. No. 9.2e-70;
ive 17; Mismatches 59;
                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 219; Conservative
Reed, Steven
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Search completed: June 22, 2004, 18:07:51 Job time: 34.8799 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 22, 2004, 16:59:04; Search time 9.93246 Seconds (without alignments) 3438.018 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-886-349A-2 1802 1 MSNSRRRSLRWSWLLSVLAA......QTKSGGTRTGNVTLAEGPPA 355

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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317.5 315.5 315.5 315.5 315.5 315.5 315.5 315.5 317.5 313.5 317.5 311.5 311.5 30.5 30.5 30.5 30.5 30.5 30.5 30.5 30	E85500	E90649	H96956	I40059	AI3349	F87590	AC0909	S75445	AD2451	H86891	AH0410	C87408	AD3418	D69109	140060	B81914
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	30	31	32	8	3.4	35	36	37	38	68	40	41	42	43	4.4	45

## ALIGNMENTS

	RESULT 1	
	F70983 probable	serine proteinase pepA - Mycobacterium tuberculosis (strain H37RV)
	C;Specier C;Date: ]	C;Species: Mycobaccerium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Dec-2002
	C;Access: R;Cole, E; Connor, Rajandres	C;Accession: F70983 R;Cole, S., Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; ; Connor, R.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
	Nature 393, A;Authors: 4 A;Title: Dec A;Reference	Nature 393, 557-544, 1998 A,Authors: Sqares, K.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MUID:98295987; PMID:9634230
	A, Access: A, Status: A, Molecul	A.Accession: F70983 A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Molecule type: DNA
****	A,Residues: 1-3 A,Cross-referen A,Experimental	A,Residues: 1-355 <col/> A,Cross-references: GB:296071, GB:AL123456, NID:g3242254, PIDN:CAB09453.1, PID:g2181967 A,Experimental source: strain H37Rv C.Ganetigs:
	A;Gene: pepA C;Superfamily:	epa mily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp:
	Query Match Best Local Matches 35	Query Match Best Local Similarity 99.4%; Pred. No. 7.5e-98; Matches 353; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	<i>〉</i> 원	1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFAALPLDPSAWVAQVA 60 
	දු පු	61 PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGGTYGVDVVG 120 61 PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGGTYGVDVVG 120
	& a	121 YDRTQDVAVLQLRGAGGLFSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGGTV 180 
	ć g	181 QASDSLIGAEETLNGLIQFDAAIQPGDSGGBVVNGLGQVVGNNTAASDNFQLSQGGQGFA 240 
	Š qa	241 IPIGOAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300 241 IPIGQAMAIAGQIRSGGGSPTVHIGFTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
<del></del>	& £	301 GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355 
	מ	GDVI IAVDGAFINGA IAMBADADAGINIE GDVICA I MENGOCINICANI

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240 AIPIGOAMAIAGOIRSGGGSPTVHIGPTAFLGLGVV-DNNGNGARVORVVGSAPAASLGI 298
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      Pred. No. 1.7e-67;
. Mismatches 58;
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36.0%; Pred. No. 2.1e-20;
tive 59; Mismatches 136;
                                    42;
           70.1%;
           Best Local Similarity 70.19
Matches 251; Conservative
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Matches 127, Conservative
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RESULT 2
847170
hypothetical protein 34K - Mycobacterium paratuberculosis
C;Species: Mycobacterium paratuberculosis
C;Species: Mycobacterium paratuberculosis
C;Species: Mycobacterium paratuberculosis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Dec-2002
C;Accession: 847170
S;Cameron, R.M.; Stevenson, K.; Inglis, N.F.; Klausen, J.; Sharp, J.M.
S;Description: Isolation and characterisation of a 34KDa protein of Mycobacterium paratulated to the EMBL Data Library, June 1993
A;Reference number: 847170
A;Accession: 847170
A;Accession: 847170
A;Accession: DAA
A;Accession: DAA
A;Residues: DAA
A;Residues: 1-361 cCAM
A;Cross-references: EMBL:223092; NID:g505550; PIDN:CAA80638.1; PID:g505551
C;Superfamily: Escherichia coli trypsin-like proteinase degs; GLGF domain homology; tryp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Accession: A87242

R. Cole, S. T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R. Cole, S. T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Vettlerford, K.M.
Nature 409, 1007-1011, 2001

A. Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A. Title: Massive gene decay in the leprosy bacillus.
A; Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable secreted serine proteinase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSNS-RRRSLRWSWLLSVLAAVGLGL-----ATAPAQAAPPALSQDRFADFPALPLDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSKSHHHRSVWWSWLVGVLTVVGLGLGSGVGLAPASAAPSGLALDRFADRPLAPIDPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 QGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 AMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQT
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                                                                                                                                                                                                                                                                                                                                                                                Length 361;
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; Pred. No. 1.9e-69;
41; Mismatches 58;
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70.4%;
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Best Local Similarity 70.4*
Matches 255; Conservative
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A Molecule type: DNA
A Residues: 1-354 <STO>
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A)Cross-references: GB:AL021999, GB:AL123456; NID:g3261538; PIDN:CAA17582.1; PID:e125391(A)Experimental source: strain H37Rv
A)Experimental source: strain H37Rv
A)Gene: Rv0983
C)Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps D.; Gordon, S.; Holroyd, S.; Cybecies: Mycobacterium tuberculosis
Cysecies: Mycobacterium tuberculosis
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Cybecies: Mycobacterium tuberculosis
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Cybecies: Mycobacterium tuberculosis
Cybecesion: C70821
Rycole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Mature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Accession: C70821
A;Accession: C70821
A;Accession: C70821
A;Molecule type: DNA
A;Residues: 1-464 <COL> ъ, 117 117 10; VVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALG 177 118 VVGYDRTQDVAVLQLRGASNLPTAVIGGDVAIGEPIVALGNTGGQGGLPSVLPGRVVALN 177 QTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMVTAASDNFQLSQGGQ 237 GPAIPIGGAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLG 297 GFAIPIGGAMEVVGAIRSGAGSNTVHIGPTAFFGLGVLDNNGNGARVARVVATGPAAMAG 296 239 57 58 75 1 MSRQPHRSLWRSWLVSTLAALGLSLAVVPGSATPSGPSTLALDRFSNRPPLPLNPAAM--1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQA---APPALSQDRFADFPALPLDPSAMVA 19 AAVGLGLATAPPAQAAPPALSQDRFADFPALPLDPSA----MVAQVAPQVVNINTKLGYNNA AVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDS 120 AASLVGFNRAPAGPSGGPVAASAAPSIPAANMPPGSVEQVAAKVVPSVVMLETDLGRQSE 76 VGAGTGIVIDPNGVVLINNHVIAGAT-----DINAFSVGSGQTYGVDVVGYDRTQDV 186 LIGABETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMVTA----ASDNFQLSQG--GQGF 7; Gaps ISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA Length 464; Indels Indels

VVAGGAANNAGV 408 C:Genetics: A;Note: MLCB373.28 C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps: C;Superfamily: Escherichia coli trypsin-like proteinase C;Keywords: hydrolase; serine proteinase VTLGK 461 F;182,224,305/Active site: His, Asp, Ser #status predicted	n, N.; Holroyd, Squares, R.; Sq 100147	12; bb 393 NAAVPKGVVLTKVDDALISSADALWAAVRSKAPGDKVSLTYQDGSGSRTVGVTLGK 449  77  RESULT 7  S74643  123 NAAVPKGVVLTKVDDRLISSADALWAAVRSKAPGDKVSLTYQDGSGSRTVQVTLGK 449  124 S74643  125 Proteinase hhoA (BC 3.4) - Synechocystis sp. (strain PCC 6803)  NAALernate names: protein sll1679  C; Species: Synechocystis sp.  C; Date: 25.Apr-1997 #sequence_revision 25.Apr-1997 #text_change 09-Dec-2002  C; Date: 25.Apr-1997 #sequence_revision 25.Apr-1997 #text_change 09-Dec-2002  C; Accession: S74643  R; Raneko, T; Sato, S; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Mi  R; Raneko, T; Sato, S; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada,  DNA Res. 3, 109-136, 1996  A; Reference number: S74322; MUID:97061201; PMID:8905231  A; Accession: S74643  A; Accession: S74643  A; Residues: 1-394 ckAN>  A; Residues: 1-394 ckAN>	351 379 Dacterium leprae 2002
AIPVDQAKRIADELISTGKASHASLGVQVTNDKDTLGAKIVEVVAGGAANAGV STGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAE 351	RESULT 5  Ha6930  Brobable secreted serine proteinase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: O.Agr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-200 C;Accession: H86930 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Mh R,; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamli eam, M.A.; Rutherford, K.M. Nature 409, 1007-1011, 2001 A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; A;Reference number: As Geger, K.; Simon, S.; Simmonds, M.; Skelton, J.; A;Reference number: As Geger, M. The leprosy bacillus. A;Recidues: preliminary A;Moccasion: H86930 A;Status: preliminary A;Residues: 1-382 <sto> A;Residues: 1-382 <sto> A;Genetics: M. /sto></sto>	Similarity 36.4%; Score 460; DB 2; Length 382; Similarity 36.4%; Pred. No. 5.3e-20; Ocoservative 52; Mismatches 121; Indels 54; Gaps; GLGIATAPAGAAPPALSQDRFADFPALPLDPSAWVAQVAPQVVNINTKLGYNNAVG; GLGIATAPAGAAPPALSQDRFADFPALPLDPSAWVAQVAPQVVNINTKLGYNNAVG; GAGPVTGPAASVPAANMPSGSVBQVAVKVVPSVVMLETDLGRQSEBGGPVTGPAASVPAANMPSGSVBQVAVKVVPSVVMLETDLGRQSE	Oy 295 SLGISTCDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAE  1

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us-09-886-349a-2.rpr

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hirA-like serine protease (with PDZ domain) [imported] - Clostridium acetobutylicum (Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Dec-2002 (Spacession: H9719)

R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Barteriol, 183, 4823-4838, 2001

A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Closi A; Reference number: A96900; MUID:21359325; PMID:21359325

A; Status: preliminary
                                                                                                                                                                                                                            R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                              A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 SQIRQETGMNIPVDKGVVIMQVMPNSPAAIAKLEQGDVLQSLQGQPVENAEQVQSLVGKL 420
                                                                                                                                    C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 SVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQV----APQVVNINTKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 VKSQVPQAFNDPFLQRFFGSQMPPMPNERVQRGTGSGFIVSNDGKIFTNAHVVDGADEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 AFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 V-TLKDGRSFPGRVMGSDPSTDVAVVKIE-AGDLPTVALGDSDHLQVGEWAIAIGNPLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNT--VTTGILSATGR--RSAD--IGVPDKRVEFIQTDAAINPGNSGGPLLNADGQVIGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTAASDNFQLSQGGGAAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTALIQNAQ----GIGFALPINKAQEIAQQLIATG--KVEH----AYLGIQMVTMTPELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- GNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH
                                                                                              serine proteinase (EC 3.4.21.-) htrA - Synechocystis sp. (strain PCC 6803)
N,Alternate names: protein s1r1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 452;
                                                                                                                                                                                                                                                                                                                                                                          Status: nucleic acid sequence not shown; translation not shown; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                              A;Reference number: S74322; MUID:97061201; PMID:8905231 A;Status: molain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.7%; Score 355.5; DB 2;
Best Local Similarity 29.2%; Pred. No. 8.1e-14;
Matches 116; Conservative 65; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AVGDEVEL-----GILRNGQQQNLTVTIGALPSAPP
                                                                                                                                                                                                           Accession: S77538
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DAR, Res. 8, 205-213, 2001.
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine proteinase [imported] - Nostoc sp. (strain PCC 7120)
C,Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG2150
234
                                                                                                                                                              265
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                                                                                                                                                                                   AVGEPVVAMGNSGGQGGTPRAVPGRVVALG--QTVQASDSLTGAEETLNGLIQFDAAIQP
                                                                                                               ----VTLGIISTLGRSAAQAGIPDKRVEFIOTDAAINP
                                                                                                                                                         GDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIG
                                                                                                                                                                                                                                                   ----GARVQRVVGSAPAASLGISTGDVITAVDGAP
                                                                                                                                                                                                                                                                                         -VOMMNITVDQAQQNNRNPNSPFIIPEVDGILVMRVLPGTPAERAGIRRGDVIVAVDGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 RSLR--WSWLLSVLAAVGL---GLATAPAQAAP-----PALSQDRFADFPALPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 QFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 GSPTVHIGPTAFLGLGV------VDNNG-----NGARVQRVVGSAPAASLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 AIG--GGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALG--QTVQASDSLTGAEETLNGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                               183 QVGDWAIAVGNPVGLDNT---
                                                                                                                                                                                                                                                 PTAFLGLGV---VDNNGN--
                                                                                                                                                                                                                                                                                                                                         312 INSATAM 318
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Matches 125; Conserv
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                                                                    148
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RESULT 12
AG0433
procession: AG0433
procession: AG0433
procession: AG0434
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Date: 02-Nov-2001 #sequence_revision N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice,
R;Parkhill, J.; Wren, E.Simmonds, M.; Skelton, J.; Stevens, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, R.M.; Mitchead, S.; Barrell, F.
Nature 413, 523-557, 200
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Stetus: preliminary
A;Residus: 1-457 eXUR>
A;Residus: 1-457 eXUR>
A;Residus: 1-457 eXUR>
A;Residus: 1-457 eXUR>
A;Residus: 1-457 eXUR>
A;Cross-references: GB:AL590842; PIDN:CAC92795.1; PID:g15981488; GSPDB:GN00175
C;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                   216 IGQVVGMNTAASDNFQLSQG---GQGFAIPIGQAMAIAGQIRSGG---GSPTVHIGPTAF 269
                                                                                                                                                                                                                                    LGLGVVDNNGN--GARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHP 327
57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 VSGSQAQQQRLPEEFKFFFGPNAPSGKESSRPFEGLGSGVIINAEKGYILTNNHVINNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 FGLGQT--ATSGIISALGR-----SGLNLEGLENFIQTDASINRGNSGGALVNLDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAI--GGGVAVGEPVVAMGNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 VVGMNTAASDNFQLSQGGQ----GFAIPIGQAMAIA-----GQIRSG-----GGSPTVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 SWLLSVLA-AVGLGLATAP---AQAAPPALSQDRFADFPALPLDPSAMVAQVAPQVVNI-
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Best Local Similarity 31.2%; Pred. No. 4.4e-13;
Matches 122; Conservative 53; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 GHHPGDVISVNWQTKSGGTRTGNVTLAEGPP 354
                                                                                                                                                                                                                                                                                                                                                                                GDVISVNWQTKSGGTRTGNVTLAE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                             GDRIKVIY-TRDGKEHTAEVTLGE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGPGKTIKIG--
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T35287
probable secreted proteinase - Streptomyces coelicolor
C;Species: Sreptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Beccesion: T35287
C;Accession: T35287
R;Seeger, K; Harris, D; Bentley, S;D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Seeger, K; Harris, D; Bentley, S;D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A;Accession: T35287
A;Reference number: 221574
A;Accession: T35287
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T3528
A;Accession: T3528
A;Accession: T352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
       A; Molecule type: DNA
A; Residues: 1-33 < KDB. ABS DIDN: AAKB0387.1; PID: G15025449; GSPDB: GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Generics:
C; Generics:
C; Generics:
C; Generics:
C; Generics:
C; Generics:
C; Guperfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 GEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 GPVVNGLGQVVGMNTAASDNFQLSQGG---GFAIPIGQAMAIAGQIRSGGGSPTVHIGP 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 TAFLGLG--VVD------NNGNGARVORVVGSAPAASLGISTGDVITAVDGAPINSATA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGAT 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGNSGGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 ILMÉGISGEAVDKSTAEQHNIPQGVYIEQIQDFSSÄQKAGMQVGDVÍTKFDGKKVTSTSD 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PAQAAPPALSQDR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDTSRTRLRRLLAPVAVPACV-LLLATGCSDAGAGTDRGSGSAREGDTAQAAAPRAASEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVA---V
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                                                                                                                                                                                                                                                                                                                                                                                                                    ----GYNNAVGAGTGIVIDPNGVVLT
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                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                               Query Match.
19.6%; Score 354; DB 2; Length 433;
Best Local Similarity 32.0%; Pred. No. 9.4e-14;
Matches 101; Conservative 51; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 362;
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19.1%; Score 345; DB 2; Length 362
Best Local Similarity 32.6%; Pred. No. 2.6e-13;
Matches 125; Conservative 49; Mismatches 154; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    50 LDPSAMVAQVAPQVVNINTKL------
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                    A; Molecule type: DNA A; Residues: 1-429 < KUR>
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD1894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 GGIAGRGMGSGFIISKDGYILTNHHVITGASEV-TIKLTDRREFKAKIIGSDEQYDVALL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52
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                                      Species: Xylella fastidiosa
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
periplasmic proteinase XF2241 [imported] - Xylella fastidiosa (strain 9a5c) C,Species: Xylella fastidiosa C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C,Accession: A82581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 AEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQG--GQGFAIPIGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NSRRRSLRWSWLLSV---LAAVGLGLATAPAQAAP--PALSQDRFADFPALPL----DP
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19.0%; Score 341.5; DB 2;
Best Local Similarity 31.6%; Pred. No. 6.1e-13;
Matches 123; Conservative 55; Mismatches 128;
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C,Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAMVAQVAPQVVNINT----KLGYNNAV-
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Grine proteinase [imported] - Nostoc sp. (strain PCC 7120)
C,Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120
C,Date: Nostoc sp. strain PCC 7120
C,Date: Nostoc sp. strain PCC 7120
C,Accession: AB2057
R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. NA, Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A,Reference number: AB1807; MUID:21595285; PMID:11759840
A,Accession: AB2057
A,Status: preliminary
A,Molecule type: DMA
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Tabata, S. 205-213, 2001
A)Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD1894
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                    A)Cross-references: GB:BA00019; PIDN:BAB72659.1; PID:g17130047; GSPDB:GN00179
A)Experimental source: strain PCC 7120
C)Genetics:
A;Genetics:
A;Genetics: alr0702
C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 VDRDKGVLVVRVLPNSPAARAGLRAGDVIQKLNGQAVTDASNVQRAVENAQVGGQLQLEL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 AQ----GLGFAIPIKTAQRISNQLIATGKVQHPYLG-IQMVGLTPQIKQNINSDPNSGLT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 AEFNDPFFRRFFGSQLPQQQERVQRGTGSGPLISADGSILTNAHVVDGADTVRVI-LKDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 LAQKASDLAVSRVDAAPP-LGNNTDPNF-----VTQVVQRVGPAVVRIEASRTVTSRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSFQGKVLGTDNLTDVAVVKIQ-ANNLPTLTVGNSDQLQPGQWAIAIGNPLGLDNT--VT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 LAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAV-
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Best Local Similarity 31.5%; Pred. No. 2e-12;
Matches 92; Conservative 57; Mismatches 115; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.6%; Score 335.5; DB 2; 29.2%; Pred. No. 1.1e-12; ive 59; Mismatches 137;
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137 GLPSAAIGGGVAV--GEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLIGAEETLN 194
                                                                                                                302 DVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGP 353 | : : : | | | | | | | 361 DIIQSINNQSVTTVVEQVQKIVENSQIGQPLQIQIE-RNGQTTQVNVSPAPLP 411
                                                                                                                                                   Search completed: June 22, 2004, 17:24:47 Job time : 10.9325 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 22, 2004, 16:46:13; Search time 5.9081 Seconds (without alignments) 3128.737 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-886-349A-2 1802 1 MSNSRRRSLRWSWLLSVLAA.....QTKSGGTRTGNVTLABGPPA 355

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		bacillus	escherich	escheri	salmonell	lactobaci	escherich	lactoco	brucella me	brucella su	3 bacillus su	haemophilus	rhizobiu	bartonel	arabidopsi	chlamydia t	chlamydia	buchnera ap	rickettsia	chlamydia	bacillus su	arabidops	buchnera ap	homo sapien	rickettsia	mus musculu	haem	рошо	homod	homo sapien	gnw	snw	ar	rhizobium
	Description	 09r9il	P31137	6606Ed	P26982	Q924h7	P09376	Q91a06	Q8yg32	044597	034358	P45129	Q52894	P54925	022609	P18584	Q9p197	P57322	Q92ja1	Q9z6t0	P39668	Q91u10	085291	043464	005942	Q9jiy5	P44947	P83110	Q92743	P83105	Q9d236	Q9r118	Q9sel7	P55377
SUMMAKIES	ID	! Щ		DEGO_ECOFI			DEGP_ECOLI	HTRA_LACLA	DEGP BRUME	DEGP_BRUSU	HTRA_BACSU	HTOA HAEIN	DEGP_RHIME	DEGP_BARHE		DEGP_CHLTR		DEGP_BUCAI	DEGP_RICCN	DEGP_CHLPN	YYXA_BACSU	DEG8_ARATH	DEGP_BUCAP		DEGP_RICPR	- 1			HRA1 HUMAN	1	- 1	RAI	PA	Y4BJ RHISN
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P52320 streptomyce	P04985 bos taurus	O53810 mycobacteri	Q50594 mycobacteri	P00777 streptomyce	Q99372 rattus norv	006794 mycobacteri	P56877 mycobacteri	Q64761 avian adeno	Q52657 rickettsia	P71933 mycobacteri	P13608 bos taurus
PRIC_STRGR	ELS BOVIN	Y747 MYCTU	YI40 MYCTU	PRTB STRGR	ELS RAT	WA22 MYCTU	Y278 MYCTU	FIB1_ADEG1	OMPA_RICCN	YQ34 MYCTU	PGCA_BOVIN
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457	747	801	515	299	864	914	957	710	2021	778	2364
0.6	8.8	8.5	8.4	8.2	8.1	8.0	7.9	7.9	7.8	7.7	7.7
162.5	158.5	153	150.5	147	146.5	145	142.5	141.5	141	139.5	139.5
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us-09-886-349a-2.rsp

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Nature 409:529-533 (2001).
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SEQUENCE FROM N.A.
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                                                                                                                                        Noone D., Howell A., Collery K.M.;

Noone D., Howell A., Collery K.D. bevine K.M.;

NydA and YvtA, HrrA-like serine proteases in Bacillus subtilis,
regage in negative autoregulation and reciprocal cross-regulation of
regage in negative autoression.

RT

YkdA and yvtA gene expression.

I. Bacteriol. 183:654-663(2001).

- - FUNCTION: May be involved in processing, maturation, or secretion
of extracellular enzymes.

- - SUBCELLULAR LOCATION: Membrane-bound (Potential).

- - INDUCTION Induced by heat shock during exponential growth and by
heterologous amylaess at the transition phase of the growth cycle.

Negatively regulates its own expression.

- - MISCELLANBOUS: Inactivation results in compensating overexpression
of htrA, especially during stress conditions.

- - SIMILARITY: Contains 1 PDZ/DHR domain.

- - SIMILARITY: Contains 1 PDZ/DHR domain.

- - CAUDION: Ref. 2 and Ref. 3 sequences differ from that shown due to

- - CAUDION: Ref. 2 and Ref. 3 sequences differ from that shown due to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 RERSLRWSWLLSVLAAV---GLGLATAP-----AQAAPPALSQDRFADFPALPLDPS 53
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Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstain E., Yoshikawa H., Danchin A., "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease; Heat shock; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.5%; Score 350.5; DB 1; Length 458; 27.6%; Pred. No. 8.3e-13;
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CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
77551045A865ASCD CRC64;
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EXTRACELLULAR (POTENTIAL).
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EMBL; 293941; CAB07968.1; ALT FRAME.
EMBL; 293941; CAB07969.1; ALT FRAME.
EMBL; 293120; CAB15290.1; ALT_FRAME.
Subtilist; BG14155; yvtA.
INTERPRO: IPR0019003; Cys_Ser_trypsin.
INTERPRO: IPR001478; PDZ.
INTERPRO: IPR001254; Peptidase_S1.
INTERPRO: IPR001254; Peptidase_S1.
Pfam; PF00595; PDZ; 1.
Pfam; PF00595; trypsin; 1.
                                                                                                                     STRAIN=168;
MEDLINE=20576168; PubMed=11133960;
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SMART; SM00228; PDZ; 1.
                                                                                                      TRANSCRIPTIONAL REGULATION.
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                                                                          Nature 390:249-256(1997)
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92
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Hydrolase; Protease; Se
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458 AA;
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Best Local Similarity
Matches 111; Conserv
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NHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGE 151
                                                                                                                                                                                    212 VVNGLGQVVGMNTAASDNFQLSQGG---QGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTA
                                                                                                                                                                                                                                                                                                                                                      302 LINASGOVIGIN----SLKVSESGVESLGFAIPSNDVEPIVDOLLONGKV-----DRP
                                                                                                                                                                                                                                                                                                                                                                                                                             269 FLGLGVVDNN-------GNGARVQRVVGSAPAASLGISTGDVITAVDGA
                                             152 PVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGP
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MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Appodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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STRAIN=K12 / MG1655;
MEDLINE=97426617; Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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Bass S., Gu Q., Goddard A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PINSATAMADAL-NGHHPGDVISVNWQTKSGGTRTGNVTLAE 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Procease degS precursor (EC 3.4.21.-)
DEGS OR HHOB OR HTRH OR B3235 OR Z4594 OR ECS4108.
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STRAIN-KI2 / W3110;
MEDLINE-S9165273; PUDMed-8576051;
Waller P.R., Sauer R.T.;
"Characterization of degq and degs, Es
"Characterization of Degp protease.";
U Bacteriol. 178:1146-1153(1996).
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EMBL; UIS661; AAC43992.1; -.
EMBL; U32495; AAC44005.1; -.
EMBL; U10897; AAA58036.1; -.
EMBL; AE000402; AAC76266.1; -.
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     MEDLINE=21156231, PubMed=11288796, Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogaswara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Scherichia coli M. Tobe T., Tope T., Shinagawa H.; Shinagawa H.; Complete ganome sequence of enterohemorrhagic Escherichia coli Ol57:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKLLRSVAIGLIVGAILLVAMPSLRSLNPLSTPQFDSTDETPASYNLAVRRAAPAVVNV-
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PRELIMINARY SEQUENCE OF 82-355 FROM N.A.
MEDLINE=88105815; PubMed=3322223;
Vogel R.F., Entian K.-D., Mecke D.;
"Cloning and sequence of the mich structural gene of Escherichia colicoding for malate dehydrogenase.";
Arch. Microbiol. 149:36-42(1987).
                                                                                                                                                                                                                                                                                                                                  Bazan J.F., Fletterick R.J.;
"Structural and catalytic models of trypsin-like viral proteases.";
Semin. Virol. 1.311-322(1990)
-!- SUBCELLULAR LOCATION: Periplasmic (Potential).
-!- SIMILARITY: Belongs to peptidase family $2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
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V -> E (IN REF. 6).
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PROTEASE DEGS.
PDZ.
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EMBL; AE000551; AAC86333.1; -
EMBL; AP002564; BAB37531.1; -
EMBL; AP02564; BAB37531.1; -
EMBL; AP02564; BAB37531.1; -
EMBL; AP0257; -
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Hydrolase; Serine protease;
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                                                                                                                                                                                                                           DVVGYDRIQDVAVLQLRGAGGLPSAAIGGGVA--VGEPVVAMGNSGGQGGTPRAVPGRVV 174
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STRAIN=K12 / M346551,
M346517, PubMed=9278503;
MBLINE=97426617, PubMed G. III, Bloch C.A., Perna N.T., Burland V.,
MRILEY M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor U., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
The complete genome sequence of Escherichia coli K-12.";
The complete genome sequence of Escherichia coli K-12.";
Cience 277:1453-14741997).
CI- FUNCTION: PROTEASE WITH A SHARED SPECIFICITY WITH DEGP/DEGP.
CI- SUBCELLUAR LOCATION: Periplasmic.
CI- SINILARITY: Belongs to operidase family S2C.
CI- SINILARITY: Contains 2 PDZ/DHR domains.
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Enterobacteriaceae, Escherichia.
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Bass S., Gu Q., Goddard A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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STRAIN=K12 / W3110;
MEDLINE=96165272; PubMed=8576051;
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DEGO OR HHOA OR B3234.
Escherichia coli.
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91 LINNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVA-- 148
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                                                                                   Mol. Microbiol. 5:401-407(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                               18.1%; Score 326; DB 1; Length 455;
30.4%; Pred. No. 1.9e-11;
iive 61; Mismatches 117; Indels 94; Gaps
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Enterobacteriaceae; Salmonella.
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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DEGP OR HTRA OR PTD OR STM0209.
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PDZ 1.
PDZ 2.
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PIR; JC6051; JC6051.
MEROPS; S01.274; -
SWISS-2DPAGE; P3909; COLI.
ECGGene; EG12612; degQ.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
PEAM; PP00089; trypsin; 1.
PRINTS; PR00894; PROTEASES2C.
SWART; SW00228; PDZ; 2.
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455 AA;
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Matches 119; Conserv
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SIGNAL 1
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P26982;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SERAILELZ / GSGS1412 / ATCC 700720;
MEDLINE=2134948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Danhee M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
Complete genome sequence of Salmonella enterica serovar Typhimurium ITZ.";
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Hydrolase; Serine protease; Heat shock; Periplasmic; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: SERINE PROTEASE THAT IS REQUIRED AT HIGH TEMPERATURE. INVOLVED IN THE DEGRADATION OF DAMAGED PROTEINS. SHARED SPECIFICITY WITH HHOA/DEGQ.
MEDLINE=91251770; PubMed=1645840; Johnson K., Charles I., Dougan G., Pickard D., O'Gaora P., Costa Johnson K., Miller I., Hormaeche C.; Miller I., Hormaeche C.; Miller I., Hormaeche C.; Miller I., Hormaeche C.; Miller I., Hormaeche C.; Miller I., Hormaeche C.; Miller I., Hormaeche C.; Miller I., Hormaeche C.; Miller I., Hormaeche C.; Miller I., Miller I., Hormaeche C.; Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Miller I., Mi
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llarity 29.1%; Pred. No. 3.2e-11;
Conservative 55; Mismatches 126; Indels 106;
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86E685BF3C1A289F CRC64;
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-i- SIMILARITY: Belongs to peptidase family S2C.
-i- SIMILARITY: Contains 2 PDZ/DHR domains.
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                                                                       236
                                                                                                     259
                                                                                                                        237 SGGALVNLNGELIGINTAILAPDGGNI---GIGFAIPSNMVKNLTSQMVEYGQVKRG--- 290
                                                                                                                                                             PTVHIGPTAFLGLGVVDNNGN------GARVQRVVGSAPAASLGISTGDVITA 306
                                                                                                                                                                                           291 -----ELGIMGTELNSELAKAMKVDAQRGAFVSQVMPNSSAAKAGIKAGDVITS 339
207
                                                               VGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAE-ETLNGLIQFDAAIQPGD
                                                                                                     SGGPVVNGLGQVVGMNTA--ASDNFQLSQGGQGFAIP-----IGQAMAIAGQIRSGGGS
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CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
BIEB677991C88707 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smeds A., Varmanen P.K., Palva A.M.; "Molecular characterization of a stress-inducible gene from
                                                                                                                                                                                                                       307 VDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                             Lactobacillus helveticus.";
J. Bacteriol. 180:6143-6153(1998).
-!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-!- SIMILARITY: Belongs to peptidase family $2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-TDE-2003 (Rel. 41, Last annotation update)
Serine protease do-like htrA (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                            413 AA
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INTERPRO) IPRO09003; CYS_Ser_trypsin.
INTERPRO; IPRO01254; Peptidase_S1.
INTERPRO; IPRO01940; Peptidase_S1.
INTERPRO; IPRO01940; Peptidase_S1C.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
SMART; SW00228; PBDZ; 1.
PROSITE; PS50106; PBZ; 1.
Hydrolase; Serine protease; Transmembra
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413 AA;
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                                                                                                   124 TODVAVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQ
                                                                                                                                                                                                                                                 238 TS---SGNQT----VIQTDAAINPGNSGGALVNSAGQVIGINSMKLAQSSDGT$VEGMAF
                                                                           67 NIKLGYNNAVGAGTGIVI---DPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDR
                                                                                                                                                                                      TIDLAVLSIDAKYVTQTAQFGDSKHLEAGQTVIAVGSPLGSEYASTVTQGIISAPARTIS
                                                                                                                                                                                                                                                                                                   AIPIGQAMAIAGQIRSGG--GSPTVHIGPTAFLG------LGVVDNNGNGARVQRVVG
                                                                                                                                                                                                                            182 ASDSLIGAEETINGLIQFDAAIQPGDSGGPVVNGLGQVVGMNI--AASDNFQLSQGGQGF
                                         Gaps
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SEGUENCE FROM N.A.

STRAIN-RIA / WAILD.

MEDLINE-812 / WAID.

Fujita N., Mori H., Yura T., Ishihama A.;

Fujita N., Mori H., Yura T., Ishihama A.;

Fujita N., Mori H., Yura T., Ishihama A.;

Fujita N., Mori H., Yura T., Ishihama A.;

Fujita N., Mori H., Yura T., Ishihama A.;

Fujita N., Mori H., Yura T., Ishihama A.;

Nayerematic sequencing of the Escherichia coli genome: analysis of the 24-41 min (110, 917-193, 643 bp) region.";

Nucleic Acids Res. 22:1637-1639(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.
Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                       24;
Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                                                                                                                                                        352 NGSAANAGIKSGDVITKVDGKKVEDVASLHSILYSHKVGDTVNV 395
 ; Score 321; DB 1; Length 41; Pred. No. 3.2e-11; 50; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                              290 SAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISV 333
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heat-inducible
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Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P09376; P15724; Created)
01-MAK-1999 (Rel. 10, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protease do precursor (EC 3.4.21.-)
PEGP OR HTRA OR PTD OR B0161 OR Z0173 OR ECS0165.
Escherichia coli, and
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BIDLINE=89057448; PubMed=3057437;

Libinska B., Sharma S., Georgopoulos C.;

"Sequence analysis and regulation of the headolis a signa 32-independent mechanism of transcription.";

Nucleic Acids Res. 16:10053-10067(1988).
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     17.8%;
31.3%;
                                       89; Conservative
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     Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hangashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T., Han C.G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Yasunaga T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genome sequence of enterohemorrhagic Escherichia coli "--"" and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli survival at
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-: FUNCTION: SERINE PROTEASE THAT IS REQUIRED AT HIGH TEMPERATURE.
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"Genome sequence of enterhament T.S., Lin J., Yen G., Schwartz D.C.,

"Genome sequence of enterhament T.S., Apodaca State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State 
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Wurgler S.M., Richardson C.C.;
"Structure and regulation of the gene for dGTP triphosphohydrolase
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MEDLINE=91222240; PubMed=2025286;
Seol J.H., Woo S.K., Jung B.M., Yoo S.J., Lee C.S., Kim K.J.,
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"Protease Do is essential for survival of Escherichia coli at high
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K12 / W3110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from Escherichia coli.";
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"The HtrA (DegP) protein, essential for Es
high temperatures, is an endopeptidase.";
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                      FROM N.A.
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A -> G (IN REF. 1).

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STIXILIMQ -> RHLPVNAVISLNPFLKTGRGSPYNL (IN
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29.8%; Pred. No. 5.7e-11;
ive 51; Mismatches 108; Indels 105; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Heat shock; Periplasmic; Repeat; Signal;
INVOLVED IN THE DEGRADATION OF DAMAGED PROTEINS. IT CAN DEGRADE ICLA, ADA, CASEIN AND GLOBIN. SHARED SPECIFICITY WITH DEGO.
-!- SUBGELLINET: MAILTHEATIC.
-!- SUBCELLINEAR LOCATION: Periplasmic.
-!- INDUCTION: By heat shock.
-!- INDUCTION: By heat shock.
-!- MISCELLANEOUS: HTRA IS INDISPENSABLE FOR BACTERIAL SURVIVAL AT TEMPERATURES ABOVE 42 DEGREES CELSIUS.
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 2 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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InterPro; IRRO19184; Peptidase_S1.
InterPro; IRRO1949; Peptidase_S1.
InterPro; IRRO1949; Peptidase_S1.
Pfam; PF00595; PDZ; 2.
Pfam; PF00893; trypsin; 1.
PRINTS; PR00814; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X12457, CAA30997.1, EMBL, D26562; BAB96738.1, EMBL, AE00125, AAC73272.1, EMBL, U70214, AAB08591.1, EMBL, AE005192, AAG54465.1, EMBL, M29955, AAA23488.1, EMBL, M31772, AAA23680.1, -
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EcoGene; EG10463; degP.
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Matches 112; Conserv
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                                                                                                                                                                                                                                                                                      204 QPGDSGGPVVNGLGQVVGMVTA--ASDNFQLSQGGQGFAIP-----IGQAMAIAGQIRS
                                                                      GGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAE-ETLNGLIQFDAAI
                                                                                                      GGGSPTVHIGPTAFLGLGVVDNNGN-------GARVQRVVGSAPAASLGISTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBL_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=2017880; PubMed=10712686; Poquet I., Saint V., Seznec E., Simoes N., Bolotin A., Gruss A.; Poquet I., saint V., Seznec E., Simoes N., Bolotin A., Gruss A.; Hirzh is the unique surface housekeeping procease in Lactococcus lactis and is required for natural protein processing."; Mol. Microbiol. 35:1042-1051(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Membrane-bound (Probable). SIMILARITY: Belongs to peptidase family S2C. SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease do-like htrA (EC 3.4.21.-) (HtrAL1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Pel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408 AA
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InterPro; IPR001478; PDZ.
InterPro; IPR001054; Peptidase Sl.
InterPro; IPR001940; Peptidase_SlC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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16-OCT-2001
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HTRA LACLA
ID HTRA LAC
AC Q9LAO6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 NA-IQTDAAINPGNSGGALINIEGQVIGITQSKITTTEDGSTSVEGLGFAIPSNDVVNII 284
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                                                                                                                                                                                                                                                                                                                                               79 GTGIVIDPNG---VVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRG-
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SEQUENCE FROM N.A.

MEDIATE 20020109; PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los DelVecchio V.G., Kapatral V., Redkar R.J., Lykilds A., Reznik G., Jaranova N., Anderson I., Bhattacharya A., Lykilds A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

Brucella melitensis.";
                                                                                                                                                                                                                                                                                                            34;
                                                                                                Transmembrane; Complete proteome
                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                       Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGP_BRUME STANDARD; PRT; 513 AA.
DEGP_BRUME STANDARD; PRT; 513 AA.
15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2004 (Rel. 43, Last annotation update)
DEGP OR HTRA, OR BMEI1330.
                                                                                                                                                                                                                                                                                                            51; Mismatches 119; Indels
                                                                                                                                                    PDZ.
CHARGE RELAY SYSTEM (POTEN
CHARGE RELAY SYSTEM (POTEN
CHARGE RELAY SYSTEM (POTEN)
581B90B55A7DF851 CRC64;
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- SUBCELLULAR LOCATION: Periplamaic (Potential).
- SUBLERITY: Belongs to peptidase family S2C.
- SIMILARITY: Contains 2 PDZ/DHR domains.
                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                       Score 310;
                                                                                                             POTENTIAL.
CATALYTIC.
                                                                                                                                                                                                                                                                                          Pred. No.
Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00814; PROTEASES2C.
SMART; SM00221; PDZ; 1.
PROSITE; PSS0106; PDZ; 1.
Hydrolase; Serine protease; Tra
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                                                                                                                                                                                                                                                                                                              93; Conservative
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302
127
157
239
408 AA;
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    Brucella abortus.
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 SV--GSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPS----AAIG--GGVAVGEPVVAMG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 TAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHH 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 EVIGINTAI --- FSPSGGSVGIAFAIPSSTAKQVVDQLIKKGSVERGWIGVQIQPVTKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Mismatches 142; Indels 136; Gaps
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CATALYTIC.
PDZ 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CA72FEF99DFC6288 CRC64;
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30-MAY_2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Drobable serine protease do-like precursor (EC 3.4.21.-).
Brucella suis, and
                                                                                                                                                                                                                                                            PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Periplasmic; Repeat; Signal;
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                     send an email to license@isb-sib.ch)
                                                                             PIR; AD3418, AD3418.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001478; PDZ.
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InterPro; IPR001940; Peptidase SIC
                                                           EMBL; AE009571; AAL52511.1; -.
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SMART; SM00228; PDZ; 2.
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Pfam; PF00089; trypsin; 1.
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182
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as lits content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                             SEQUENCE FROM N.A.

SECURES abortub. STRAIN=2308;

MEDIANE=93165990; PubMed=7861951;

Tatum F.M., Cheville N.F., Morfitt D.;

Tatum F.M., characterization and construction of htrA and htrA-like mutants of Brucella abortus and their survival in BALB/c mice.";

Microb. Pathog. 17:23-36(1994).
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CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29461, 235;
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Hydrolase; Serine protease; Periplasmic; Repeat; Signal;
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PROBABLE SERINE
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Interpro; IPR001478; PDZ.
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InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 2.
PRIMTS; PR0089; trypsin; 1.
PRIMTS; PR00894; PROTEASES2C.
SWART; SM00228; PDZ; 2.
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Xunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Xunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Xunst F., Ogasawara N., Moszer I., Albertini A.M., Borchert S.,
Xa Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Xa Azevedo V., Beruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Xa Groi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Xa Erriz C., Fujita M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Xa Entian K.D., Errington U., Fabret C., Ferrari E., Foulger D.,
Xa Ghim S.Y., Glaser P., Goffeau A., Golighily E.J., Grandi G.,
Xa Ghiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Xi Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Xa Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Xa Kurita K., Levine A., Lardinois S., Lauber J., Lazarevic V.,
Xa Kobayashi Y., Koetter P., Koningstein G., Madigue C.,
Xa Kobayashi Y., Koetter P., Mizuno M., Moselt D., Nakai S., Noback M.,
Xa Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Madigue C.,
Xa Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Xa Rieger M., Rivolta C., Rocha B., Rapoport G., Rey M., Reynolds S.,
Xa Rieger M., Rivolta C., Rocha B., Rapoport G., Schie F.,
Xa Sordyun A., Tacconi E., Roche B., Roche B., Sorffone F.,
Xa Sordyun A., Tarakoshi A., Tanaka H., Takanath H., Takanatu K.,
Xa Takeuchi M., Tamakoshi A., Tanaka T., Takanath H., Takanatu K.,
Xa Takeuchi M., Tamakoshi A., Tanaka F., Vannaler F., Vannaretti A.,
Xa Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
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------GYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAF 106
                                                                                                                                                                                 107 SV--GSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPS----AAIG--GGVAVGEPVVAMG
                                                                                                                                                          158 NSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLG
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28-FEB-2003 (Rel. 42, Last sequence update)
10-071-2003 (Rel. 42, Last sequence update)
Probable sezine protease do-like htrA (EC 3.4.21.-).
HTRA OR BSU12900.
Bacillus subschils.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
111 TAXID=1423;
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MEDLINE=98044033; PubMed=9384377;
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Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zunstein B., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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MEDLINE=20158875; PubMed=10692364;
Noone D., Howell A., Devine K.M.;
"Expression of ykdA, encoding a Bacillus subtilis homologue of HtrA, is heat shock inducible and negatively autoregulated.";
J. Bacteriol. 182:1592-1599(2000). MEDLINE=20576168; PubMed=11133960; MEDLINE=20576168; PubMed=11133960; Noone D., Howell A., Collery R., Devine K.M.; Noone D., HurA-like serine proteases in Bacillus subtilis, engage in negative autoregulation and reciprocal cross-regulation ykdA and yvtA gene expression.; J. Bacteriol. 183:654-663(2001). protease; Heat shock; Transmembrane; POTENTIAL. EXTRACELLULAR (POTENTIAL) POLY-SER. CYTOPLASMIC (POTENTIAL) PERS, A66643, A69643.
MEROPS, S01.273;
MEROPS, S01.273;
MEROPS, S01.273;
MILLIAET, BG12608; htrA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1.
Pfam; PP00595; PDZ. 1.
Pfam; PR00595; PDZ; 1.
PFAM; SWART; SW00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1. EMBL; AJ002571; CAA05570.1; -. EMBL; Z99110; CAB13147.1; -. Hydrolase; Protease; Serine Complete proteome. TRANSCRIPTIONAL REGULATION. TRANSCRIPTIONAL REGULATION. TRANSCRIPTIONAL REGULATION. Nature 390:249-256(1997). 44 67 449 108 45 68 103 STRAIN=168 FRANSMEM 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                              PROSITE: PSSO106; PD2; 2.
Hydrolase; Serine protease; Periplasmic; Repeat; Signal;
Complete proteome.
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 9.9e-10; 54; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.4%; Score 295; DB 1; 28.1%; Pred. No. 9.9e-10;
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InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                          Pfam; PF00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                               EMBL; U32805; AAC22906.1; -. PIR; A64113; A64113.
MEROPS; S01.274; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150
226
26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        30
                                                                                                                                                                                      FIGR; HI1259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Simines 108;
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Q52894;
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ACT_SITE
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ACT_SITE
SEQUENCE
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DEGP_RHIME
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                                                                                                                                                                                                                                  SDMVEDLSPAIVGITNLQAQSNSSLFGSSSSDSSEDTESGSGSGVIFKKENGKAYIITNN 178
                                                                                                                                                                                                                                                                                                                                                  212
                                                                                                                                                                                                                                                                        HVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG--GGVAVGEP 152
                                                                                                                                                                                                                                                                                                                                                                                    294
                                                                                                                                                                                                                                                                                                                                                                                                                        270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 DLEQVPQNYQEGTLGLFGSQLNKGVYIREVASGSPAEKAĞLKAEDIIIGLKGKEIDTIGSE 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 GLGVVDNN-------GNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATA 317
                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                          VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGABETLNGLIQFDAAIQPGDSGGPV
                                                                                                                                                                                                   SAMVAQVAPQVVNINTKLGYNNA--------VGAGTGIVI-DPNG--VVLTNN
                                                                                                                                                                                                                                                                                                        179 HVVEGASSLKV-SLYDGTEVTAKLVGSDSLTDLAVLQISDDHVTKVANFGDSSDLRTGET
                                                                                                                                                                                                                                                                                                                                                                              238 VIAIGDPLGKDLSRTVTQGIVSGVDRTVSMS---TSAGETSINVÍQTDAAINÞGNSGGPL
                                                                                                                                                                                                                                                                                                                                                                                                                  213 VNGLGQVVGMNT--AASDNFQLSQGGQFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95350630; PubMed=7542800; Playton R.A., Kirkness B.F., Plaischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., McKenlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom B. Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -: SUBCELLULAR LOCATION: Periplasmic (Potential).
-: SIMILARITY: SEBNS TO BE A INTERMEDIATE FORMS BETWEEN E.COLI HTRA (PROTEASE DO) AND HHOA.
-: SIMILARITY: Belongs to peptidase family S2C.
-: SIMILARITY: Contains 2 PDZ/DHR domains.
                                                                                                                                                                     45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                 DB 1; Length 449;
                                      CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
E12B07A9018EE414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable periplasmic serine protease do/hhoA-like precursor
                                                                                                                             16.4%; Score 295.5; DB 1; Length 29.3%; Pred. No. 8.9e-10; tive 53; Mismatches 126; Indels
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     POLY-SER.
PDZ.
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                                                                                         47713 MW;
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                                                                                                                                                                 Conservative
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     152
437
179
209
290
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                                                                                           449 AA;
                                                                                                                                                Similarity
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                                                                                                                                                             93;
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P45129;
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DOMAIN
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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 HIGPTAFLGLGVVDNNGN------GARVQRVVGSAPAASLGISTGDVITAVDGAP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LLGIKGGELNADLAKAFNVSAQQGAFVSEVLPKSAAEKAGLKAGDIITAMNGQK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 VLAAVGLGLATAP-----AQAAPPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VLNSIALGLSVLSTSFVAHVAQATLPSFVSEQNSLAP------MLEKVQPAVVTLSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- LGYNNAVGAGTGIVIDPN-GVVLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 PVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEE-TLNGLIQFDAAIQPGDSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 NHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSA--AIGGGVAVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 FTVAIGNPFGLGQT--VTSGIVSALGRS-----TGSDSGTYENYIQTDAAVNRGNSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 ALVNINGELIGINTAI---ISPSGGNAGIAFAIPSNQASNLVQQILEFGQVRRG-----
POTENTIAL.
PROBABLE PERIPLASMIC SERINE PROTEASE
DO/HHOA-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                              98;
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PSFANVDAVSPAVORRENVEDDESNFTFDFGGRGF

EDLEDPELREFFAFENDRADFWRDRRGFRGEGRLR

RAQGSGFFITEDGYLVTNNHVYSDGSA -> AVSPWWSTPF

RRRSSPSACHYNASATWKATSPSISAAGSRICKKTIRCG

VSSANSLRVWATVPIVGATAAVRAVVVSVRGRKAPASSSP

KTVTSSPTTTSSPTRAT (IN REF. 1)

KSADDVLKVINNAKKDGRSKALFQIEQGSRFVALPICG STRAIN=1021;
MEDIINE=96146524; PubMed=8550509;
Glazebrook J., Ichige A., Walker G.C.;
Genetic analysis of Rhizobium meliloti back-phoA fusion results in identification of degP: two loci required for symbiosis are closely linked to degP."; MEDLINE=21396507; PubMed=11481430;
MEDLINE=21396507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Capela D., Barloy-Hubler F., Gouzy J., Edelu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.",
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
-: SUMCELLULAR LOCATION: Periplasmic (Potential).
-: SIMILARITY: Belongs to peptidase family \$2C.
-: SIMILARITY: Contains 2 PDZ/DHR domains. POTENTIAL. PROBABLE SERINE PROTEASE DO-LIKE. PDZ 2. CHARGE RELAY SYSTEM (POTENTIAL). CHARGE RELAY SYSTEM (POTENTIAL). CHARGE RELAY SYSTEM (POTENTIAL) LL -> PV (IN REF. 1). DEGPI OR DEGP OR RO1021 OR SMC02365.
Milazobium melliloti (Sinorhizobium melliloti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium. NRQTIFSR (IN REF. 1). D7E82BB9981EA23C CRC64; FESR (IN REF. InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 2.
Pfam; PF00893; Irrypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2. CATALYTIC. EMBL, U31512, AA43669.1, ALT_INIT. EMBL, AL591785, CAC45593.1, -. MEROPS, SO1.273, -. J. Bacteriol. 178:745-752(1996). 504 AA; 53035 MW; 26 286 286 286 286 1140 1270 1440 1447 1151 504 Complete proteome FROM N.A. SEQUENCE FROM N.A. 464 NCBI_TaxID=382; STRAIN=1021; ACT SITE ACT SITE ACT SITE CONFLICT SEQUENCE CONFLICT SEQUENCE DOMAIN SIGNAL DOMAIN SON THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS TO THE TENERS T

79 GTGIVIDPNGVVLTNNHVIAGATDINAFSV--GSGQTYGVDVVGYDRTQDVAVLQL--RG 134

Gaps

38;

117; Indels

39; Mismatches

Conservative

97;

Matches

135 AGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLN

à g ò 셤 ò 셤 ò

195 GLIQFDAAIQPGDSGGPVVNGLGQVVGNNTAASDNFQLSQGGQG--FAIPIGQAMAIAGQ  IRSGG----GSPTVHIGPTA----FLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDV 288 LIKDGTVSRGWLGVQIQPVTKDIAESLGL----SEANGALVVEPQAGSPGEKAGIKNGDV

253

304 ITAVDGAPINSATAMADALNGHHPGDVISVN-WQTKSGGTRTGNVTLAEGP 353 

181 KFTYVSFÅDDEKVRVGDWVVAVGNPFGLGGTVTÅ--GIISÅRGRDIGSG------PYD

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InterPro; 198001478; PDZ_
InterPro; 198001478; PDZ_
InterPro; 198001954; Peptidase_S1.
InterPro; 198001954; Peptidase_S1.
Pfam; PR00059; PDZ; 2.
PRINTS; PR00089; trypsin; 1.
PRINTS; PR000814; PROTEASES2C.
PROSTTE; PS50106; PDZ; 2.
PROSTTE; PS50106; PDZ; 2.
PROSTTE; PS50106; PDZ; 2.
PROSTTE; PS50106; PDZ; 2.
PROSTANIAL.
19 PROBABLE PERIPLASMIC SERINE PROTEASE DOCHAIN
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATC 49882 / Houston 1;
MEDLINE=94299828; PubMed=8027347;
MEDLINE=94299828; PubMed=8027347;
Maderson B., Sims K., Regnery R., Robinson L., Schmidt M.J.,
Goral S., Hager C., Edwards K.;
"Detection of Rochalimaea henselae DNA in specimens from cat scratch
disease patients by PCR.";
J. Clin. Microbiol. 32:942-948(1994).
--- SUBCELLULAR LOCATION: Periplasmic (Potential).
--- SIMILARITY: Belongs to peptidase family S2C.
--- SIMILARITY: Contains 2 PDZ/DHR domains.
               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probble periplasmic serine protease DO-like precursor (EC 3.4.21.-)
CAntigen htrA)
                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bartonellaceae; Bartonella.
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STANDARD;
BARHE
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Score 291; DB 1; Length 504; Pred. No. 1.8e-09;

16.1%;

Query Match Best Local Similarity

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DEGINARY STANDARD; FRI; 437 AA.

16-0CT-2001 (Rel. 40, Last sequence update)

16-0CT-2001 (Rel. 41, Last agreence update)

Procease Do-like 1, chloroplast precursor (EC 3.4.21.-).

BEGPI OR DEGP OR AT3027925 OR KINNIZ.18

ARABAIGORSIS thallana (Mouse-ear cress).

BURATYOLA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; NCBI_TAXID=3702;

NCBI_TAXID=3702;
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MEDLINE=98175982; PubMed=9507020;
Itzhaki H., Naveh L., Lindahl M., Cook M., Adam Z.;
"Identification and characterization of DegP, a serine protease associated with the luminal side of the thylakoid membrane.";
J. Biol. Chem. 273:7094-7098(1998).
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-!- ENZYME REGULATION: Inhibited by phenylmethylsulfonyl fluoride and
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Kieselbach T., Bystedt M., Schroeder W.P., Submitted (JUL-2000) to Swiss-Prot.
-!- FUNCTION: Serine protease that is required at high temperature.
May be involved in the degradation of damaged proteins. In vivo,
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LL -> V (IN REF. 2).
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                                                                                                                                                                                                                            -!- INDUCTION: By heat shock.
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
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PROTEASE DO-LIKE 1.
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InterPro; IPR001403; BpZ.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001294; Peptidase_S1C.
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EMBL; AP000371; BAB02539.1; -.
EMBL; AP001302; BAB02539.1; JOINED.
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PROSITE; PS50106; PDZ; 1.
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GVSADLLVGQKVFAIGNPFGLDHT--LTTGVISGLRREI--SSAATG--RPIQDVIQTDA 273
                                                          AIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPT 261
                                                                                                              ----- 324
                                                                                                                                                                VHIGPTAFLGLGV------VDNNG-NGARVQRVVGSAPAASLGIST-----GD 302
                                                                                                                                                                                                                    325 VRFGKVTRPILGIKFAPDQSVEQLGVSGVLLLDAPPSGPAGKAGLQSTKRDGYGRLILGD 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis.";
Science 282:754-759(1998).
Science 282:754-759(1998).
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 2 PDZ/DHR domains.
-!- CAUTION: REF.1 SEQUENCE WAS INCORRECT: DUE TO SEQUENCING ERRORS THE AUTHORS TRANSLATED THEIR PUTATIVE 59 kba IMMUNOGENIC PROTEIN ON THE COMPLEMENTARY STRAND TO THAT OF WHAT SEEMS TO BE THE REAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-Serovar L2;
MEDLINE=90337348; PubMed=2379836;
KABARDE S., Weinstein Y., Sarov I.;
"Cloning, characterization and sequence of a novel 59-kDa protein of Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P18554, 084830, 0.0. Crated)
01-NOV-1990 (Rel. 16, Crated)
30-NAY-2000 (Rel. 14) Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-) (59 kDa immunogenic protein) (SK59).
                                                                                             274 AINPGNSGGPLLDSSGTLIGINTAIXSPSGAS-SGVGFSIPVDTVGGIVDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                           VITAVDGAPINSATAMADALNGHHPGDVISV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497 AA
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PHOL-2DPAGE, P18864,
INCEPPO, IPRO09031 CYS Ser_trypsin.
INCEPPO, IPRO19178, PDZ.
INCEPPO, IRRO19254, Peptidase 31.
INCEPPO, IRRO19254, Peptidase 51.
INCEPPO, IPRO19340, Peptidase 51E.
INCEPPO, IPRO0995, POZ, 2.
Fam, PF00599, PDZ, 2.
PEam, PF00599, LYPSin, 1.
PRINTS, PR00894, PROTEASESC.
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                                                                                                                                                                                                                                                                                                                                                                                                                         193 LNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQG--GQGFAIPIGQAMAIA 250
                                                                                                                                                                                                                                                                                                             251 GOIRSGGGSPTVHIGPTAFLGLGVVDN------NGNGARVQRVVGSAPAASLGISTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 DOLISDGOVTRGFLGVT----LOPIDSELATCYKLEKVYGALVTDVVKGSPAEKAGLROE
                                                                                                                                                                                                                                                                                           GTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGL
                                                                                                                                                                                                                                                            44; Gaps
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                                                             POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
CATALYTIC.
                                                                                                                                         CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
                                                                                                                                                                                                                          Length 497;
                                                                                                                                                                                                                        ; Score 288; DB 1; Length 49:
; Pred. No. 2.6e-09;
46; Mismatches 109; Indels
                                                                                                                                                                                             86A5E31BB84A38BA CRC64;
                                Repeat; Signal; Antigen;
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32.3%;
SMART, SM00228, PDZ, 2.
PROSITE, PS50106, PDZ, 2.
Hydrolase, Serine protease;
                                                                                                                                                                                                                                             1 Similarity 32.3 95; Conservative
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497 AA;
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June 22, 2004, 16:55:54; Search time 29.0268 Seconds (without alignments) 3858.816 Million cell updates/sec
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1802
1 MSNSRRRSLRWSWLLSVLAA......QTKSGGTRTGNVTLAEGPPA 355
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	007175 mycobacteri	Q7u2s9 mycobacteri	Q50320 mycobacteri	Q9ccy9 mycobacteri	Q8vka4 mycobacteri	Q7u0x2 mycobacteri	O53896 mycobacteri	Q9cd67 mycobacteri	Q9z5g6 mycobacteri	Q9fbk9 streptomyce	Q93j30 streptomyce	Q8dg87 synechococc	P72780 synechocyst	Q82fm9 streptomyce	Q82il8 streptomyce	Q8fr17 corynebacte
SUMMARIES	ΙD	007175	Q7U2S9	Q50320	Q9CCY9	Q8VKA4	Q7U0X2	053896	Q9CD67	Q9Z5G6	Q9FBK9	093J30	Q8DG87	P72780	Q82FM9	Q82IL8	Q8FR17
		16	16	7	16	16	16	16	16	~	16	16	16	16	16	16	16
	% Query Match Length DB	355	355	361	354	446	464	464	382	452	542	519	375	394	472	619	473
	% Query Match	99.4	99.4	72.5	70.6	26.1	26.1	26.0	25.5	25.5	22.6	22.0	21.7	21.2	21.2	21.2	21.1
	Score	1792	1792	1306	1272.5	469.5	469.5	468.5	460	460	407	396	391	382	382	382	379.5
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	Q8pmv4 xanthomonas Q8ns10 corynboacte P73354 synechooyst Q8ptt ralsconia s Q8xptt ralsconia s		V./Kasy Synechococc Q7u495 synechococc Q92qe6 rhizobium m Q8pb56 xanthomonas Q8d128 synechococc Q89rp2 bradyrhizob	×
Q9KJN6 Q8YTF9 Q89QJ8 Q8G6T3	Q8PMV4 Q8NS10 P73354 Q8XPT5	Q97GD5 Q8DMV9 Q8R756 Q89915	Q7U8K9 Q7U495 Q92QE6 Q8PB56 Q8DL28 Q89RP2	Q982R5 Q987R2 Q98D1R0 Q99D1R0 Q99BA3 Q97UX54 Q8YXZ0
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SM00228; PDZ; 1.
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                                                                                                                Similarity
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                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
                                                                                                                                                                                                                                                                                                                                                                             1 MSNSRRRSIRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
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STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
                                                                                                                                                                                                                                                                                                                                                    ·,
                                                                                                                                                                                                                                                                                                                       99.4%; Score 1792; DB 16; Length 355; 99.4%; Pred. No. 3.5e-87; tive 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1765;
                                                                                                                                                                                                                                            PROSITE; PS50106; PDZ; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Hypothetical protein; Serine protease; Protease;
                                                            Tuberculist; Rv0125; ...
Tuberculist; Rv0125; ...
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:000508; P:protecolysis and peptidolysis; IEA.
InterPro; IPR00403; Cys_Ser_trypsin.
InterPro; IPR004254; Peptidase_S1.
InterPro; IPR004254; Peptidase_S1.
InterPro; IPR004056; Peptidase_S1.
InterPro; IPR00595; Poz; 1.
Pfam; PF00599; Poz; 1.
                                                                                                                                                                                                                                                                                                 355 AA; 34926 MW; 16CE9E21A97BF192 CRC64;
SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable serine protease PEPA (EC 3.4.21.-).
                                                                                                                                                                                                       PRINTS; PRO0834; PROTEASESC.
PRINTS; PRO0839; V8PROTEASE.
SMART; SMO0228; PDZ; 1.
-i- SIMILARITY: TO SERINE PR
EMBL; Z96071; CAB09453.1; -.
EMBL; AE006925; AAK44357.1;
PIR; F70983;
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 99.4
Matches 353; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium bovis.
                                                                                                                                                                                                                                                                                     Complete proteome.
SEQUENCE 355 AA;
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                                                     TIGR; MT0133;
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X MEDLINE=95005449; PubMed=7921248; MEDLINE=95005449; PubMed=7921248; MEDLINE=95005449; PubMed=7921248; MEDLINE=95005449; PubMed=7921248; M. Cameron R.M., Stevenson K., Inglis N.F., Klausen J., Sharp J.M.;
T "Identification and characterisation of a putative serine protease expressed in vivo by Mycobacterium avium subsp paratuberculosis."; Microbiology 140:1977-1982 (1994).

- I Microbiology 140:1977-1982 (1994).

- I SIMILARITY: CONTAINS I PDZ/DHR DOMAIN.

R PIR; $23092; CAA80638.1; - I PZ/DHR DOMAIN.

R PIR; $47170; $47170.

R PIR; $74170; $74170.

R PIR; $74170; $74170.

R GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0006203; F:peptidase activity; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR009403; Cys Ser_trypsin.
                                                                                                                                                                                                                                                                                                                                                             1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 QASDSLIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
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                                                                                                                                                                                                                       99.4%; Score 1792; DB 16; Length 355; 99.4%; Pred. No. 3.5e-87;
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                                                                                                                                                                                                                                                                           Indels
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Last annotation update)
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Mycobacterium paratuberculosis.
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InterPro; IPR001940; Peptidase_SIC.
Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
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354; 7

DB 16; Length 58; Indels

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59 -VAPQVVNISTRLGYNSAVGAGTGIVIDSSGVVLTNNHVISGATDISAFDVGNGKTYGVD 117
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.,
                                                                                                                                                                                                                                                                                                                  1 MSNSRRRSIRWSWLLSVLAAVGLGLATAPAQA---APPALSODRFADFPALPLDPSAMVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                    tease; Complete proteome. 612F23261BC9EA4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; I
GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys.Ser_trypsin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
10-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat shock protein HtrA, putative.
                                                                                                                                                                                                                                         ; Score 1272.5; DE; Pred. No. 9e-60; 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446
               InterPro; IPR001254; Peptidase 51.
InterPro; IPR001254; Peptidase 51.
InterPro; IPR001956; Peptidase 51B_VB.
InterPro; IPR001996; Peptidase_SIC_Pfam; PF00059; trypsin; 1.
Pfam; PF00099; trypsin; 1.
PRINTS; PR000834; PROTBASES2C.
PRINTS; PR000834; PROTBASE.
SWART; SW00228; PDZ; 1.
PK0SITE; PS50106; PDZ; 1.
PK0SITE; PS50106; PDZ; 1.
PK0SITE; PS50106; PDZ; 1.
PK0KOIRS; Protease; Scrime protease; SEQUENCE 354 AA; 35265 WW; 612F232
                                                                                                                                                                                        protease;
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Best Local Similarity 70.1%
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RI Mature 409:1007-1011(2001).

- Isminanty T. To Serine Professes, TRYPSIN FAMILY.

- Isminanty T. To Serine Professes, TRYPSIN FAMILY.

- Part Man MacSe9.
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                                                                                                                                                                                                                                                                                                                                                                                          300 AAAGIAPGDVITGVDTVPINGATSMTEVLVPHHPGDTIAVHFRSVDGGERTANITLABGP
                                                                                                                                                                                MSKSHHHRSVWWSWLVGVLTVVGLGLGLGSGVGLAPASAAPSGLALDRFADRPLAPIDPS
                                                                                                                                                                                                                     AMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 -GGGGFAIPIGRAMAVANQIRSGAGSNTVHIGPTAFLGLGVTDNNGNGARVQRVVNTGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 ASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGP
                                                                                                                                               1 MSNS-RRRSLRWSWLLSVLAAVGLGL----ATAPAQAAPPALSQDRFADFPALPLDPS
                                                                                                              Gaps
                                                                                                              .,
                                                                         Length 361;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                              58; Indels
                                  30FEF78FD6F3C411 CRC64;
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GO; GO:000742; P:intracellular signaling cascade; II
GO; GO:0005608; P:proteclysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                     72.5%; Score 1306; DB 2; 70.4%; Pred. No. 1.6e-61; iive 41; Mismatches 58;
 Serine protease, Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probable secreted serine protease.
                                  35709 MW;
                                                                                                            255; Conservative
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 Protease;
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                                  361 AA;
                                                                                         Local Similarity
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Hydrolase;
                   SIGNAL
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                                                                         Query Match
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                                                                                                                                                                                                                                                                                             - AGNONTVLDAIQTDAAINPGNSGGALVNMNAQLVGVNSAIATLGADSADAQSGSIGLGF
                                                                                                                                                                                                                                                                                                                                                                                  240 AIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV-DNNGNGARVQRVVGSAPAASLGI
                                                                                                                                                                                                AASLVGFNRAPAGPSGGPVAASAAPSIPAANMPPGSVEQVAAKVVPSVVMLETDLGRQSE
                                                                                                                                                                                                                                                   162 -- EGSGIILSAEGLILTNNHVIAAAAKPPLGSPPPKTTVTFSDGRTAPFTVVGADPTSDI
                                                                                                                                                                                                                                                                            AVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGOGGTPRAVPGRVVALGQTVQASDS
                                                                                                                                                                                                                                                                                                                                186 LIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA----ASDNFQLSQG--GQGF
                                                                                                                                                                                                                                                                                                                                                                                                            AIPVDOAKRIADELISTGKA----SHASLGVQVTNDKDTPGAKIVEVVAGGAAANAGV
                                                                                                                                                                       19 AAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSA---MVAQVAPQVVNINTKLGYNNA
                                                                                                                                                                                                                         76 VGAGTGIVIDPNGVVLTNNHVIAGAT-----DINAFSVGSGOTYGVDVVGYDRTQDV
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
EMBL; BX248337; CAD93870.1; -
EMBL; BX248337; CAD93870.1; -
EKYCOLASE; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 PKGVVVTKVDDRPINSADALVAAVRSKAPGATVALTFQDPSGGSRTVQVTLGK 443
                                                                                                                                                                                                                                                                                                                                                                                                                                     STGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAE 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.1%; Score 469.5; DB 16; Length 464; 36.0%; Pred. No. 2.9e-17;
                                                                                                                     DB 16; Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable serine protease (Serine proteinase) (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59; Mismatches 136; Indels
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00059; PDZ; 1.
PRIMTS; PR00834; PROTEASESC.
SMART; SM00228; PDZ; 1.
PROSTIE; PS50106; PDZ; 1.
SEQUENCE 446 AA; 44484 MW; 54170CBEA8FE872B CRC64;
                                                                                                                    26.1%; Score 469.5; DB 16; 36.0%; Pred. No. 2.8e-17; ive 59; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 AA
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01-0CT-2003 (TrEMBLrel. 25, Last seqn
01-0CT-2003 (TrEMBLrel. 25, Last ann
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STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
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Best Local Similarity 36.0%
Matches 127, Conservative
                                                                                                                                   Best Local Similairy Construe Matches 127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium bovis.
                                                                                                                                  Local Similarity
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                                                                                                                       Query Match
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                                                           186 LTGABETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGNNTA----ASDNFQLSQG--GQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 AIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV-DNNGNGARVQRVVGSAPAASLGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 PKGVVVTKVDDRPINSADALVAAVRSKAPGATVALTFQDPSGGSRTVQVTLGK 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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26.0%; Score 468.5; DB 16; Length
Best Local Similarity 36.0%; Pred. No. 3.3e-17;
Matches 127; Conservative 59; Mismatches 136; Indels
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Hydrolase; Protease; Serine protease; Complete proteome.
SEQUENCE 464 AA; 46452 MW; AE93BFCC53BIEC8F CRC64;
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GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR099003; Cys. Ser_trypsin.
InterPro; IPR091478; PDZ.
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Last sequence update)
Last annotation update)
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    VGAGTGIVIDPNGVVLTNNHVIAGAT---
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InterPro; IPR001940; Peptidase SlC.
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SMART; SM00228; PDZ; 1.
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Pfam; PF00089; trypsin; 1.
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RV0983 OR MTV044.11.
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128 AVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDS 185
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                                                                                      120 AASLVGFNRAPAGPSGGPVAASAAPSIPAANMPPGSVEQVAAKVVPSVVMLETDLGRQSE 179
 75
                                                                                                                                                     |||: || ||: || ||: || 355 AIPVDQAKRIADELISTGKA-----SHASLGVQVINDKDTLGAKIVEVVAGGAAANAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.; Woodward J.R.,
AAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSA---MVAQVAPQVVNINTKLGYNNA
                                                                                                                                                                                                186 LTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA----ASDNFQLSQG--GQGF
                                                                                                                                                                                                                 240 AIPIGOAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV-DNNGNGARVQRVVGSAPAASLGI
                                                                 -- DINAFSVGSGQTYGVDVVGYDRTQDV
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R GO; GO: 000823; F: peptidase activity; IEA.
R GO; GO: 000823; F: peptidase activity; IEA.
R GO; GO: 0008295; F: trypsin activity; IEA.
R GO; GO: 0004295; F: trypsin activity; IEA.
R GO; GO: 000542; P: proteclysis and peptidolysis; IEA.
R GO; GO: 0005608; P: proteclysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_SI.
DR InterPro; IPR001254; Peptidase_SI.
DR InterPro; IPR001494; Peptidase_SIC.
DR Pfam; PF00555; PDZ; 1.
DR Pfam; PR00555; PDZ; 1.
DR Pfam; PR00595; PDZ; 1.
DR PKINTS; PR00128; PDZ; 1.
DR RNART; SM00228; PDZ; 1.
KW Hydrolase; Protease; Serine protease; Complete protecome.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible secreted serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                              382 AA
                                                                 76 VGAGTGIVIDPNGVVLTNNHVIAGAT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium leprae
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Length 382;

DB 16;

Score 460;

25.5%;

Query Match

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12;
                                                                            182 ASDSLIGABETINGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAA-----SDNFQLSQG 235
                                                                                                                                                            210 TTGE-SGNONTVLDAİQTDAAİNPGNSGGALVNMGGQLVGVNSAIATLGADSGDAQSGSI 268
                                                                                                                                                                                            AGTGIVIDPNGVVLTNNHVIAGA------TD1NAFSVGSGQTYGVDVVGYDR 123
                                                                                                     TQDVAVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQ 181
                                                                                                                                                                                GQGFAIPIGQAMALAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGN-GARVQRVVGSAPAA 294
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                                      GLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA----PQVVNINTKLGYNNAVG
         54; Gaps
                                                                                                                                                                                                                                                                                                                                                       Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
Best Local Similarity 36.4%; Fred. No. 7.3e-17;
Matches 130; Conservative 52; Mismatches 121; Indels
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Harris D., Taylor K.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                         452
                                                                                                                                                                                                                                                                                                                                       Putative serine protease.
MLCB373.28.
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                                                                                                                                  GAGPVIGPAASVPAANM------PSGSVEQVAVKVVPSVVMLETDLGRQSE-- 164
                                                                                                                                                                                                     AGTGIVIDPNGVVLTNNHVIAGA------TDINAFSVGSGQTYGVDVVGYDR 123
                                                                                                                                                                                                                                                     165 EGSGVILSADGLILTNNHVVAVAAKPGGGPGGGLSPKTTVTFF---DGRTASFTVVGADP 221
                                                                                                                                                                                                                                                                                                     TQDVAVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQ 181
                                                                                                                                                                                                                                                                                                                                                     222 TSDIAVVRVQSISGLTPITMGSSADLRVGQPVVAVGSPLGLAGT--VTSGIVSALNRPVS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                     280 TIGE-SGNQNIVLDAIQIDAAINPGNSGGALVNMGGQLVGVNSAIATLGADSGDAQSGSI 338
                                                                                                                                                                                                                                                                                                                                                                                                       182 ASDSLIGAEETLNGLIGFDAALOPGDSGGPVVNGLGQVVGMNTAA----SDNFQLSQG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 GOGFALPIGQAMALAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGN-GARVQRVVGSAPAA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 GLGFAIPVDQAKRIADELISTG--KATH----ASLGVQVATDKGTPGAKVMDVVAGGAAA 392
                                                                                                     22 GLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA----PQVVNINTKLGYNNAVG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 NAAVPKGVVLTKVDDRLISSADALVAAVRSKAPGDKVSLTYQDQSGSSRTVQVTLGK 449
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
25.5%; Score 460; DB 2; Length 452; 36.4%; Pred. No. 9e-17;
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                  52; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saunders D., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                          36.48;
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01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
                                               Matches 130; Conservative
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STRAIN=A3(2) / M145;
                          Similarity
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SCOS149 OR SCP8.12
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140 SAAIGG--GVAVGEPVVAMGNSGGGGTPRAVPGRVVALGQTVQA-SDSLTGAEETLNGL 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 IVIDPNGVVLTNNHVI--AGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 FVLDGRGHILTNNHVVEPAGSGGEITVTFNSGDTAEAEVVGRDSGYDLAVVKVKGVTGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 IQFDAAIQPGDSGGPVVNGLGQVVGMNTA-----ASDNFQLSQGGQGFAIPIGQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 LÓTDAPINPGNSGGPLLDARGRAIGINSAIRSADSGSTESDDGQAGSIGLGFAIPINÒGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIAGQIRSGGGSPTVHIGPTAFLGLGV-VDNN--GNGARVQ------RVVGSAPAASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 GISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEG 352
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'Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 542;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.6%; Score 407; DB 16; Length 5 32.6%; Pred. No. 7e-14; tive 56; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase, Protease, Serine protease, Complete proteome
SEQUENCE 542 AA, 53761 MW, 620F7D889DF7212D CRC64;
                        coelicolor A3(2).";
Nature 417:141-147(2002).
Nature 417:141-147(2002).
EMBL; AL939122; Postidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys.Ser_trypsin.
InterPro; IPR001478; PDZ.
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Last annotation update)
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                                                                                                                                                                                                                                                                           InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PP00595; PDZ; 1.
Pfam; PP00089; trypsin; 1.
SMART; SM00284; PDZEASESC.
PROSITE; PSS0106; PDZ; 1.
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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SC03977 OR SCBAC25E3.14.
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nes 116;
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432

12;

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232 LSQGGQ----GFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARV--QR 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 VVGS-----APAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445 VGGSDPVEKGGPADDAGIKPGDVITKLDDRVIDSGPTLIGEIWTHKPGDEVTVTYE-RGG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGYDRIQDVAVLQLRGA-GGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGOTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA----ASDNFQ 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 POVININTKLGYNNAVGAGTGIVIDPNGVVITNNHVIAGATDINAFSV--GSGQTYGVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LLSVLAAVGLG------LATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
                                                                    Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hopwood U.A.;

"Complete genome sequence of the model actinomycete Streptomyces celicolor A3(2).";

"Complete genome sequence of the model actinomycete Streptomyces celicolor A3(2).";

In Nature 417:141-147(2002).

In ReMEL, AL931118;

GO, GO:0008233; F:peptidase activity; IEA.

GO; GO:0002425; F:trypsin activity; IEA.

GO; GO:0002425; F:trypsin activity; IEA.

GO; GO:0006508; P:proteclysis and peptidolysis; IEA.

InterPro; IPR001409; PDZ.

InterPro; IPR001549; Peptidase_S1C.

InterPro; IPR001549; Peptidase_S1C.

InterPro; IPR001549; Peptidase_S1C.

R Pfam; PF000834; PROTEASES2C.

SMART; SM00228; PDZ; 1.

R SMART; SM00229; PDZ; 1.

R SMART; SM00220; Trypsin; 1.

R SMART; SM00220; Trypsin; 1.

R SMART; SM00220; Tryp SPC; 1.

Mydrolase; Protease; Serine protease; Complete protecome.
                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=A3(2) / M145.
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; Parke L., Murphy L., Oliver K., O'Neil S., Reabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S., Senders D., Sharp S., Squares R., Squares S., Taylor K., Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.;
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                                      STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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nes 119; Conservative
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MEDLINE-2225144;

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Kiyokawa C., Kohara M., Mateumnoto M., Matanaki N.,

Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

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Bacteria, Cyanobacteria, Chroococcales, Synechococcus.
                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 33.6
Matches 108; Conservative
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RESULT: P72780 ω

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111 GQTYGVDVVGYDRTQDVAVLQLRGA-GGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPR 167
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Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.; Shinose M., Kikuchi H., Shiba T., Cakaki Y., Hattori M., Omura S.; Shinose M., Kikuchi H., Shiba T., Complete genome sequence and comparative analysis of the industrial microorganism Exreptomyces avermitilis.",
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EMBL; Ap005038; BAC71935.1;
GO; GO:0008239; Firtypsin activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0005038; P:proteclysis and peptidolysis; IEA.
InterPro; IPR003003; Cys_Ser_trypsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21477403; PubMed=11572948; MEDLINE=21477403; PubMed=11572948; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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SEOUENCE 472 AA; 46086 MW; AE04FAA409A3B7E0 CRC64;
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
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Last annotation update)
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(TrEMBLrel. 24, I
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
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                               312 INSATAM 318
                                                                               350 ISDGARL 356
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Matches 102; Conserv
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01-OCT-2003
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence" analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3.109-136 (1956).

-! SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.

EMBL; D90900; BAA16795.1; -.
                                                                                                                                                                                                                                                                                                                                             Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Myajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.himpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
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SEQUENCE 394 AA, 41336 MW, AD59D94811B8F57B CRC64;
                                                                                                                                                                                Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.274; -... GO; GO:0004295; F:trypsin activity; IEA. GO; GO:0007242; P:intracellular signaling cascade; I: GO; GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR009003; CYS_Ser_trypsin.
                                             01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
394 AA
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InterPro; IPR008353; Peptidase S1B tx.
InterPro; IPR008256; Peptidase S1B V8.
InterPro; IPR001940; Peptidase S1C.
PRT;
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MEDLINE=97061201; PubMed=8905231;
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PRINTS, PRO0834, PROTEASES2C.
SMART; SMO0228, PDZ; 1.
SMART; SM0020, TYP, SPC; 1.
PROSITE; PS50106, PDZ; 1.
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Pfam; PF00089; trypsin; 1.
PRELIMINARY;
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Matches 116; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --AGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG--GVAVGEPV 153
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                                               : : | | | : : | | | : : | | | 394 TEQGASGS--DAITPNGPAAKAGLKPGDVITKLDDMVIDSGPTLIGEIWTHRPGATVKLT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ikeda H., Ishikawa U., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial microorganism Streptonyces avarmitilis."; microorganism Streptonyces avarmitilis."; EMBL, APO05033, BAC70826.1; ... GO, GO.0004225; Fitrypsin activity, IEA. GO, GO.0007427; Fitracellular signaling cascade; IEA. GO, GO.000508; Piproteolysis and peptidolysis; IEA. InterPro; IPRO09003; Cys. Ser_trypsin.
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Best Local Similarity 33.7%; Pred. No. 1.7e-12;
Matches 114; Conservative 53; Mismatches 127; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa U., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
Genome sequence of an industrial microorganism Streptomyces
avermitilis; deducing the ability of producing secondary
metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
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SEQUENCE 619 AA; 64251 MW; D2D3C72A67D3B3A6 CRC64;
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MEDLINE=22608306; PubMed=12692562;
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Last annotation update)
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InterPro; IPR001940; Peptidase_S1C.
Pfam; PP00595; PD2; 1.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00894; PROTEASESCC.
SMART; SM00228; PDZ; 1.
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                                                                                                                                              335 WQTKSGGTRTGNVTLAE 351
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(TrEMBLrel. 24, I
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                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
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Maximum |
                                            Run on:
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No
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σ	Ada26365 Mycobacte	Aay32070 Mycobacte	Aae29710 Mycobacte	Aael7574 Mycobacte	Aau74599 Antigenic	Aao22142 Ra12-H9-3	00	~	Ada26373 Mycobacte	Aae29731 Mycobacte	Ada26364 Mycobacte	Aae29709 Mycobacte	-	Ada26374 Mycobacte	Aau74588 Antigenic	Aay32059 Mycobacte	Aae29704 Mycobacte	Aael7568 Mycobacte	Aay32071 Mycobacte
ADA26369	ADA26365	AAY32070	AAE29710	AAE17574	AAU74599	AA022142	AAE29708	AAE17572	ADA26373	AAE29731	ADA26364	AAE29709	AAE17573	ADA26374	AAU74588	AAY32059	AAE29704	AAE17568	AAY32071
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26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Mycobacterium tuberculosis mature Ra35 antigenic protein AAE29702 standard; protein; 330 AA

Vaccine; immunity; diagnostic agent; gene therapy; Ra35 antigen. /note= "Encoded by GAG" Location/Qualifiers

/note= "Encoded by

#505

New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium

Disclosure; Page 79-80; 155pp; English.

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymucleotide sequence encoding an antisen or an antisement from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, M15, and 6H polymucleotides. Sequences of the invention

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CORI-) CORIXA CORP.
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                       Skeiky Y,
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          useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymotleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis mature Ra35 (N-terminus of MTB32A; RA35FL) antigenic protein
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                                                                                                                                                                                                                       PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
                                                                                                                                                                                                                                              GVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQP 180
                                                                                                                                                                                                                                                          240
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  They are
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  used in methods for eliciting immune response in mammals.
                                                                                                            Length 330;
                                                                                                                                 Indels
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                                                                                                            Query Match 100.0%; Score 1698; DB 5; Best Local Similarity 100.0%; Pred. No. 1.9e-122; Matches 330; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium sp. MTB32A (Ra35FL) mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide"
                                                                                                                                                                                                                                                                                                                                                                                                  HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
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/note= "Ra35 N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by GAG'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE17566 standard; protein; 330 AA.
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01-FEB-2001; 2001US-0265737P.
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Mycobacterium species antiques to instant proteins compositions compositions compositions compositions to include two or more individual M. Tuberculosis antigens which increase particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. Tuberculosis antigens which increase the sarchogical sensitivity of sera from individuals infected with treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral mycobacterium, in vitro and in vivo assays for detecting humoral mycobacterium, in vitro and in vivo assays for detecting humoral infection or monitoring of disease progression, as intibodies or cell-mediated immunity against M. tuberculosis, for the ingential anti-M. Luberculosis and an on-human animal Sequences of the invention are also used as vaccines. MTB32A full intradermal skin test. The present sequence is Mycobacterium species MTB32A (MTB32A) mature protein
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                                                                        Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
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                                                                                                                                                                                                                                                            present invention relates to fusion proteins containing at least two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 PTAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH
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Pred. No. 1.9e-122;
; Mismatches 0;
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                                                                                                                                                                                    Claim 70; Fig 6; 136pp; English.
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Best Local Similarity 100.
Matches 330, Conservative
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N-PSDB; AAD28336
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New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium
                 Vaccine; immunity; diagnostic agent; gene therapy; Ra35FLMutSA; mutant;
Mycobacterium tuberculosis Ra35FLMutSA mutant antigenic protein.
                                                                                             /note= "Wild type Ser substituted with Ala"
                                                                                                                                                                                                                                                                                                           Disclosure, Page 81-82; 155pp; English.
                                                                         Location/Qualifiers
                                                                                                                                                                                                                Guderian J;
                                                                                                                                                      13-MAR-2002; 2002WO-US008223.
                                                                                                                                                                         13-MAR-2001; 2001US-0275837P
                                             Mycobacterium tuberculosis. Synthetic.
                                                                                                                                                                                                               Brannon M,
                                                                                                                                                                                           CORIXA CORP
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                                                                                                                                                                                                                                            N-PSDB; AAD47078
                           antigen; mutein.
                                                                                   Misc-difference
                                                                                                                WO200272792-A2
                                                                                                                                                                                                                                                                                            tuberculosis
                                                                                                                                                                                                              Skeiky Y,
                                                                                                                                                                                            (CORI-)
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous bolynculeotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis Ra35FIMutSA mutant antigenic protein Length 330; 99.8%; Score 1695; DB 5; 99.7%; Pred. No. 3.2e-122; Sequence 330 AA;

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PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
                                                                                                                                                                                                    PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
                                                                                                                                                                                                                                            GVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQP 180
                                                                                                                                                                                                                                                                                 GVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQP 180
                                                                                                                                                                                                                                                                                                                          GDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIG 240
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                                                                               1 MHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVID
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                                      Indels
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                                    1; Mismatches
                 Best Local Similarity 99.7
Matches 329; Conservative
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Mycobacterium species Ra35FL mature protein mutant (S183A), Ra35FLMutSA
                                                                                             Fusion protein, antigen; serological sensitivity; immune response;
tuberculosis; infection; vaccine; Ra32FLMutSA protein; mutant; mutein.
                                                                                                                                                     'note= "Wild type Ser substituted with Ala"
                                                                                                                                                            199. .330
/note= "Ra35 C-terminal peptide, Ra12"
                                                                                                                                        /note= "Ra35 N-terminal peptide"
      301 HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
301 HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                            Location/Qualifiers
                                           Ā
                                           AAE17567 standard; protein; 330
                                                                    (first entry)
                                                                                                                 Mycobacterium sp.
                                                                                                                                                Misc-difference
                                                                     22-APR-2002
                                                        AAE17567;
                                                                                                                                                             Region
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Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject Claim 73; Fig 6; 136pp; English. WPI; 2002-147798 N-PSDB; AAD28337

Alderson M;

Reed S,

Skeiky Y,

2002-147798/19.

20-JUN-2000; 2000US-00597796. 01-FEB-2001; 2001US-0265737P. 20-JUN-2001; 2001WO-US019959.

WO200198460-A2

27-DEC-2001

(CORI-) CORIXA CORP

useful for eliciting an immune response in a mammal, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WIB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species Ra32FL mature protein mutant (S183A), Ra35FLMutSA The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nuclectides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M tuberculosis antigens which increase the servological sensitivity of sera from individuals infected with tuberculosis and methods for that use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are

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Gaps

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Length 330, Indels 9 9 180

180 240 240

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MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypucclotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
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                                                                                                                                                                                                                                                      1 MHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVID
                                                                                                                                                                                                                                                                                                                                                                             GVAVGEPVVAMGNSGGOGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQP
                                                                                                                                                                                                                                                                                                                                                                                                           121 GVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQP
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                                                                                                                                                         Score 1695; DB 7;
Pred. No. 3.2e-122;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
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N-PSDB; ADA26353.
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Mycobacterium sp.
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                                                                                                                                                              PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
                                                                                                                                                                                               PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
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                                                                                                                       1 MHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVID
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                                                                                          1 MHHHHHHAPPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVID
                                                      Gaps
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ilosis; tuberculostatic; gene therapy; vaccine; mutant; mutein.
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                  Length 330;
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                                                      Indels
 Score 1695; Db J,
No. 3.2e-122;
0;
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                                                        Mismatches
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                    99.8%;
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                                                          Conservative
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                                       Similarity
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Mycobacterium sp.
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(CORI-) CORIXA CORP
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                                                   The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antiqen, or MTB32A, MTB32A and BBS5A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                       Length 723;
                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                    lery Match 99.8%; Score 1695; DB 7; st Local Similarity 99.7%; Pred. No. 8.6e-122; tches 329; Conservative 1; Mismatches 0;
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                Claim 4; Fig 2; 112pp; English.
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N-PSDB; ADA26355.
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Best Local Similarity
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New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH
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tuberculosis; tuberculostatic; gene therapy; vaccine.
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99.8%; Score 1695; DB 7;
Best Local Similarity 99.7%; Pred. No. 1.3e-121;
Matches 329; Conservative 1; Mismatches 0;
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                                                                                                                                                                       Claim 6; Fig 4; 112pp; English
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Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
                                                                                                                                                                                                                                                                Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHPGDVIS
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                                                                             Guigueno
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Best Local Similarity 100.0%; Pred. No. 2.5e-118;
Matches 323; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                      Claim 32; Fig 50D; 309pp; French
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97FR-00010404.
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De La Salmoniere
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                                                                                                                          WPI; 1999-181045/15.
N-PSDB; AAX34251.
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 355 AA;
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11-SEP-1997;
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                                                                             New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB33 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                      The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A
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                                                                                                                                                                                                                                                   polynucelotide of the invention may have a use in gene therapy, and as vacchie. The methods and compositions of the present invention are usef for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                          Disclosure; Fig 19; 112pp; English
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                              WPI; 2003-697554/66
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 329; Conserv
                                                                                                                                                                                                                                                                                                                                 Sequence 330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium
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                Skeiky Y,
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Gaps ; 0

67 92 127 152 187 212 247

us-09-886-349a-4.rag

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 (busion polypeptide, comprising a polynucleotide sequence of Fal2, a 14 (busion polypeptide) servine protease annigen MTB32A of a 14 (busion tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both as an antigen for detecting servine antibodies. The presence of servine antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as cources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antipens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This sequence represents the Mycobacterium tuberculosis MTB32A protein
                                                                                                                                                                                                                                                                                Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 39pp; English
                                       06-OCT-2000; 2000WO-US027652.
                                                                                   99US-0158585P.
                                                                                                                                                                         Guderian
                                                                                                                                                                                                                   WPI; 2001-266299/27.
                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                        N-PSDB; AAL40768.
                                                                                   07-OCT-1999;
12-APR-2001
                                                                                                                                                                         Skeiky Y,
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Sequence 355 AA;

212 127 152 187 247 272 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307 332 67 92 33 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT NNHVI AGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP VNGLGQVVCMNTAASDNPQLSQGGQGPAIPIGQAMAIAGQIRSGGSPTVHIGPTAFLGL 93 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 8 APPALSQDRFADFPALPLDPSAWVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT VVAMGNSGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV .; 0 Length 355; 0; Indels 96.9%; Score 1645; DB 4; L 100.0%; Pred. No. 2.5e-118; iive 0; Mismatches 0; 330 VTWQTKSGGTRTGNVTLAEGPPA Matches 323; Conservative Best Local Similarity 213 248 89 273 308 128 333 dd g ò g ò ò 셤 ò

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AAG81110 standard; protein; 355

AAG81110

RESULT 11
AAG81110
ID AAG81
XX
AC AAG81

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This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polymuleotide sequences AAHS1947 - AAHS2092 represent DNA encoding proteins AAG81266 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDBNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 NNHVIAGAIDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 VVAMGNSGGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV
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                                 Mycobacterium tuberculosis potential drug target protein SEQ ID
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                                                                   Drug target; growth; organism viability; characterisation
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100.0%; Pred. No. 2.5e-118;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       Marcotte EM;
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                                                                                                                                                                                                                                                        12-NOV-1999; 99US-0165086P.
12-NOV-1999; 99US-0165124P.
01-FEB-2000; 2000US-0179531P.
                                                                                                                                                                                                                       13-NOV-2000; 2000WO-US031152
                                                                                                                                                                                                                                                                                                                                                                         Rotstein SH,
                                                                                                          Mycobacterium tuberculosis
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Matches 323, Conservative
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                                                                                                                                                WO200135317-A1,
                                                                                                                                                                                                                                                                                                                                                                         Eisenberg D,
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VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                          357 VTWQTKSGGTRTGNVTLAEGPPA 379
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DR;
                                                                                                                                                                   AAW32367 standard; protein; 355
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95US-00532136.
96US-00620280.
96US-00658800.
96US-00688033.
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                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
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4, Twardzik
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N-PSDB; AAT91414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1997
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                                                                                                                                                                                                           AAW32367;
                      308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 VNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                     Secreted protein, Mycobacterium, primer, PCR; amplification, probe, hybridisation, detection, vaccine; immunisation, infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guigueno A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.9%; Score 1645; DB 2; L
100.0%; Pred. No. 2.7e-118;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pelicic V,
                                                                                                                                                                                                                               Mycobacterium species protein sequence 50F.
333 VTWQTKSGGTRTGNVTLAEGPPA 355
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                                                                                                   AAY04830 standard; protein; 379
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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TBRa35. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection.
                                                                              Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant, skin testing; M.tuberculosis.
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Mycobacterium tuberculosis antigen TbRa35
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APPALSQDRFADFPALPLDFSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDFNGVVLT NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP

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153 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV VNGLGQVVGMNTAASDNFQLSQGGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL

188

128 VVAMGNSGGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV

This polypeptide comprises Mycobacterium tuberculosis soluble antigen TDRa35. It is encoded by a DNA sequence (see AAV4455) isolated from a M. tuberculosis stann H37Ra expression library with rabbit anti-sera raised against M. tuberculosis supernatant. No significant homology was found between TDRa35 and Genebank database sequences. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAM64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transference or transference or transference or transference calls. Also claimed are methods and diagnostic kits for GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307 to 273 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHFEGDVIS New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis. В. Houghton Tuberculosis; infection; diagnosis; antigen; TbRa35. Skeiky YAW, Dillon DC, Campos-Neto A, ;, Twardzik DR, Lodes MJ; Mycobacterium tuberculosis antigen TbRa35 Mycobacterium tuberculosis; strain H37Ra Example 3; Page 115-116; 250pp; English. VTWOTKSGGTRIGNVTLAEGPPA 330 Á AAW64307 standard; protein; 355 96US-00729622. 97US-00818111. 97WO-US018214 (revised)
(first entry) WPI; 1998-251292/22. N-PSDB; AAV44355. (CORI-) CORIXA CORP. WO9816645-A2 07-OCT-1997; 11-OCT-1996; 13-MAR-1997; 17-OCT-2003 09-NOV-1998 Reed SG, Sk Vedvick TS, 23-APR-1998 AAW64307; 308 248 RESULT 15 AAW64307 g QY Db g ð o, 67

Query Match

96.2%; Score 1634; DB 2; Length 355;
Best Local Similarity 99.4%; Pred. No. 1.7e-117;
Matches 321; Conservative 0; Mismatches 2; Indels

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detecting M. tuberculosis infection in a patient using the above polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS , field)
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4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Length 355 Indels

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128 VVAMGNSGGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                      33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 92
APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 67
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96.2%; Score 1634; DB 4; Length 355;
Best Local Similarity 99.4%; Pred. No. 2.6e-131;
Matches 321; Conservative 0; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DAPA:
APPLICATION NUMBER: US/08/818,111
FILLING DATE: 13-MAR-1997
CLASSIFRCATION: 424
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: si
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STATE: Washing
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US-08-818-111-80
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ö 8 APPALSQDRFADFPALPLDPSAWVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT Gaps

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93 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP 152
                                                                                                                                                                                                     128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                                                                                                                                                                                                               188 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 247
                                                                                                                                                                                                                                                                                                                           248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
                                                                                                                                                                                                                                                                                                                                                                                                                 33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 92
                                                                                                            68 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                     8 APPALSODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCRANTION:

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Davin C.

APPLICANT: Davin C.

APPLICANT: Davin C.

APPLICANT: Houghton, Raymond

APPLICANT: Wardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Hendrickson, Ronald C.

TILLE OF INVENTION: COMPOUNDS AND METHODS FOR INMUNOTHERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 355

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 99104-7092
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTANG SYSTEM: PC-DOS/MS-DOS
SOFTANG SYSTEM: PC-DOS/MS-DOS
SOFTANGE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 VNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 VTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 79, Application US/09072967; Patent No. 6592877; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 355 amino acids
amino acid
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Washington
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US-09-072-967-79
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STATE: Wa
COUNTRY:
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                                                                                                                                                                               212
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                                                                     93 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGGVAVGEP 152
                                                                                                                                                                                                                                                                      213 VNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 272
                                                                                                                                                                                                                                                                                                                   248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 92
                                                                                                                                                              VNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                           68 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
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Patent No. 6458366

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Netc, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Meda'tck, Daniel R.
APPLICANT: Meda'tck, Daniel R.
APPLICANT: Meda'tck, Daniel R.
APPLICANT: Meda'tckgon, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF I
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ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OCHEVING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-M2-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121,417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                          308 VIWOTKSGGTRIGNVILAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                              333 VNWQTKSGGTRTGNVTLAEGPPA 355
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INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 355 amino acids
amino acid
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Best Local Similarity 99.4
Matches 321; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: single
linear
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US-09-072-596-80
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CITY: Se
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10S-09-287-849-2
Sequence 2, Application US/09287849
Parent No. 6627198
GENERAL INFORMATION:
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neco, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Rusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
                                                                                                               187
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                                        535 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
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68 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                                                                                               VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV
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; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-223-040-2
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Best Local Similarity 100.0%; Pred. No. 7.9e-76;
Matches 195; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                      188 VNGLGQVVGMNTAAS 202
                                                                                                                                                                                                                                                                                              582 VNGLGOVVGMNTAAS 596
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Best Local Similarity
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APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Boilon, Davin C.

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Contra Corporation

TITLE OF INVENTION: This on Their Uses

FILE REPRENCE: 1999-009200S

CURRENT APPLICATION NUMBER: US 08/818,112

PRIOR FILING DATE: 1997-03-13

PRIOR PLING DATE: 1997-03-13

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-04-07

PRIOR PLING DATE: 1998-04-07

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   Score 1634; DB 4; Length 355;
Pred. No. 2.6e-131;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 VIWOTKSGGIRIGNVILAEGPPA 330
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      96.2%;
99.4%;
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                                     Similarity 99.4
1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                           Matches 321;
                                                                                                                                                                                                                                            68
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         Query Match
Best Local 9
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; TYPE: PRT
) ORGANISM: Artificial Sequence
; FEATURE:
) OTHER INFORMATION: Description of Artificial Sequence:bi-fusion US-09-287-849-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 RTGNVTLAEGPPA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 RIGNVILAEGPPA 330
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Sequence 28, Application US/09287849

Sequence 28, Application US/09287849

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

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APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

BRIOR APPLICANTON NUMBER: US 09/025,197

PRIOR APPLICANTON NUMBER: US 09/025,197

PRIOR APPLICANTON NUMBER: US 09/025,197

PRIOR APPLICANTON NUMBER: US 09/025,197

PRIOR APPLICANTON NUMBER: US 09/025,197

PRIOR APPLICANTON NUMBER: US 09/023,040

PRIOR APPLICANTON NUMBER: US 09/023,040

PRIOR APPLICANTON NUMBER: US 09/023,040

PRIOR FILING DATE: 1998-12-30

NUMBER OF SEQ ID NO 28

LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            655 VVAMGNSGGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDDAIQPGDSGGPV 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          535 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGGVAVGEP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 APPALSODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.1%; Score 987; DB 4; Length 729; Best Local Similarity 100.0%; Pred. No. 7.9e-76; Matches 195; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR PAPLICATION NUMBER: US 08/942,578
PRIOR PILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR PRIOR PLING DATE: 1998-04-07
PRIOR PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENT NOT: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 VNGLGOVVGMNTAAS 202
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                        US-08-818-112-66
) Sequence 66, Application US/08818112
) Patent No. 6220969
) GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Resky, Yasir A.W.
APPLICANT: Campose.Neto, Antonio
APPLICANT: Campose.Neto, Antonio
APPLICANT: Twadrick, Thomas S.
APPLICANT: Twadrick, Daniel R.
APPLICANT: Twadrick, Daniel R.
APPLICANT: Twadrick, Daniel R.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Wedvick, Thomas S.
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
     Length 231;
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39.5%; Score 670; DB 3; Length 132;
Best Local Similarity 99.2%; Pred. No. 8e-50;
Matches 131; Conservative 0; Mismatches 1; Indels
Query Match 39.8%; Score 676; DB 4; Length 23 Best Local Similarity 99.2%; Pred. No. 5.2e-50; Matches 132; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY. USA

ZIP: 98104-7022

COMPUTER READABLE FORM:
MEDIUT TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFTATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: MAX., DAVIA J.
REGISTRATION NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 682-6031
INFORMATION POR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: AMINO acids
TYPE: AMINO acids
TYPE: AMINO acids
TYPE: AMINO acids
TYPE: AMINO acids
TYPE: AMINO acids
TYPE: AMINO acids
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US-08-818-112-66
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TREATME

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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Skelky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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                                                                                                       Sequence 66, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 632-4900
TELEPHONE: (206) 632-6031
INFORMATION FOR SEC ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.5%;
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 99.2
Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seattle
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 630
                                                                                    US-09-056-556-66
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APPLICANT:
APPLICANT:
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                                                                                                                       259 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR 318
                                                                                                                                                        61 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR 318
TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 258
                                   1 TAASDNFQLSQGGGGAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yashr A.W.

APPLICANT: Skeiky, Yashr A.W.

APPLICANT: Campos-Neto, Antonia

APPLICANT: Houghton, Raymond

APPLICANT: Houghton, Raymond

APPLICANT: Twardzik, Thomas S.

APPLICANT: Twardzik, Thomas S.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SECHENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and Purner.
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99.2%; Pred. No. 8e-50;
tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 67, Application US/08818111 Patent No. 6338852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 amino acids
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Best Local Similarity 99.2'
Matches 131; Conservative
                                                                                                                                                                                                                                               319 TGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                         121 TGNVTLAEGPPA 132
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STRANDEDNESS: sir
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CITY: Seattle
STATE: Washingt
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TOPOLOGY:
US-08-818-111-67
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Score 670; DB 4; Length 132;
Pred. No. 8e-50;
0; Mismatches 1; Indels
 Sequence 819, Application US/09636215
Patent No. 6620922
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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99.2%;
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Vedvick, Thomas S.
Carter, Darrick
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Best Local Similarity
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                 TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
NOTRESPONDENCE ADDRESS:
CARREPOUNDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                         COMPUTER: TELPOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORFIGNATING SYSTEM: PC-DOS/MS-DOS
SOFTWARD: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKA, DAVIG J.
REGISTRATION NUMBER: 31.392
REGISTRATION NUMBER: 210121.417C9
TELECOMMUTCATION INFORMATION:
TELEFHONE: (206) 622-4900
TELEFAK: (206) 622-6031
TELEFAK: (206) 622-6031
TELEFAK: (206) 642-6031
TELEFAK: (206) 642-6031
TELEFAK: (206) 642-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.5%; Score 670; DB 4.
99.2%; Pred. No. 8e-50;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 132 amino acids TYPE: amino acid
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Best Local Similarity 99.2
Matches 131; Conservative
                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                    STATE: Washington
COUNTRY: USA
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                                                                                        Seattle
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US-09-072-596-67
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CITY: Se
STATE: V
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259 VORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR 318
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                                                        199 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR
                                                                                                                1 TAASDNFQLSQGGGFAIPIGGAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR
Gaps
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121/1007/1007/1009/636,215
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFFWARE: FastSEQ for Windows Version 3.0
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; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-636-215-819
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ô 0; Gaps Query Match 39.5%; Score 670; DB 4; Length 132; Best Local Similarity 99.2%; Pred. No. 8e-50; Matches 131; Conservative 0; Mismatches 1; Indels දුරු ප්

199 TAASDNFOLSQGGGGFALPIGGAMALAGOIRSGGGSPTVHIGFTAFLGLGVUDNNGNGAR 258 

319 TGNVTLAEGPPA 330

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ò Op Op 121 TGNVTLAEGPPA 132

Search completed: June 22, 2004, 17:27:28 Job time: 11.78 secs

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June 22, 2004, 17:23:10 ; Search time 30.5644 Seconds (without alignments) 3048.105 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                     1 MIHHHHAPPALSQDRFADF.....QTKSGGTRTGNVTLAEGPPA 330
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NBW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1163542 seqs, 282313646 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		, ok			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	1698	100.0	:	12	US-09-886-349A-4	Sequence 4, Appli
0	1698	100.0		14	US-10-098-732A-4	Sequence 4, Appli
т	1698	100.0		15	US-10-369-983-19	Sequence 19, Appl
4	1695	99.8		12	US-09-886-349A-6	Sequence 6, Appli
Ŋ	1695	8.66		14	US-10-098-732A-6	Sequence 6, Appli
, <b>ω</b>	1695	99.8	330	15	US-10-369-983-20	Sequence 20, Appl
7	1695	8.66		15	US-10-369-983-2	Sequence 2, Appli
æ	1695	99.8		15	US-10-369-983-4	Sequence 4, Appli
a	1645	96.9		σ	US-09-712-363-161	Seguence 161, App
10	1634	96.2		12	US-09-886-349A-2	Sequence 2, Appli
11	1634	96.2		14	US-10-193-002-80	Sequence 80, Appl
12	1634	96.2		14	US-10-084-843-79	Sequence 79, Appl
13	1634	96.2	355	14	US-10-098-732A-2	Sequence 2, Appli
14	1003.5	59.1		15	US-10-369-983-18	Sequence 18, Appl
Ļ	000	au			712_10_269_983_16	Semience 16 Aprol

173888888888888888888888888888888888888	equence 848 equence 819 equence 848 equence 819 equence 848
0-369-983-11 0-369-983-11 0-369-983-11 0-369-983-11 0-369-983-11 0-369-988-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349A-1 0-369-349-349A-1 0-369-349-349-349-349-349-349-349-349-349-34	US-09-759-1 US-09-780-6 US-09-780-6 US-09-822-8 US-09-822-8 US-09-895-7
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                                                                      GENERAL INVOCATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Adderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proceins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-0090700S
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 330
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100.0%; Pred. No. 1.1e-121;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MTB32A (Ra35 mature)
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
               ; Sequence 4, Application US/0986349A; Publication No. US20040086523A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 330, Conservative
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US-09-886-349A-4
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Similarity
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Best Local Simi
Matches 330;
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LENGTH: 330
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                                   121 GVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQP 180
                                                                               240
                                                                                                              GDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIG 240
                                                                                                                                                          241 PTAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH 300
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APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrrey
APPLICANT: Goderian, Jefrrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-01201005
CURRENT APPLICATION WUMBER: US/10/098,732A
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR APPLICATION NUMBER: US 60/275,837
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 100.0
Matches 330; Conservative
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LENGTH: 330
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                                                      GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Red, Steven
APPLICANT: Red, Steven
APPLICANT: Red, Steven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: Old458-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
SUNTHER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Cotixs Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-0097003
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 50
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llarity 100.0%; Pred. No. 1.1e-121;
Conservative 0; Mismatches 0; 1
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Sequence 19, Application US/10369983 Publication No. US20030235593A1
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61 PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
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APPLICANT: Skeiky. Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Red, Steven
TUTLE APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPRENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR PILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 20
IENGTH: 330
TYPE: PRT
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ilarity 99.7%; Pred. No. 1.8e-121;
Conservative 1; Mismatches 0;
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APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US; TITLE OF INVENTION: US/10/098,732A; CURRENT APPLICATION NUMBER: US/10/098,732A; CURRENT FILING DATE: 2001-03-13
FRIOR PRIOR PRICATION NUMBER: US 60/275,837
FRIOR FILING DATE: 2001-03-13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 330
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; OTHER INFORMATION: Description of Artificial Sequence:Ra35FLMutSA
(8-10-098-732A-6
                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Ra35FLMutSA
US-09-886-349A-6
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99.8%; Score 1695; DB 14;
Best Local Similarity 99.7%; Pred. No. 1.8e-121;
Matches 329; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.7%; Pred. No. 1.8e-121;
Matches 329; Conservative 1; Mismatches 0;
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ORGANISM: Artificial Sequence
                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 330
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US-10-098-732A-6
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Pred. No. 7e-121;
1; Mismatches 0;
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PRIOR PELING DATE: 2000-01-28
PRIOR PELING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: PC1/19,531
PRIOR PILING DATE: 1000-02-01
PRIOR PILING DATE: 1099-01-29
PRIOR PILING DATE: 1999-01-29
PRIOR PELING DATE: 1999-02-01
PRIOR PELING DATE: 1999-02-01
PRIOR PELING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR PELING DATE: 1999-03-26
PRIOR PELING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR PELING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR PELING DATE: 1999-05-14
PRIOR PELING DATE: 1999-05-14
PRIOR PELING DATE: 1999-15-14
PRIOR PELING DATE: 1999-11-12
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/712,363 CURRENT FILING DATE: 2000-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 161, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Elsenberg, David
                                                                                                                                                                                                                                         99.8%;
                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                     Matches 329; Conservative
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Best Local Similarity
SOFTWARE: Patentin
                                              1010
                    SEQ ID NO 4
LENGTH: 10
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                                                                                                                                               APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
TOTIAN CORINA CORPORATION
TITLE OF INVENTION FUSION Proteins of Mycobacterium Tuberculosis
FILE REPRENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 723
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; Sequence 4, Application US/10369983
; Publication 0. US2003023553A1
; Publication 0. US2003023553A1
; GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
; APPLICANT: Goderian, Jeff
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT APPLICATION NUMBER: US/10/369,983
; PRIOR APPLICATION NUMBER: US/10/369,983
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:mutated
OTHER INFORMATION: MTB32-MTB39F fusion protein (MTB32MutSA)
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                                                                                    Sequence 2, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
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Matches 329; Conservative
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61 PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
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                                                                                                                                                                                                                                                                                                         1 MHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVID
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OTHER INFORMATION: Description of Artificial Sequence:MTB-102F fusion OTHER INFORMATION: protein US-10-369-983-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
PILE REFERENCE: 07419-03201
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0
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180

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VVAMGNSGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                                                                 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 247
                                                                                                                                                              248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
                       Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIAGNOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHODS FOR
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99.4%; Pred. No. 8.9e-117;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-U1-2002
CLASSIFICATION: <ur>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND ME.
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                 308 VTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                           333 VNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 80, Application US/10193002 Publication No. US20030135026A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 355 amino acids
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INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Best Local Similarity 99.4
Matches 321; Conservative
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APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-00907005
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR PILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR PILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1
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                                                                                                             96.9%; Score 1645; DB 9; L
100.0%; Pred. No. 1.3e-117;
iive 0; Mismatches 0;
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ORGANISM: Mycobacterium tuberculosis
                                                 ) ORGANISM: Mycobacterium tuberculosis
US-09-712-363-161
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US-09-886-349A-2
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Matches 321; Conservative
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Best Local Similarity 100.
Matches 323; Conservative
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US-09-886-349A-2
            LENGTH: 355
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Sequence 2, Application US/10099732A

Sequence 2, Application US/10099732A

Publication No. US2030175294A1

GENERAL INFORMATION:

APPLICANT: Skelky, Yasir

APPLICANT: Brannon, Mark

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

FILE REFERENCE: 014058-012010US

CURRENT APPLICATION NUMBER: US/10/098,732A

CURRENT FILING DATE: 2001-03-13

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE Patentin Ver. 2.1

SEQ ID NO 2.
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                                                                                           96.2%; Score 1634; DB 14;
99.4%; Pred. No. 8.9e-117;
live 0; Mismatches 2;
                 SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-084-843-79
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US-10-098-732A-2
                                                                                                                    Best Local Similarity 99.4
Matches 321; Conservative
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8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
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Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.30
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REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTWQTKSGGTRTGNVTLAEGPPA 330
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Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
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TYPE: amino acid
STRANDEDNESS: single
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N FOR SEQ ID NO: 79:
NCE CHARACTERISTICS:
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                                    247
                                                                213 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSFTVHIGFTAFLGL 272
                                                                                                    248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
                                                                                                                            273 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 714
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153 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETINGLIQFDAAIQPGDSGGPV 212
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GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeff

APPLICANT: Gracia Corporation

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

FILE REFERENCE: 014058-00908108

FILE REFERENCE: 014058-00908108

CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT APPLICATION NUMBER: US/003-02-18

FRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 18

FERRENCE: 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:fusion protein; OTHER INFORMATION: MTB103F (MTB72F-85b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15; Length 1016;
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                                                                                                                                                                          308 VTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                        333 VNWQTKSGGTRTGNVTLAEGPPA 355
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US-10-369-983-16
; Sequence 16, Application US/10369983
; Publication No. US20030235593A1
; GENERAL INPORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Guderian, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.9°
Matches 207; Conservative
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US-10-369-983-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence:fusion protein; OTHER INFORMATION: MTB114F (MTB72F-mTCC#2)
US-10-369-983-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPI--NSATAMADA 296
APPLICANT: Accu, correct APPLICANT: Accu, corrival APPLICANT: Corriva Corporation TITLE OF INVENTION Fusion Proteins of Mycobacterium Tuberculosis FILE REPERENCE: 014058-009031US CURRENT APPLICATION NUMBER: US/10/369,983 CURRENT FILING DATE: 2003-02-18 PRIOR FILING DATE: 2003-02-15 NUMBER OF SEQ ID NOS: 22 SOFTWARE: Patentin Ver. 2.1 SOFTWARE: Patentin Ver. 2.1 SOFTWARE: Patentin Ver. 2.1 LENGTH: 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 73.2%; Pred. No. 2.4e-67;
Matches 213; Conservative 13; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: June 22, 2004, 18:07:52
ne : 31.5644 secs
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ORGANISM: Artificial Sequence
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 22, 2004, 16:59:04; Search time 9.233 Seconds (without alignments) 3438.018 Million cell updates/sec Run on:

US-09-886-349A-4 1698 1 MHHHHHHAPPALSQDRFADF......QTKSGGTRTGNVTLAEGPPA 330 Title: Perfect score: Sequence:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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serine proteinase	htrA-like protein	proteinase DO (EC	trypsin-like prote	serine proteinase	trypsin-like prote	periplasmic serine	proteinase (EC 3.4	probable periplasm	heat shock protein	serine proteinase	serine proteinase	proteinase DO (EC	proteinase DO (EC	proteinase DO (EC	proteinase DO - He
140060	I40059	AI3349	JC6051	D69109	AC0909	F72359	AG0433	B81914	S15337	C87336	A69643	\$45229	E85500	五90649	H71936
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ALIGNMENTS

E	
FESULT F70983 probabl	KESULI 1 1770983 probable serine proteinase pepA - Mycobacterium tuberculosis (strain H37RV)
C,Speci C,Date:	C,Species: Mycobacterium tuberculosis C.pate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Dec-2002
 C,Acces R,Cole, , Conno Rajandr	C;Accession: F/U983 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. , Connor, R.; Bavies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S., Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature A,Authc A;Title A;Refer	Nature 333, 537-544, 1998 A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A,Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome t A,Reference number: A70500; MUID:98295987; PMID:9634230
A,Accession A,Status: p A,Molecule	A,Accession: F70983 A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Rolecule type: DNA
 A;Residues: A;Cross-ref A;Experimen	A;Residues: 1-355 <col/> A;Cross-references: GB:296071; GB:AL123456; NID:g3242254; PIDN:CAB09453.1; PID:g2181967 A;Experimental source: strain H37Rv
 A;Gene: pepA C;Superfamil)	Jene: pepA Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps
Query Ma Best Loo Matches	Query Match Best Local Similarity 100.0%; Pred. No. 9.4e-90; Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
\triansland \trian	8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 67
 , yo	68 INHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVIQLRGAGGLPSAAIGGGVAVGEP 127
 λ d d	128 VVAMGNSGGGGGTPRAVPGRVVALGGTVQASDSLFGAEFTLNGLIQFDAAIQPGDSGGPV 187
 Qy	188 VNGLGQVVGMNTAASDNPQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 247
 QJ QD	248 GVVDNNGNGARVQRVVGSAPAASIGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
Qy Dp	308 VTWQTKSGGTRTGNVTLAEGPPA 330

188

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248 272

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Chaccesion: C70821
Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Combor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Halroyd, S.; Rature 393, 537-544, 1998
Abdure 393, 537-544, 1998
Apture 393, 537-544, 1998
Apture 394, Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: J.464 <CCL>
A; Residues: J.464 <CCL>
A; Cross-references: GB:AL021999; GB:AL123456; NID:93261538; PIDN:CAA17582.1; PID:e1253910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable serine proteinase Rv0983 - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Dec-2002
37 PSTLAIDRESNRPPLPLNPAAWVA---PQVVNISTRLGYNSAVGAGTGIVIDSSGVVLTN
                                                                                                                                                                                                                   NHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPV
                                                                                                               129 VAMGNSGGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVV
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Cantetics:
A;Gene: Rv098
C; Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF
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C;Species: Mycobacterium paratuberculosis
C;Species: Mycobacterium paratuberculosis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Dec-2002
C;Accession: 847170
R;Cameron, R.M.; Stevenson, K.; Inglis, N.F.; Klausen, J.; Sharp, J.M.
submitted to the EMBL Data Library, June 1993
A;Description: Isolation and characterisation of a 34KDa protein of Mycobacterium paratu
A;Reference number: 847170
                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:223092; NID:9505550; PIDN:CAA80638.1; PID:9505551
C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
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;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
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A;Residues: 1-354 <STO>
A;Cross-references: GB:AL450380; NID:g13093863; PIDN:CAC32191.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable secreted serine proteinase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APSGLALDRFADRPLAPIDPSAMVGQVGPQVVNIDTKFGYNNAVGAGTGIVIDPNGVVLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 APPALSODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.5%; Score 1231.5; DB 2; Length 361; Best Local Similarity 73.1%; Pred. No. 1.8e-65; Matches 236; Conservative 38; Mismatches 48; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTWQTKSGGTRTGNVTLAEGPPA 330
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                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-361 <CAM>
                                                                                                                                                                                                                                                                                         Status: preliminary
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domain homology; tryps

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Indels 31; Gaps

Length 464;

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H86930
probable secreted serine proteinase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002
C;Accession: H86930
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq, A;Utter massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUD:21128732; PMID:11234002
A;Accession: H86930
A;Accession: H86930
A;Accession: H86930
A;Accession: Bachiminary
A;Molecule type: DNA
A;Residues: 1-382 <STO>
A;Genetics:
C;Genetics:
A;Genetics:
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A;Genetimily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp TASSULT 6
TASA48

probable serine proteinase (EC 3.4.21.-) MLCB373.28 [similarity] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #text_change 09-Dec-2002
C;Acession: T45448
R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, February 1998
A;Rcference number: Z22967
A;Rcference number: Z22967
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Matches
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Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
                                                                                                                                                                                                                                                                                                                                                    R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                  Serine proteinase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: Ag2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                            -ADALN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Cross-references: GB:BA000019; PIDN:BAB74457.1; PID:g17131851; GSPDB:GN00179
A.Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GGVAVGEPVVAMGNSGGOGGTPRAVPGRVVALG--QTVQASDSLTGAEETLNGLIQFDA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNNVQVGDWAIAVGNPLGFDNT-----VTLGIVSTLKRSSAQVGITDKRLDFIQTDA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVDGILVMRVLPGTPAERAGIRRGDVIVAVDGTPISDGARLQRIVEQAGLNKALKLDLLR 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---VDNNG-----NGARVQRVVGSAPAASLGISTGD 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GAGTGIVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                               207 LSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGV---VDNNGN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 407;
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                                                                                                            ---GARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.7%; Score 368; DB 2;
31.5%; Pred. No. 1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 SAMVAQVGPQVVNINTKLGYNNAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 VHIGPTAFLGLGV-----
                                                                                                                                                                         312
                                                                                                                                                                                                       GDRR---LSLTVOT 386
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                                                                                                                                                                         GHHPGDVISVTWQT
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Matches 110; Conserv
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1-407 <KUR>
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A;Molecule type: DNA
A;Residues: 1-407 <KUF
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 201
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97199
A;Status: preliminary
A;Molecule type: DNA
A;Residues: J-433 «KUR>
A;Residues: ACUR>
A;Cross-references: GB:AE001437; PIDN:AAK80387.1; PID:g15025449; GSPDB:GN00168
A;Cross-references: GB:AE001437; PIDN:AAK80387.1; PID:g15025449; GSPDB:GN00168
A;Cross-references: Clostridium acetobutylicum ATCG224
C;Genetics: CAC2433
C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps
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A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77538
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-452 cKAN>
A;Residues: 1-452 cKAN>
A;Cross-references: EMBL:D90905; GB:AB001339; NID:g1652360; PIDN:BAA17385.1; PID:g1652465;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: http://doi.org/10.1009/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.10099/10.1009/10.10099/10.10099/10.1009/10.10099/10.1009/10.1009/10.10099/10.1009/10.1009/10.1009/10.1009/
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N.Alternate names: protein s1r1204
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Decies: Synechocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Dec-2002
C;Accession: S77538
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA, Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 LIVSQIVKKVSPAVVGVSTKTIVTQNDFDSFFGSSNGNGSSTQEGMGSGIIFNNDGYILT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVA---V 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAFLGLG--VVD------NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GYNNAVGAGTGIVIDPNGVVLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Match 20.8%; Score 353; DB 2; Length 43 Local Similarity 32.0%; Pred. No. 8.2e-14; Indels 101; Conservative 50; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDPSAMVAQVGPQVVNINTKL-
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IDSIKSKHNSGDTVQV 415
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15;

Gaps

82;

20.7%; Score 352; DB 2; Length 452; llarity 30.2%; Pred. No. 9.8e-14; Conservative 59; Mismatches 113; Indels

Best Local Similarity Matches 110; Conserval

H97199
htrA-like serine protease (with PDZ domain) [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Dec-2002 C;Accession: H97199

RESULT 9

Query Match

Db 113 GQDDEGGIAGRGAGGIISKDGYILTNHHVITGASEV-TIKLTDRREFKAKIIGSDEGY 171 Qy 101 DVAVLQIRGAGGIPSAAIGGGVAVGEPVVAMGNSGGOGTPRAVPGRVVALGQIVQAS 158 172 DVALLKI-DAKNLPTVRIGDSSSLKSGGWVVAIGSPFGLDHSVTAGIVSALGRS 224 Qy 159 DSLIGAEETLAGLIQPDAAIQPGDSGGPVVNGIGGVVGMYTAASDNFOLSGG-GGGFAI 216		9y BAPALSQURFADEPALPLDEAWAYQUONINILAGINNAYAGIGITININING STATEMENT OF STAPLAS ON THE STAPLAND STAPLAGIN ON THE STAPLAS ON THE S	SULT 13 2057 rine protein Species: Nos Note: Nostoo
Qy 24 PLDPSAMVAQVGPQVVNINTKLGYNNAV	Qy 274 STGDVITAVDGAPINSATAMADAINGHHPGDVISVTWQTKSGGTRTGNVTLAEG 327 : : : : :	A; Residues: 1-514 <sim> A; Residues: 1-514 <sim> A; Cossidues: 1-514 <sim 1-514="" <sim="" a;="" brio<="" briones:="" cossidues:="" td=""><td>18; Mismatches I INTKLGYNNAV ETVITRKKVGKRRGIPL</td></sim></sim></sim></sim></sim></sim></sim></sim></sim></sim>	18; Mismatches I INTKLGYNNAV ETVITRKKVGKRRGIPL

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19.6%; Score 332; DB 2; L 29.6%; Pred. No. 1.4e-12; live 49; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVVDNNGNGARVQRVVGSAPAASLGIS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 NLSDYYSVLEDKKPDDEVRVT 378
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A; Cross-references: GB: AE002017;
A; Experimental source: strain R1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.6*
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
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C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AB2057
K;Xaneko, T.; Makamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Atle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Accession: AB2057
A;Accession: AB2057
A;Accession: Barbanary
A;Residues: 1-416 <KUR>
A;Residues: 1-416 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73707.1; PID:g17131098; GSPDB:GN00179
C;Genetics:
A;Gene: all2008
C;Genetics:
A;Gene: all2008
C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
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Experimental source: strain Nichols
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Science 281, 375-388, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 VAVGNSEVLQPGEAVIAIGNPLGLNNS--VTSGIISATGR----SGSDIGASDKRVDYLQ 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAIGGGVAV--GEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 FDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGG 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 416;
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19.6%; Score 312; DB 2; Length 398;
Best Local Similarity 32.4%; Pred. No. 1.3e-12;
Matches 104; Conservative 42; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%; Score 333; DB 2; Length 41'
29.0%; Pred. No. 1.2e-12;
ive 63; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 DPS---AMVAQVGPQVVNINTKLGYNNAV------
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Matches 101; Conserv
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C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Species: Dec.1999 #sequence_revision 03-Dec-1999 #text_change 09-Dec-2002
C.Accession: E7535
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, I.M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, J.S.; Smith, H.O.; Venter, J.J.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R.A.Reference number: A75250; MUID:20036896; PMID:10567266
A.Accession: E75357
A.Accession: E75357
A.Scatus: preliminary
A.Molecule rype: DMA.
                                                                             190
                                                                                                                                       137 QGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVG 196
                                                                                                                                                                                                         191 LART--LTVGVVSALARPIQNKGSI-----IRNMIQTDAAINPGNSGGPLLDTQGRMIG 242
                                                                                                                                                                                                                                                                           MNTAASDNFQLSQGGGGAIPIGQAMAIA-----GQIRSG---GGSPTVHIGPTAFLGL 247
                                                                                                                                                                                                                                                                                                                           ---TGDVITAVDGAPIN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GGAPATGTGSGFFVNAQGDIVTNNHVVD 155
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                                                   81 FSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG----VAVGEPVVAMGNSGG
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C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF
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Search completed: June 22, 2004, 17:24:48 Job time : 10.233 secs

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US-09-886-349A-4 1698 1 MHHHHHHAPPALSQDRFADF.....QTKSGGTRTGNVTLAEGPPA 330

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9r9il bacillus su	Q9z4h7 lactobacill							Q52894 rhizobium m	bacillus s	escherichi	P45129 haemophilus	bartonella	chlamydia	P57322 buchnera ap	chlamydia	Q9z6t0 chlamydia p	arabidopsi	rickettsi	bacillus s	arabidopsi	O85291 buchnera ap	005942 rickettsia	O43464 homo sapien	haemoph	Q92743 homo sapien	homo	mus	Ď,	mus	mus muscul	arabidopsi	rhiz
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ALIGNMENTS

28-FEB-20 128-FEB-20 128-FEB-20 Probable Probable Probable Probable STRAIN=1 SEQUENCE STRAIN=1 Noone DE- Noone =1 MEDLINE-	PACSU YUTA BACSU STANDARD; PRT; 458 AA. 909BJI; 035021; 035039; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 42, Last sequence update) 10-007-2003 (Rel. 42, Last annotation update) 10-007-2003 (Rel. 42, Last annotation update) Probable serine procease yvtA (EC 3.4.21). YUTA OR YUTB OR BSU33000. Bactilus subtalis. Bacterria; Firmicutes; Bacillales; Bacillus.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=169; STRAIN=169; Noone D., Howell A., Devine K.M.; Noone D., Howell A., Devine K.M.; Streasino of ykdA, encoding a Bacillus subtilis homologue of HtrA, is heat shock inducible and negatively autoregulated."; J. Bacteriol. 182:1592-1599 (2000). [2] SEQUENCE FROM N.A. MEDLINE=98015415; PubMed=9353931; Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.; Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.; Microbiology 143:3305-3308 (1997). [3] Microbiology 143:3305-3308 (1997).	STRAIN=168; MEDLINE=98044033; PubMed=9384377; MEDLINE=98044033; PubMed=9384377; MOSZER I., Albertini A.M., Alloni G., Azevedo V., Bartero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A. Ehrlich S.D., Emmerson P.T., Fritz C., Fujita M., Fujita Y., Funa S., Gallizzi A., Galleron N., Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Hasono S., Hullo M.F., Itaya M., Jones L., Jorls B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Vobayashi Y., Koetter P., Konligstein G., Krogh S., Kumano M.,	ca K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
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Best Local Similarity
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Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSS0106; PD2; 1. Hydrolase; Heat shock; Transmembrane; Hydrolase; Protease; Serine protease;
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77551045A865ASCD CRC64;
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EMBL, 29341; CAB07968.1; ALT FRAME.
EMBL, 293420; CAB07968.1; ALT_FRAME.
EMBL, 293420; CAB12300.1; ALT_FRAME.
Subtilist; BR014155; yvta,
InterPro; IPR001975; yvta,
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_S1.
Pfam; PF00595; PDZ; 1.
Pfam; PF00595; PDZ; 1.
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92 PC
458 EX
440 PDC
217 CH
298 CH
48717 MW;
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Best Local Similarity 28.4%
Matches 101; Conservative
                                                                                                    Nature 390:249-256(1997).
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458 AA;
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                                            231 VASFGDSSQLRTGEKVIALGNPLGQQFSGTVTQGIISGLNRTIDV-DTTQGTVEM--NVL 287
                                                                                                                                                                                288 QTDAAINPGNSGGPLINASGQVIGIN----SLKVSESGVESLGFAIPSNDVEPIVDQLL 342
                                                                                                                                                                                                                                                                                                                                             343 QNGKV-----DRPFLGVQMIDMSQVPETYQENTLGLFGDQLGKGVYVKEVQANSPAEKA 396
                                                                                                                                                                                                                                                                                   ----GNGARVQRVVGSAPAASL 271
                                                                                                                                       173 QFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGG---QGFAIPIGQAMAIAGQIR
115 SAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLI
                                                                                                                                                                                                                                                                                                                                                                                                                   GISTGDVITAVDGAPINSATAMADAL-NGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
BL68677991C88707 CRC64;
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Molacular characterization of a stress-inducible gene from Lactobacillus helveticus.";
J. Bacteriol. 180:6143-6153(1998).
-I. SURCELLUIAR LOCATION: Wenbrane-bound (Potential).
-I. SURCELLUIAR LOCATION: Wenbrane-bound (Potential).
-I. SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Serine protease do-like htrA (EC 3.4.21..).
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InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001404; Peptidase S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRNRTS; PR00834; PROTEASES2C.
SWART; SW00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
Hydrolase; Serine protease; Transmembrane.
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                                                                                                                                                                                                                                                                           230 SGGGSPTVHIGPTAFLGLGVVDNN---
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MEROPS; S01.273; -.
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413 AA;
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Length 413;

Score 326; DB 1; Pred. No. 8.7e-12;

19.2%; 31.6%;

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                                                                                                 178 TIDLAVISIDAKYVTQTAQFGDSKHLBAGQTVIAVGSPLGSBYASTVTQGIISAPARTIS 237
                                                                                                                                                                           215 AIPIGQAMAIAGQIRSGG--GSPTVHIGPTAFLG------LGVVDNNGNGARVQRVVG 264
                                                                                                                                                                                                   292 AIPSNEVVTIVNELVKKGKITRPQLGVRVIALQGIPEGYRSRLKIKSNLKNGIYIAFVSR 351
                         98
                                       119 SSKNGKLETYSEGSGVVYMKSNGKGYIVTNNHVISGSDAVQVL-LANGKTVNAKVVGKDS
                                                                        99 TQDVAVLQLRGAGGLPSAAIGGG---VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQ
                                                                                                                                         238 TS---SGNQQT---VIQTDAAINPGNSGGALVNSAGQVIGINSMKLAQSSDGTSVEGMAF
                                                                                                                          157 ASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNT--AASDNFQLSQGGQGF
                        NTKLGYNNAVGAGTGIVI - - - DPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-2104935; PubMed=11206551;

MEDLINE-2104935; PubMed=11206551;

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Shao Y., Miller L., Rotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli, and
Escherichia coli, ol57.H7.
Escherichia coli 0157.H7.
Escherichia coli 0157.H7.
Enterobacteriaceae; Escherichia.
MCBI_TaxID=562, 83334;
24;
                                                                                                                                                                                                                           265 SAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVT 309
                                                                                                                                                                                                                                           : ||: || :||| || :: || 352 NGSAANAGIKSGDVITKVDGKKVEDVASLHSILYSHKVGDTVAVT 396
Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
STRAIN=K12 / W3110;
SUBMILTED (O.Q., GO) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Protease degS precursor (EC 3.4.21...)
DEGS OR HHOB OR HTRH OR B3235 OR Z4594 OR ECS4108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waller P.R., Sauer R.T.;
"Characterization of degQ and degS,
homeograp of the DegP protease.",
homeograp of the Pigg Pactease.",
homeograp of the Pigg Pactease."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=K12 / W3110;
MEDLINE=96165272; PubMed=8576051;
50;
Conservative
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STRAIN-0157:H7 / RIMD 0509952;
MDELINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli Ol57:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGA-------GTGIVID
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MEDLINE=88105815; PubMed=3322223;
Vogel R.F., Entian K.-D., Mecke D.;
"Cloning and sequence of the mdn structural gene of Escherichia colicoding for malate dehydrogenase.";
Arch. Microbiol. 149:36-42(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bazan J.F., Fletterick R.J.;
"Structural and catalytic models of trypsin-like viral proteases.";
Semin. Virol. 1:311-322(1990).
--: SUBCELLULAR LOCATION: Periplasmic (Potential).
--: SIMILARITY: Belongs to peptidase family S2C.
--: SIMILARITY: Contains 1 PDZ/DHR domain.
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PROTEASE DEGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_SI.
InterPro; IPR001940; Peptidase_SIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1032495; AAC44006.1; -..., V18997; AAA58037.1; -..., ABOUGLO; AAC76267.1; -..., ABOUGS51; AAC8303.1; -..., APO02564; BAB37531.1; -..., M24777; -:, NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SWART; SM0228; PDZ; 1.
PROSITE; PS50166; PDZ; 1.
Hydrolase; Serine protease; Per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37581 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.8%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U15661; AAC43993.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M24777; -; NOT ANNO
PIR; D91142; D91142.
PIR; JG6052; JG6052.
MEROPS; S01.275; -
EcoGene; EG11652; hhob.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326
326
126
201
253
307
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126
201
253
307
355 AA;
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InterPro; IPR001940; Peptidase_S1C
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                                                                                                                                                       ACT SITE
ACT SITE
ACT SITE
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                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                        DOMAIN
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DEGP_BRUME
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                                                             172
                                                                                                                            --IG 219
                                145
                                                                                   191 QTDASINHGNSGGALVNSLGELMGINTLSFDKSNDGETPEGIGFAIPFQLATKIMDKLIR 250
61 PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolotin A., Wincker D., Manager S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis LIL403."
Genome Res. 11:731-753(2001)
-!- FUNCTION: DEGRADES ABNORMAL EXPORTED PROTEINS. NEEDED FOR THE PRO-PEPTIDE PROCESSING OF A NATURAL PRO-PROTEIN AND FOR THE PRO-PATIVE PROTEIN. RESPONSIBLE FOR THE HOUSEKEEPING OF EXPORTED
                      GVA---VGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV-QASDSLTGAEETLN----GLI
                                                                                                                                                                                                                        251 DGRVİRGYİGIĞGR----EİAPLHAQĞGĞI--DQLQĞIVVNEVSPDGPAANAĞİQVNDLİ
                                                                                                                                                                                         QAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poquet I., Saint V., Seznec E., Simoes N., Bolotin A., Gruss A., "HtrA is the unique surface housekeeping protease in Lactococcus lactis and is required for natural protein processing."; Mol. Microbiol. 35:1042-1051(2000).
                                                                                                                                                                                                                                                        280 TAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGP 328
                                                                                                                                                                                                                                                                                       305 ISVDNKPAISALETMDQVAEIRPGSVIPVV-VMRDDKQLTLQVTIQEYP 352
                                                                                                                            OFDAAIQPGDSGGPVVNGLGQVVGMNTAASD--NFQLSQGGQGFAIP----
                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2011 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine protease do-like htrA (EC 3.4.21.-) (HtrALI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLUIAR LOCATION: Membrane-bound (Probable).
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                       408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=1L1403;
MEDLINE=20177820; PubMed=10712686;
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006442; AAK06234.1; -. PIR; H86891; H86891.
MEROPS; S01.273; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF155705; AAF61294.1; -.
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTRA OR LL2136.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 NA-IQTDAAINPGNSGGALINIEGQVIGITQSKITTTEDGSTSVEGLGFAIPSNDVVNII 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GQIRSGGGSPTVHIGPTAFLGLGVVD-----NNGN------GARVQRVVGSAPAA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 NKLEADG-----KİSRPA-LGIRMYDLSQLSTNDSSQLKLPSSVTGGVVVXSVQSGLPAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAILE-16M / ATCC 23456 / Biotype 1;
MEDLINE-20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 SLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 GTGIVIDPNG---VVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:: :| |||||||:: | |||||:: | ||||:: ||||:: ||||:: ||||:: |||:: |||:: |||:: ||:: |||:: ||:: |||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 HVKDVATFADSSKLTIGEPALAVGSPLGSQFANTATEGILSATSRQVTLTQE-NGQTTNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 -AGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA---ASDNFQLSQGGQGFAIPIGQAMAIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                             Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8YG32;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HTRA OR BMEI1330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.6%; Score 315; DB 1; Length 40 llarity 31.6%; Pred. No. 3.6e-11; Conservative 51; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               581B90B55A7DF851 CRC64;
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--- SUBCELLULAR LOCATION: Periplasmic (Potential).
--- SIMILARITY: Belongs to peptidase family S2C.
--- SIMILARITY: Contains 2 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   513 AA.
                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                  CATALYTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41648 MW;
Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
                                                                                                                                                              PROSITE: PS50106; PDZ; 1.
Hydrolase; Serine protease;
TRANSMEM 6 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                 302
127
157
157
239
408 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Heidelberg J.F.,

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                                                                                                                                              185 VLKINA----PKRKFVYVAFGDDNKVRVGDWVVAVGNPFGLGGT--VTSGIVSARGRDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 AG------PYDDFIQIDAAVNKGNSGGPAFDLSGEVIGINTAI---FSPSGGSVGIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIPIGOAMAIAGOIRSGG----GSPTVHIGP----TAFLGLGVVDNNGNGARVQRVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 VLQLRGAGGLPS----AAIG--GGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 ASDSLIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQG--F
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MEDLINE=95165990; PubMed=7861951;
Tatum F.M., Cheville N.F., Morfitt D.;
Cloning, characterization and construction of htrA and htrA-like mutants of Brucella abortus and their survival in BALB/c mice.";
Microb. Pathog. 17:23-36(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
CATALYTIC.
PDZ 1.
PDZ 2.
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.1%; Score 307.5; DB 1; Length 513; 34.3%; Pred. No. 1.2e-10; ive 36; Mismatches 118; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERINE PROTEASE DO-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Periplasmic; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEICEF1959472806 CRC64;
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FINEL, AE014368; AAN29540.1; -...
FIR, BRO661; 140060.
TIGR, BRO611; -...
InterPro; IRR001903; Cys_Car_trypsin.
InterPro; IRR0019478; PDZ.
InterPro; IRR001944; Peptidase_S1C.
Pfam, PR00595; PDZ; 2...
Pfam, PR0089; trypsin, 1...
SMART; SM00228; PDZ; 2...
PRO81TE; PS50106; PDZ; 2...
PROSITE; PS50106; PDZ; 2...
PROSITE; PS50106; PDZ; 2...
PROSITE; PS50106; PDZ; 2...
PROSITE; PS50106; PDZ; 2...
PROSITE; PS50106; PDZ; 2...
PROSITE; PS50106; PDZ; 2...
PROSITE; PS50106; PDZ; 2...
PROSITE; PS50106; PDZ; 2...
PROSITE; PS50106; PDZ; 2...
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513 AA;
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     not removed. Usage by and for commercial reement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||::
|185 VLKINA----PKRKFVYVAFGDDNKVRVGDWVVAVGNPFGLGGT--VTSGIVSARGRDIG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 ASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQG--F 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 AIPIGQAMAIAGQIRSGG----GSPTVHIGP-----TAFLGLGVVDNNGNGARVQRVVGS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIPSSTÁKQVVDÓLIKKGSVERGWIGVOJOPVTKDIAASLGLA----EEKGÁLVASPQDD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 APAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 GYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSV--GSGQTYGVDVVGYDRTQDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE
CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDZ 1.
PDZ 2.
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
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                                                                                                      PIR, ADD418, 1. ADD4003; Cys. Br. Lrypsin.

DR InterPro; IPR001478; PDZ.

DR InterPro; IPR001478; PDZ.

R InterPro; IPR00140; Peptidase_S1.

R InterPro; IPR00140; Peptidase_S1.

Pfam; PF00595; PDZ; 2.

Pfam; PR00039; trypsin; 1.

PRNTTS; PR00814; PROTEASESC.

R SMART; SM00228; PDZ; 2.

R PROSITE; PS50106; PDZ; 2.

R Advolase; Serine protease; Periplasmic; Repeat; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; Signal; 
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Brucellaceae; Brucella.
NCBI_TaxID=29461, 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEGP_BRUSU
DEGP_BRUSU
DEGP_BRUSU
AC 44597,
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FRE-2003 (Rel. 41, Last amnotation update)
DT 28-FRE-2003 (Rel. 41, Last amnotation update)
DE Probable serine protease do-like precursor (EC 3.4.21.-).
DE Brucella suis, and
OS Brucella abortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C472FEF99DFC6268 CRC64;
modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   25 PC
513 PR
299 CA
391 PD
500 PD
152 CH
257 CH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
300
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513 AA;
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Matches 104;
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DOMAIN
DOMAIN
DOMAIN
ACT SITE
ACT SITE
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103

Gaps

45;

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MEDLINE=91251770; PubMed=1645840;
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                                                                                                                                                                                                                                                                         78 DDLPDQPAQPFE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Salmonella
                                                                                                                                                                     47205 MW;
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                       214 ;
455 AA;
                                                                                                                                                                                                           Similarity
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                                                                                          28
258
355
109
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                                                                                                                                                                                                          Sest Local Simi
Matches 101;
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P26982;
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                                                                                                                 DOMAIN
ACT SITE
ACT SITE
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                                                                                          CHAIN
DOMAIN
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  288 AIPSSTAKQVVDQLIKKGSVERGWIGVQIQPVTKDIAASLGLA----EEKGAIVASPQDD 343
                           266 APAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLA 325
                                                   344 GPAAKAGIKAGDVITAVNGETVQDPRDLARKVANIAPGEKAALTVWRKNKAEEI-NVTIA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=KI2 / MGIG55,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                               Waller P.R., Sauer R.T.;
Characterization of degQ and degS, Escherichia coli genes encoding
homologs of the DegP protease.";
J. Bacteriol. 178:1146-1153(1996).
                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- FUNCTION: PROTEASE WITH A SHARED SPECIFICITY WITH DEGP/DEGP.
-!- SUBCELJUIAR LOCATION: Periplasmic.
-!- SUBCELJUIAR: Belongs to peptidase family S2C.
-!- SIMILARITY: Belongs to peptidase family.
                                                                                                                                                                                                                                                                                                                                        STRAIN=K12 / W3110;
Bass S., Gu Q., Goddard A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proctase degQ precursor (EC 3.4.21.-).
DEGQ OR HHOA OR B3234.
                                                                                                                                                                      455 AA.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 28-32 STRAIN=K12 / W3110;
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SWISS-2DPAGE; P39099; COLI.
ECOGRACA: P39099; COLI.
InterPro; IPR009003; Cys. Ser_trypsin.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1.
Pfam; PP00595; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96165272; PubMed=8576051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U15661; AAC43992.1; -. EMBL; U32495; AAC44005.1; -. EMBL; U18997; AAA58036.1; -.
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PIR; JC6051; JC6051.
MEROPS; S01.274; -.
                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                               326 EGP 328
                                                                                                                                                                                                                                                              Sscherichia coli
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GAIDINAFSVGSGQIYGVDVVGYDRIQDVAVLQLRGAGGLPSAAIGGG--VAVGEPVVAM 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 QAQKI-SIQLNDGREFDAKLIGSDDQSDIALLQIQNPSKLTQIAIADSDKLRVGDFAVAV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 GNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAE-ETLNGLIQFDAAIQPGDSGGPVVNG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LLGIKGTEMSADIAKAFNLDVQRGAFVSEVLPGSGSAKAGVKAGDIITSLNGKPLNS 324
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STRIN=LI2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; Bubmed=11677609;
MEDLINE=21534948; Bubmed=11677609;
MCCIelland M., SanFeubmed K.B., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 DRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPN-GVVLTNNHVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 GNPFGLGQT--ATSGIVSALGR-----SGINLEGLENFIQTDASINRGNSGGALLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 PTAFLGLGVVDNNGN------GARVQRVVGSAPAASLGISTGDVITAVDGAPINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.0%; Score 305.5; DB 1; Length 455; 29.7%; Pred. No. 1.4e-10; ive 49; Mismatches 101; Indels 89
                                                                                                                                                                                                                                                                             CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Periplasmic; Repeat; Signal;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                             6A090F93AC021C83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 ATAMADALNGHHPGDVISVTWQTKSGGTRTG-----NVTL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 FAELRSRIATTEPGT-----KVKLGLLRNGKPLEVEVTL 358
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01-AUG-1992 (Rel. 23, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Protease do precursor (EC 3.4.21.-).
BGP OR HTRA OR PTD OR STM0209.
Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475 AA
                                                                                                                                                                         PROTEASE DEGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSGVIIDAAKGYVVTNNHVVDNASVIKV-QLSDGRKFDAKVVGKDPRSDIALIQIQNPKN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGN-------GARVQRVVGSAPA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGIVID-PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPSAAIGGGVA--VGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAE-ETLN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 GLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA--ASDNFQLSQGGQGFAIP-----IGQA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
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Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Heat shock; Periplasmic; Repeat; Signal;
Complete proteome.
                                                                                            LTZ.";
Nature 413:852-856(2001).
-!- FUNCTION: SERINE PROTEASE THAT IS REQUIRED AT HIGH TEMPERATURE.
-!- FUNCTION: SERINE PROTEASE THAT IS REQUIRED AT HIGH TEMPERATURE.
SPECIFICITY WITH HHOA/DEGQ.
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- INDUCTION: By heat shock.
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 2 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
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CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
86E685BF3C1A289F CRC64;
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PROTEASE DO.
PDZ 1.
PDZ 2.
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PURD, AE008704; AAL19173.1; --
PUR, S1337; S15337.
MEROPS; S01.273; --
Stydene; SG10773; degp.
InterPro; IPR001773; degp.
InterPro; IPR00178; DDZ.
InterPro; IPR00154; Peptidase_S1.
InterPro; IPR00154; Peptidase_S1.
Pfam; PF0069; trypsin; 1.
Pfam; PF0069; trypsin; 1.
PRINT; SM00228; PDZ; 2.
SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
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les 96, Conservative
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475
372
467
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281
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475 AA;
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                         STETETETE SUBSTRANCE SOURCE SOURCE SUBSTRANCE SOURCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SUBSTRANCE SU
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PROBABLE SERINE PROTEASE DO-LIKE.
CATALYTIC.
PDZ 1.
PDZ 2.
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
LL -> PV (LIN REP. 1).
LL -> PV (LIN REP. 1).
ESTANVDAYSPAVVSYNQARENSDESNETEDFOGRGF
EDLFEDHPLRFFFREFAPRENDRADEWEDREPREGERLRP
RAGGSGFFIERDEGYLVATHVSDGSA -> AVSPWNSTPF
RRRSSPSACHHVNASATWRATSPSISAAAGSRTCRKTIRCG
VSSANSLRVKMTVPIVGATAAVRAKVYSVRGRKAPASSSP
                                                                                                                                                                                                             STEAIN=1021;
MEDLINE=96146524; PubMed=8550509;
Glazebrock J., Ichige A., Walker G.C.;
"Genetic analysis of Rhizobium meliloti bacA-phoA fusion results in
identification of degP: two loci required for symbiosis are closely
linked to degP.";
                                                                                                                                                                                                                                                                                                                                                                       Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Bedker A., Boukry M., Cadieu E., Dreano S., Gloux S., Poil T., Coffeeu A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).

-: SIMILARITY: Belongs to peptidase family S2C.

-: SIMILARITY: Contains 2 PDZ/DHR domains.
                             30-May-2000 (Rel. 39, Created)
30-May-2000 (Rel. 39, Last sequence update)
30-May-2003 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP1 OR DEGP OR RO1021 OR SWC02365.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiane Rhizobiane Sinorhizobium/Bnsifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Periplasmic; Repeat; Signal;
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504
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InterPro; IPR001478; PDZ.
InterPro; IPR001244; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 2.
Pfam; PR008094; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U31512; AAC43669.1; ALT_INIT.
EMBL; ALS91785; CAC45593.1; -.
MEROPS; S01.273; -.
                                                                                                                                                                                                                                                                                                               Bacteriol. 178:745-752(1996).
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Hydrolase; Serine protease;
 STANDARD;
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Complete proteome.
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                                                                                                                                                                                                                                          54 GIGIVIDPNGVVLTNNHVIAGATDINAFSV -- GSGQTYGVDVVGYDRTQDVAVLQL--RG 109
                                                                                                                                                                                                                                                                                                      110 AGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSITGAEETLN 169
                                                                                                                                                                                                                                                                                                                                                                                                      170 GLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQG--FAIPIGQAMAIAGQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 IRSGG----GSPTVHIGPTA----FLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 LIKDGTVSRGWLGVQIQPVTKDIAESLGL----SEANGALVVEPQAGSPGEKAGIKNGDV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Barwado V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S., Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Benizot F., Derhort C., Errington J., Pabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Ferna S., Galizzi A., Galleron N., Fritz C., Fujita M., Fujita Y., Ferna S., Galizzi A., Galleron N., Guiseppi G., Guy B.J., Haga K., Hatch J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Kasahara Y., Klearr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Amellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parkoon E., Pujic P., Purnelle D., Porrettelle D., Porsecott A.M., Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y., Rieger M., Rivolta C., Roche B., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Socifone F.,
                      KSADDVLKVINNAKKDGRSKALFQIEAQEGSRFVALPITQG
                                                                                                                                                                                                                                                                                                                                                                                                                                 181 KFTYVSFADDEKVRVGDWVVAVGNPFGLGGTVTA--GIISARGRDIGSG-----PYD
                                                                                                              ; Score 296; DB 1; Length 504;
; Pred. No. 5.2e-10;
39; Mismatches 116; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the Bacillus subtilis genome between xlyA and ykoR.", (NoV-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 VTALNGEPVKDPRDLARRVAALRPGSTAEVTLW--RSGKSETVNLEIGTLP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                             D7E82BB9981EA23C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable serine protease do-like htrA (EC 3.4.21.-).
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                                                                   53035 MW;
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                                                                                                                                                              Conservative
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                                                                 504 AA;
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HTRA OR BSU12900
                      464
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034358;
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                      CONFLICT
                                                                 SEQUENCE
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"A novel two-component regulatory system in Bacillus subtilis for the survival of severe secretion stress.";

Mol. Microbiol. 41:1159-1172(2001)

Mol. Microbiol. 41:1159-1172(2001)

Mol. Microbiol. 41:1159-1172(2001)

Mol. Microbiol. 41:1159-1172(2001)

G. FUNCTION: May be involved in processing, maturation, or secretion of extracellular enzymes.

G. FUNCTION: Membrane-bound (Potential)

G. INDUCTION: Transcription is css dependent. Induced by heat shock during exponential growth and by heterologous amylases at the transition phase of the growth cycle. Negatively regulates its own expression during exponential growth and during heat shock.

G. INDUCTION: Inactivation results in compensating overexpression of ytvA, especially during stress conditions.

G. INTIARITY: Belongs to peptidase family S2C.

G. INTIARITY: Contains I PDZ/DHR domain.
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Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorckin A., Tacconi E., Takagi T., Tarkahashi H., Takemaru K., Takakeroli M., Tamakseli A., Tanaka T., Terpetra P., Tognoni A., Tosto V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Noone D., Howell A., Devine K.M.;
"Expression of ykdA; encoding a Bacillus subtilis homologue of HtrA, is heat shock inducible and negatively autoregulated.";
J. Bacteriol. 182:1592-1599(2000).
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"YkdA and YvtA, HtrA-like serine proteases in Bacillus subtilis,
engage in negative autoregulation and reciprocal cross-regulation of
ykdA and yvtA gene expression ";
J. Bacteriol. 183:654-663(2001).
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Vitikainen M., Sarvas M., Pragai Z., Bron S., van Dijl J.M.,
Kontinen V.P.,
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InterPro; IPR0014078 PD2.
InterPro; IPR001244; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF000895; PD2; 1.
Pfam; PF00089; trypsin; 1.
PRINITS; PR000834; PROTEASES2C.
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MEDLINE=20158875; PubMed=10692364;
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MEDLINE=21439741; PubMed=11555295;
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STRAIN=K12 / MG1655
 SDMVEDLSPAIVGITNLQAQSNSSLFGSSSSDSSEDTESGSGSGVIFKKENGKAYIITNN 178
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                                                                                                                                                                                                                   179 HVVEGASSLKV-SLYDGTEVTAKLVGSDSLTDLAVLQISDDHVTKVANFGDSSDLRTGET 237
                                                                                                                                                                                                                                      VVAMGNSGGOGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                                                                                                                                                                                                                                        238 VIAIGDPLGKDLSRTVTQGIVSGVDRTVSMS----TSAGETSINVIQTDAAINPGNSGGPL 294
                                                                                                                                                                                                                                                                               188 VNGLGQVVGMNT--AASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFL 245
                                                                                                                                                                                                                                                                                                                       246 GLGVVDNN------GNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATA 292
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                                                                                                                                                                                                                                                                                                  295 LNTDGKIVGINSMKISEDDVE----GIGFAIPSNDVKPIAEELLSKGQIERPYIG-VSML
                                                                                                                                                        ----VGAGTGIVI-DPNG--VVLTNN
                                                                                                                                                                                                70 HVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQIRGAGGLPSAAIG--GGVAVGEP
                                                                                                                                     Gaps
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STRALN=K12 / Wallo;
STRALN=K12 / Wallo;
MEDLINE=S261430; PubMed=8202364;
Fujita N., Mori H., Yura T., Ishihama A.;
Fujita N., Mori H., Yura T., Ishihama A.;
Fujita N., Mori H., Yura T., Ishihama A.;
Fujita N., Mori H., Yura T., Ishihama A.;
Fujita N., Mori H., Yura T., Ishihama A.;
Fujita N., Mori H., Yura T., Ishihama A.;
Nucleic Acids Res. 22:1637-1639(1994).
                                POLY-SER.
POLY-SER.
POLY-SER.
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
W, E12807A9018EE414 CRC64;
                                                                                                                                     45;
                                                                                                                  DB 1; Length 449;
                                                                                                                                    52; Mismatches 127; Indels
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL)
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P09376; P15724;
D1-MAR-1998 (Rel. 10, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protease do precursor (EC 3.4.21.-).
DEGP OR HTRA OR PID OR B0161 OR 20173 OR ECS0165.
Escherichia coli, and
Escherichia coli 0157:H7.
                                                                                                                  Score 294.5; DB 1
Pred. No. 5.6e-10;
                                                                                                                                                          28 SAMVAQVGPQVVNINTKLGYNNA-----
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MEDLINE-89057448; PubMed-3057437;
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NCBI_TaxID=562, 83334;
                                                                                             47713 MW;
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29.3%;
                                                                                                                                        93; Conservative
     449 AA;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-015:11, / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurckawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara M., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kuhate genome sequence of enterohemorrhagic Escherichia coli 0157.H7 and genomic comparison with a laboratory strain K-12.";
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Lipinska B., Zylicz M., Georgopoulos C.;
"The HIAN (Depl) protein, essential for Escherichia coli survival at
high temperatures, is an endopeptidase.";
J. Bacteriol. 172:1791-1797(1990).
MEDIJINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
STRAIN=0157:H7 / EDL933 / ATCC 700927;
STRAIN=21074935;
Perna N.T., Plunkett G. III, Bexlin V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Bexlin V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkparifer H.A.,
Grosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grocbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Machor R.A., Blattner F.R.)
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
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MEDLINE-90207273; PubMed=2157212;
MEDLINE-90207273; PubMed=2157212;
Murgler S.M., Richardson C.C.;
"Structure and regulation of the gene for dGTP triphosphohydrolase from Escherichia coli.";
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E
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MEDLINE=98263247; PubMed=9600841;
Wilkins M.R., Gasteiger E., Tonella L., Ou K., Tyler M.,
Sanchez J.-C., Gooley A.A., Walsh B.J., Bairoch A., Appel R.D.,
Williams K.L., Hochstrasser D.F.,
"Protein identification with N and C-terminal sequence tags in
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Bairoch A., Appel R.D.,
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Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=90323597; PubMed=2165018;
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MEDLINE=91222240; PubMed=2025286;
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EMBL; U32805; AAC22906.1; -. PIR; A64113; A64113.
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P45129;
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                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstarion the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                  A -> R (IN REF. 1, 7 AND 8).
E -> Q (IN REF. 7).
A -> G (IN REF. 1).
STILLIMQ -> RHLPVNAVISLNPFLKTGRGSFYNL (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Heat shock; Periplasmic; Repeat; Signal;
Seol J.H., Woo S.K., Jung E.M., Yoo S.J., Lee C.S., Kim K.J., Tanaka K., Ichihara A., Ha D.B., Chung C.H.; Procrease Do is essential for survival of Escherichia coli at high temperatures: is identity with the htra gene product."; Biochem. Biophys. Res. Commun. 176:730-736(1991).
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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
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InterPro; IPR001478; PDZ_
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 2.
Pfam; PF000894; Irrypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SWART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                    EMBL; M36536; AAA23994.1; -
EMBL; D26562; BAB9697.1; -
EMBL; D26562; BAB96738.1; -
EMBL; AE000125; AAC73272.1; -
EMBL; AE005192; AAC73272.1; -
EMBL; AE005192; AAG8465.1; -
EMBL; AP002550; BAB33868.1; -
EMBL; AP002550; EMB33868.1; -
EMBL; M31772; AAA23717.1; -
EMBL; M31772; AAA23680.1; -
FIR; E85500; E85500.
FIR; E85500; E85500.
FIR; S45229; S45229.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   54 GTGIVIDPN-GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221
                                                                                                                                                                                                                                                                                                              114 GSGVIIDADKGYVVTNNHVVDNATVIKV-QLSDGRKFDAKNVGKDPRSDIALIQIQNPKN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                          223 NFIQTDAAINRGNSGGALVNLNGELIGINTAILAPDGGNI---GIGFAIPSNMVKNLTSQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 MAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGN--------GARVQRVVGSAPA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 MVEYGQVKRG------ELGIMGTELNSELAKAMKVDAQRGAFVSQVLPNSSA 325
                                                                                                                                                                                                                                                                                                                                                                                            LPS--AAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAE-ETLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 GLIQFDAAIQPGDSGGPVVNGLGQVVGNNTA--ASDNFQLSQGGGGAIP-----IGQA
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-!- SUBCELLUIAR LOCATION: Periplasmic (Potential).
-!- SIMILARITY: SEEMS TO BE A INTERMEDIATE FORMS BETWEEN E.COLI HTRA
(PROTEASE DO) AND HODA.
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MEDLINE=95350630; PubMed=7542800;

Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb., Tomb., C.A., Gocayne J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                          17.3%; Score 294.5; DB 1; Length 474; 33.6%; Pred. No. 5.9e-10; ive 42; Mismatches 81; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NOBL_TaxID=727;
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Frobable periplasmic serine protease do/hhoA-like precursor (EC 3.4.21.-)
474 AA; 49354 MW; 5482E596F74B6D5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to peptidase family S2C.
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                                                                                                                                                             Conservative
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                                                                                                               Local Similarity
les 89; Conserv
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-!- SIMILARITY: Contains 2 PDZ/DHR domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 NFRGLGSGVIINASKGYVLTNNHVIDGADKITV-QLQDGREFKAKLVGKDEQSDIALVQL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 RGAGGLPSA--AIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-TLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQG--FAIPIGQAM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 SGTYENYIQTDAAVNRGNSGGALVNLNGELIGINTAI---ISPSGGNAGIAFAIPSNQAS 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 NLVQQILEFGQVRRG------LLGIKGGELNADLAKAFNVSAQQGAFVSEVLPK 312
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STRAINAATCC 49882 / Houston 1;
MEDLINE=94299828; bubMed=8027347;
MEDLINE=94299828; bubMed=8027347;
Anderson B., Sims K., Regenery R., Robinson L., Schmidt M.J.,
Goral S., Hager C., Edwards K.;
"Detection of Rochalinaea henselae DNA in specimens from cat scratch
disease patients by PCR.";
J. Clin. Microbiol. 32:942-948(1994).
J. Clin. Microbiol. 32:942-948(1994).
-:- SUBCELLULAR LOCATION: Periplasmic (Potential).
-:- SIMILARITY: Belongs to peptidase family S2C.
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable periplasmic serine protease DO-like precursor (EC 3.4.21.-)
(Antigen herA).

Bartonella henselae (Rochalimaea henselae)
Bartonella cecea; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteobacteria; Alphaproteob
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PDZ 1.
PDZ 2.
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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
ED050A00047B5851 CRC64;
             TIGR: H11259; -...
IIGETPRO; IPR001903; Cys_Ser_trypsin.
InterPro; IPR001254; PbZ-
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 2.
Pfam; PF00595; PDZ; 2.
R Pfam; PF00228; PDZ; 2.
R PR05ITE; PS50106; PDZ; 2.
R PR05ITE; PS50106; PDZ; 2.
R Hydrolase; Serine protease; Periplasmic; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 APAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | |: ||:||:|| |: | |:| | 313 SABEKAĞLKAĞDIITAMNGQKİSSFABIRAKİATTGAĞKEISLTY 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.0%; Pred. No. 8e-10; ive 42; Mismatches 101; Indels
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nes 94; Conservative
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458
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226
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466
MEROPS; S01.274; -.
TIGR; HI1259; -.
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466 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 TA--GIVSARGR----DIGTG---VYDDFIQIDAAVNRGNSGGPTFDLNGKVVGVNTAI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 GSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG--GGVAVGEPVVAMGNSGGQGGTP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 RAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 SDNFQLSQGGQG--FAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 ---FSPSGGNVGIAFAIPAATANEVVQQL-------IEKGLVQRGWLGVQI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 QRV-----VG-----SAPAASLGISTGDVITAVDGAPINSATAMADALNG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 -----YN----YN------NAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
PROBABLE PERIPLASMIC SERINE PROTEASE DO-
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P18564; 084830;
01-NOV-1990 (Rel. 39, Last sequence update)
30-MMY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-) (59 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 115;
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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PP00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00894; PROTEASES2C.
SMART; SM00229; PDZ; 2.
PROSTTE; PS20166; PDZ; 2.
Hydrolase; Serine protease; Periplasmic; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6CD9F4743282AF9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .4e-09;
es 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 HHPGDVISV-TWQTKSGGTRTGNVTLAEGP 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.0%; Score 288.5;
                                                                                                                                                                                                                                                                             Interpro; IPR009003; Cys_Ser_trypsin.
Interpro; IPR001478; PDZ.
Interpro; IPR001254; Peptidase_S1.
Interpro; IPR001940; Peptidase_S1C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54114 MW;
                                                                                                                                                                                                                         EMBL; L20127; AAA97430.1; -.
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419
143
173
247
503 AA;
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                                                                                                                                                                                                                                                           MEROPS; S01.273; -
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RESULT 15
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                                                                                                                                                                                       STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                  Kahane S., Weinstein Y., Sarov I.; "Cloning, characterization and sequence of a novel 59-kDa protein of Chlamydia trachomatis.";
                         Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
86A5E31EB84A38BA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.0%; Score 288; DB 1; Length 497 llarity 32.5%; Pred. No. 1.4e-09; Conservative 45; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Repeat; Signal; Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; H71465; H71465.
PHCI-2DPAGE; P18584; ...
InterPro; IPR009003; Cys. Ser_trypsin.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase SI.
InterPro; IPR008256; Peptidase_SIB_V8.
InterPro; IPR001940; Peptidase_SIG
                                                                (1)
SEQUENCE FROM N.A.
STRAIN=SEROVAR L2;
MEDLINE=90337348; PubMed=2279836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE001355; AAC68420.1; -.
EMBL; M31119; AAA23116.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASESC.
SMART; SM00228; PDZ; 2.
    (SK59).
  immunogenic protein)
DEGP OR HTRA OR CT823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143
173
247
497 AA;
                                                                                                                                                    Gene 90:61-67(1990)
                                                                                                                                                                           SEQUENCE FROM N.A.
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Les 95; Conserv
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SIGNAL 1
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DOMAIN
DOMAIN
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Matches
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54 GTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGL 113

40; Gaps

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    167
                                                                                                                  288
                                                                                                                                                  226 GOIRSGGGSPTVHIGPTAFLGLGVVDN------NGNGARVQRVVGSAPAASLGISTG 276
                                                                                                                                                                                     289 DÓLISDGOVTRGFLGVT----LÓPIDSELATCYKLEKVYGALVTDVVKGSPAEKAGLROE 344
114 PSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQT----VQASDSLTGAEET
                      185 PFLTFGNSDQLQIGDWAIAIGNPFGLQAT--VTVGVISAKGRNQLHIVDFED-----
                                                                        168 INGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQG--GQGFAIPIGQAMAIA
                                                                                                            235 ---FIQTDAAINPGNSGGPLLNINGOVIGVNTAIVSG---SGGYIGIGFAIPSLMAKRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
                                                                                                                                                                                                                           277 DVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGP 328
                                                                                                                                                                                                                                                 ||| | : | : | : | : | : | 345 DVIVAYNGKEVESLSALRNAISLAMPGTRV-VLKIVREGKTIEIPVTVTQIP 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20445173; PubMed=10993077; Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS."; Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Signal; Complete proteome.
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PROBABLE SERINE PROTEASE DO-LIKE
CATALYTIC.
PDZ 1.
PDZ 2.
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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR BU228.
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868E8732CAC50629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to peptidase family S2C.-!- SIMILARITY: Contains 2 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ_
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfan; PR00595; PDZ; 2.
Pfan; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP001118; BAB12943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
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Hydrolase; Serine protease;
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238
27
87
478 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=TOKYO 1998;
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Query Match
Best Local Similarity 30.9%; Pred. No. 1.6e-09;
Matches 99; Conservative 50; Mismatches 109; Indels 40; Gaps 12;
                                                                                                                                                      113 LPSAAI--GGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAE-FTLN 169
                                                                                         170 GLIQEDAAIOPGDSGGPVVNGLGQVVGMJTA--ASDNFQLSQGGGFAIPIGQAMAIAGQ 227
                                                                                                                             225 NFIQTDAAINRGNSGGALVNLKGELIGINTAILAPDGGNI---CIGFAIFCNMVKNLTAQ 281
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1698
1 MHHHHHHAPPALSQDRFADF......QTKSGGTRTGNVTLAEGPPA 330
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	007175 mycobacteri	Q7u2s9 mycobacteri	Q50320 mycobacteri	Q9ccy9 mycobacteri	Q8vka4 mycobacteri	Q7u0x2 mycobacteri	O53896 mycobacteri	Q9cd67 mycobacteri	Q9z5g6 mycobacteri	Q93j30 streptomyce	Q8dg87 synechococc	Q9fbk9 streptomyce	Q82fm9 streptomyce	Q82il8 streptomyce	Q8fr17 corynebacte	P72780 synechocyst	
COMMERCE	Οï	007175	Q7U2S9	Q50320	Q9CCY9	Q8VKA4	Q7U0X2	053896	Q9CD67	Q925G6	083430	Q8DG87	Q9FBK9	Q82FM9	Q82IL8	Q8FR17	P72780	
	gth DB	355 16	355 16	361 2	354 16			464 16		452 2	519 16	375 16	542 16	472 16	91 619	473 16	394 16	
	% Query Match Length DB				70.6												22.0	
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Q8ytf9 anabaena sp Q8dmv9 synechococc Q8ds10 corynebacte Q8ns10 corynebacte Q7v5c8 prochloroco Q89915 clostridium Q97d56 clostridium Q8r756 thermoanaer P7354 synechocyst Q8prp2 bradyrhizob Q8pmv4 xanthomonas Q9kjn6 myxococcus Q7u495 synechococc Q8xpt5 raletonia s Q8xpt5 raletonia s Q8d128 synechococc Q8d128 synechococc Q8d128 synechococc Q8d128 synechococc Q8d128 synechococc Q8d128 synechococc Q8d128 synechococc Q8d128 synechococc Q8d128 synechococc Q8d18 synechococc Q8d18 synechococc Q8d18 synechococc Q9coc Anionia fas Q9bba3 xylella fas Q9bba3 xylella fas Q9coc Anionium m	Q9748 11120Junm m Q9748 11120Junm m Q8756 xanthomonas Q8740 anabaena sp Q83752 treponema p Q97484 deinococcus Q7va24 prochloroco
16 QBYTP9 16 QBDMV9 16 QBGGT3 16 QBOSTD 16 QBOSTD 16 QBOSTD 16 QBPTS 16 QBPTS 16 QBPTS 16 QBPTS 16 QBDTS 16 QBCTO 16 QBC	O .
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ALIGNMENTS

RESULT O07175 ID O AC O	RESULT 1 007175 ID 007175 AC 007175;	PRELIMINARY;		355 AA.
TC	1997	(TrEMBLrel. (TrEMBLrel. (Creat	ed) seguence update)
i E	01-OCT-2003	(TremBLrel. 25,	25, Last anr	Last annotation update)
G E	Hypothetical PEPA OR RV01	protein (Se: 25 OR MTCI418	rine proteas 3B.07 OR MT(Hypothetical protein (Serine protease, putative). PEPA OR RV0125 OR MTC1418B.07 OR MT0133.
SO	Mycobacteriu	Mycobacterium tuberculosis.	is.	
ပ္ပ	Bacteria; Ac	tinobacteria	; Actinobact	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Ö	Corynebacter	ineae; Mycob	acteriaceae,	Corynebacterineae; Mycobacteriaceae; Mycobacterium.
X X	NCBI_TaXID=1773; [1]	773;		
RP	SEQUENCE FROM N.A	M N.A.		
RC	STRAIN=H37Rv;			
RX	MEDLINE=9829	MEDLINE=98295987; PubMed=9634230;	=9634230;	
æ	Cole S.T., B	Cole S.T., Brosch R., Parkhill J.,	rkhill J., (Garnier T., Churcher C., Harris D.,
R.	Gordon S.V.,	Eiglmeier K	., Gas S., I	Barry C.E. III, Tekaia F.,
RA	Badcock K.,	Basham D., B.	rown D., Chi	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA	Davies R., D	evlin K., Fe	ltwell T., (Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
R.A	Hornsby T.,	Jagels K., K	rogh A., McI	Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA	Oliver S., O	Sporne J., Q	Lail M.A., F	Rajandream M.A., Rogers U.,
R.A	Rutter S., S	eeger K., Sk	elton S., Sc	quares S., Squares R.,
RA	Sulston J.E.	, Taylor K.,	Whitehead	S., Barrell B.G.;
RT	"Deciphering	the biology	of Mycobact	"Deciphering the biology of Mycobacterium tuberculosis from the
ET.	complete gen	complete genome sequence.";		
RL	Nature 393:5	37-544 (1998)		
KN n	[2]	;		
국 t 구 t	SECOENCE FROM N.A.	JM IN . A.		
7 K	Fleischmann	DOL / CELLKUS.	T. Hasim	STRAIN=CDC 1951 / OSHKOSH; Bleischmann B D. Alland D. Risen T.A., Camenter L., White O.,
S S	Peterson J.,	DeBoy R., Do	odson R., G	winn M.L., Haft D., Hickey E.,
RA	Kolonay J.F.	, Nelson W.C	., Umayam L	.A., Ermolaeva M.D., Salzberg S.L.,
RA	Delcher A.,	Utterback T.	, Weidman J	., Khouri H., Gill J., Mikula A.,
RA	Bishai W.;			
RT	"Whole genom	ne comparison	of Mycobact	"Whole genome comparison of Mycobacterium tuberculosis clinical and
RT	laboratory s	strains.";		laboratory strains.";
RI	Submitted (A	VPR-2001) to	the EMBL/Ger	nBank/DDBJ databases.

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FROM N.A.
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01-NOV-1996
01-NOV-1996
01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                          93 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLDSAAIGGGVAVGEP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 VVAMGNSGGOGGTPRAVPGRVVALGOTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 212
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                                                                                                                                                                                                                                                                                                                                                                              33 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                             8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
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Pubmed=12788972;
Garnier T. Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Rarnier M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                   PROSITE; PS50106; PDZ; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Hypothetical protein; Serine protease; Protease;
                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                           Tuberculist, Rv0125; -. GO; GO:0004295; F:trypsin activity; IEA. GO; GO:0007242; P:trrypsin activity; IEA. GO; GO:0007508; P:trracellular signaling cascade; IEA. GO; GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR009003; Cys_Ser_trypsin. InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                   355 AA; 34926 MW; 16CE9E21A97BF192 CRC64;
SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable serine protease PEPA (EC 3.4.21.-).
PEPA OR MB0130.
                                                                                                                                                                                                                                                                                                           96.9%; Score 1645; DB 16;
100.0%; Pred. No. 2.4e-81;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 AA.
                                                                                                                                   InterPro, IPR001254, Peptidase S1.
InterPro, IPR008256, Peptidase S1B V8.
InterPro, IPR001940, Peptidase S1C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
          PEAM; PR00595; PDZ; 1.
PEAM; PF00089; trypsin; 1.
PRINTS; PR00834; PR0TBASES2C.
PRINTS; PR00839; VBPROTEASE.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 100.
Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 355 AA;
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                                                                                                                                                                                                                                                                                                             Query Match
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Q7U2S9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
                                                                                                                                                                                                                                                                                                                                                                                                                    67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                                                                                                                                                                                                                                                                                                                                                                                                    8 APPALSODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Microbiology 140:1977-1982(1994).

EMBL; 223092; CAA80638.1; --
PIR; 547170; S47170.
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.F. Barkhill J., Barrail B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium Sov.; Broc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

Brac. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

Hydrolase; Complete Droteome.

SEQUENCE 355 AA, 34926 MW; 16CE9E21A97BF192 CRC64;
                                                                                                                                                                                                                                                                                  DB 16; Length 355;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                                                                                               Indels
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GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0007247; P:intracellular signaling cascade; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR009003; Gys.Ser_trypsin.
InterPro; IPR001478; PDZ.
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(TremBirel. 01, Last sequence update)
(TremBirel. 25, Last annotation update)
                                                                                                                                                                                                                                                                       Query Match

96.9%; Score 1645; DB 16;
Best Local Similarity 100.0%; Pred. No. 2.4e-81;
Matches 323; Conservative 0; Mismatches 0;
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InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
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Mycobacterium paratuberculosis.
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Gaps

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

PORTAIN-CDC 1551 / Oshkosh;

PORTAIN-CDC 1551 / Oshkosh;

PORTAIN-CDC 1551 / Oshkosh;

PORTAIN-CDC 1551 / Oshkosh;

PORTAIN-CDC 1551 / Oshkosh;

PORTAIN-CDC 1551 / Oshkosh;

PORTAIN-CDC 1551 / Haft D., Haft D., Hackey E.,

PORTAIN-CDC 1551 / Oshkosh;

RA Felestedmann R.D., Famolaeva M.D., Salzberg S.L.,

RA Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

Bishai W.;

RY MAD Genome comparison of Mycobacterium tuberculosis clinical and

RT laboracory strains.";

SUBMITHER (APR-2001) to the EMBL/GenBank/DDBJ databases.

L Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

BRBL, AR06589; F:trypsin activity; IEA.

GO; GO:0006508; P:trypsin activity; IEA.

RO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

RICEPPRO; IPRO01478; PDZ.

RICEPPRO; IPRO01478; PDZ.

RICEPPRO; IPRO01496; Peptidase_S1.

RICEPPRO; PRO01496; Peptidase_S1.

RICEPPRO; PRO0595; PDZ; 1.

PRE PEAM; PPO0595; PDZ; 1.

PRE PEAM; PPO0595; PDZ; 1.

PRE PEAM; PPO0595; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 VVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISV 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 NHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGGVAVGEPV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 NHVISGATDISAFDVGNGKTYGVDVVGXDRTQDVAVLQLRGASNLPTAVIGGDVAIGEPI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 VAMGNSGGGGTPRAVPGRVVALGOTVQASDSLTGAEFTLNGLIOFDAAIQPGDSGGPVV
                                                                                                                                                                                                                                                                                                                                                                                   37 PSTLALDRESNRPPLPLNPAAWVA---PQVVNISTRLGYNSAVGAGTGIVIDSSGVVLTN
                                                                                                                                                                                                                                                                                                                                                       PPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTN
                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                      70.6%; Score 1198; DB 16; Length 354; 72.0%; Pred. No. 3.1e-57; ive 40; Mismatches 46; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                              protease; Complete proteome
                                                                                                                                                                                           612F23261BC9EA4A CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat shock protein HtrA, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 TWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 NYRSAGGGDLTANVTLAEGPPA 354
Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
PRINTS; PR00839; VBRCTEASES.
SMART; SM00228; PDZ; 1.
FNOSITE; PS50106; PDZ; 1.
Hydrolase; Protease; Serine prot SEQUENCE 354 AA; 35265 MW; 6
                                                                                                                                                                                                                                                                         al Similarity 72.03
232; Conservative
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Best Local
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Q8VKA4
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Nature 409:1007–1011(2001).

Strain B.G., Marsis S., Seevens K., Simon S., Simon S., Woodward J.R., Nature 409:1007–1011(2001).

Strain B.G., Seevens K., Taylor K., Whitehead S., Woodward J.R., Nature 409:1007–1011(2001).

Strain B.G., Seevens K., Taylor K., Whitehead S., Woodward J.R., Nature 409:1007–1011(2001).

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Strain B.G., Seevens K., Simon S., Simon S., Woodward J.R., Nature 409:1007–1011(2001).

Strain B.G., Seevens K., Taylor K., Whitehead S., Woodward J.R., Nature 409:1007–1011(2001).

Strain B.G., Seevens K., Taylor K., Whitehead S., Woodward J.R., Nature 409:1007–1011(2001).

Strain B.G., Seevens K., Taylor K., Whitehead S., Woodward J.R., Nature 409:1007–1011(2001).

Strain B.G., Seevens K., Taylor K., Whitehead S., Woodward J.R., Nature 409:1007–1011(2001).

Strain B.G., Seevens K., Simon B.G., Woodward J., Woodward J., Romania B.G., Seevens K., Whitehead S., Woodward J.R., Nature 409:1007–1011(2001).

Strain B.G., Seevens K., Simon B.G., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Woodward J., Wood
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                                                                                                                                                                                                                           8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
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H
                                                                                                                72.5%; Score 1231.5; DB 2; Length 361; 73.1%; Pred. No. 4.9e-59; ive 38; Mismatches 48; Indels 1;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                               30FEF78FD6F3C411 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9CCY9;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable secreted serine protease.
              Hydrolase; Protease; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 AA
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                                        1 38 PC
361 AA; 35709 MW;
                                                                                                                                                Best Local Similarity 73.1%
Matches 236, Conservative
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                                                               SEQUENCE
                                                                                                                      Query Match
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128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 AA
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                                                                                                                                                                                                                                                                                          301 HPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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InterPro; IPR001940; Peptidase_S1C.
Bram, PP000595; PDZ; 1.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
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MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50106; PDZ;
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                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                 186
                                                                                                                                                                                                                                                                                                                                                                                                              128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 VLAIGSPLGLEGT--VTTGIVSALNRPVSTTGE-AGNONTVLDAIGTDAAINPGNSGGAL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 VNGLGQVVGMNTA----ASDNFQLSQG--GQGFAIPIGQAMAIAGQIRSGGGSPTVHIGP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 TAFLGLGVV-DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 HASLGVQVTNDKDTPGAKIVEVVAGGAAANAGVPKGVVVTKVDDRPINSADALVAAVRSK 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGEP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 PPLGSPPPKTTVTFSDGRTAPFTVVGADPTSDIAVVRVQGVSGLTPISLGSSSDLRVGQP 264
                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                 -----DINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGEP
                                                                                                                                                                                                                                                                                                                                                             187 PPLGSPPPKTTVTFSDGRTAPFTVVGADPTSDIÁVVRVQGVSGLTPISLGSSSDLRVGQP
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Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Degett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
Hydrolase; Complete proteome.
SEQUENCE 464 AA; 46436 MW; AB93A4BB3FFA9BE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                 27.1%; Score 460.5; DB 16; Length 446; 37.4%; Pred. No. 2.5e-17;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable serine protease (Serine proteinase) (EC 3.4.21.-).
                                                                                                                                                                    55; Mismatches 118; Indels
                                                                     446 AA; 44484 MW; 54170CBEA8FE872B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
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01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last anno
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PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
                    SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
SEQUENCE 446 AA; 44484
                                                                                                                                                                  Conservative
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Matches 122; Conservative
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                                                                                                                                          Similarity
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                                                                                                                                        Local Simi.
nes 122;
                                                                                                                      Query Match
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                                                                                                                                     322 VNWNAQLVGVNSAIATLGADSADAQSGSIGLGFAIPVDQAKRIADELISTGKA----S 375
                                                                                                                                                                                                                                                    242 TAFLGLGVV-DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH 300
265 VLAIGSPLGLEGT--VTTGIVSALNRPVSTTGE-AGNONTVLDAIQTDAINPGNSGGAL 321
                                                                                    VNGLGQVVGMNTA----ASDNFQLSQG--GQGFAIPIGQAMAIAGQIRSGGGSPTVHIGP 241
                                                                                                                                                                                                                                                                                                                               376 HASLGVQVTNDKDTPGAKIVEVVAGGAAANAGVPKGVVVTKVDDRPINSADALVAAVRSK 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Mytchead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RV0983 OR MTV044.11.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
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Nature 393:337-544(1998).
-!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
EMBL, ALO21999; CAA17882.1;
Tuberculist; RO983;
Tuberculist; Ro983;
Tuberculist; Ro983;
F: Peptidase activity; IEA.
GO; GO:00004295; F: trypsin activity; IEA.
GO; GO:0007422; P: intracellular signaling cascade; IEA.
GO; GO:0006508; P: proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR0090478; PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterineae; Mycobacteriaceae; Mycobacterium
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GGSPTVHIGPTAFLGLGVVDNNGN-GARVQRVVGSAPAASLGISTGDVITAVDGAPINSA 290
59 ASVPAANM-PSGSVEQVAVKVVPSVVMLETDLGRQSE--EGSGVILSADGLILTINNHVVA 115
                                                                     GA-2-----TDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG 119
                                                                                                                                                                                                                                                  178 IQPGDSGGPVVNGLGQVVGMNTAA----SDNFQLSQGGGFAIPIGQAMAIAGQIRSG 231
                                                                                                                                                                                                                                                                                               230 INPGNSGGALVNMGGQLVGVNSALATLGADSGDAQSGSIGLGFAIPVDQAKRIADELIST 289
                                                                                               120 GG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAA
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                                                                                                                                                                                                                                                                               242 TAFLGLGVV-DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH 300
                                                                                                                                                                                                                                                                                                       376 HASLGVQVTNDKDTLGAKIVEVVAGGAAANAGVPKGVVVTKVDDRPINSADALVAAVRSK 435
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A WREDINE=21128732; PubMed=11234002;
A Wheeler P.R., Honore N., Garnier T., Churcher C., Harrie D.,
A Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
A Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
A Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.; Stevens K., Taylor K., Whitehead S., Woodward J.R.,
I. Marure 409:1007-1011(2001).
I. Nature 409:1007-1011(2001).
I. SIMILARIY: TO SERINE PROTEASES, TRYPSIN FAMILY.
REMBL; AL533917; CAC29684.1; -.
                                                                                                                                                                                        188 VNGLGQVVGMNTA----ASDNFQLSQG--GQGFAIPIGQAMAIAGQIRSGGGSPTVHIGP 241
         -----DINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGEP 127
                                   205 PPLGSPPPKTTVTFSDGRTAPPTVVGADPTSDIAVVRVQGVSGLTPISLGSSSDLRVGQP
                                                                                                                          26.5%; Score 450; DB 16; Length 382; 37.5%; Pred. No. 7.6e-17; tive 52; Mismatches 116; Indels 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium leprae.
Bacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae; Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; Hebbook, MCO. Company of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of the person of 
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SEQUENCE 382 AA; 37084 MW; 3DD8DDBAB32A80D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Possible secreted serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 AA
                                                                                                                                                                                                                                                                                                                                                                          301 HPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                                                                                                                                                                                                                                                                                                                    436 APGATVALTFQDPSGGSRTVQVTLGK 461
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Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                  128
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12;
290 G--KATH----ASLGVQVATDKGTPGAKVMDVVAGGAANAAVPKGVVLTKVDDRLISSA 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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26.5%; Score 450; DB 2; Length 45
Best Local Similarity 37.5%; Pred. No. 9.3e-17;
Matches 126; Conservative 52; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Harris D., Taylor K.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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BMBL, AL035500, CAB36690.1;

BMBL, AL035500, CAB36690.1;

GO, GO:0008233; F:peptidase activity; IEA.

GO, GO:0007442; P:intracellular signaling cascade; I.

GO; GO:0007542; P:intracellular signaling cascade; I.

GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPRO90003; Cys. Ser. Lrypsin.
                                                                                                                                                                                                                                                                                                                                                                          01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterineae, Mycobacteriaceae, Mycobacterium NOBI_TaxID=1769;
                                                                   291 TAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                              452
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InterPro; IPR00124; Peptidase S1.
InterPro; IPR001940; Peptidase S1.
Pfam; PF00595; PDZ; 1.
Pfam; PF00699; trypsin; 1.
SMART; SM00228; PDZ; 1.
Hydrolase; Protease; Serine protease.
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Query Match
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                                                               186 VAAKPGGGPGGGLSPKTTVTFF---DGRTASFTVVGADPTSDIAVVRVQSISGLTPITMG 242
                                                                                                  177
                                                                                                                                                                  INPGNSGGALVNMGGQLVGVNSAIATLGADSGDAQSGSIGLGGFAIPVDQAKRIADELIST 359
             ASVPAANM-PSGSVEQVAVKVVPSVVMLETDLGRQSE--EGSGVILSADGLILTNNHVVA 185
                                                                                                                                                                                                     232 GGSPTVHIGPTAFLGLGVVDNNGN-GARVQRVVGSAPAASLGISTGDVITAVDGAPINSA 290
                                                                                                                                                                                                                   243 SSADLRVGQPVVAVGSPLGLAGT--VTSGIVSÁLNRPVSTTGE-SGNQNTVLDAÍQTDAÁ 299
                                                                                                                                                    178 IQPGDSGGPVVNGLGQVVGMNTAA----SDNFQLSQGGQGFAIPIGQAMAIAGQIRSG 231
ADFFALPLDPSAMVAQVG----PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA 73
                                                74 GA------TDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG
                                                                                                  120 GG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAA
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Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Hondra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitesh E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A., "A set of ordered cognids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I., Barrell B.G., Rajandream M.A.;
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                       TAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                                                                                                                                                                                     519 AA.
                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
Bentley S.D., Parkhill J.,
Submitted (JUL-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                           Putative protease.
SC03977 OR SCBAC25E3.14.
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins M., Harris D.;
Submitted (JUL-2001) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 SAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSV--GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 GQTYGVDVVGYDRTQDVAVLQLRGA-GGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 GKKYDAEVVGHAQGYDVAVIKLENAPSDLKPLALGDSDKVAVGDSTIAIGAPFGLSNT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 AVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ASDNFQLSQGGQ---GFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 STGNGGFGTGQAGSIGLGFAIPVNQAKFVAQQLIKSGKPVYAKIGASVSL----EETTN
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Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watamabe A., Irigunoi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Nimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Nimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Nermosynechococue structure of the thermophilic cyanobacterium Thermosynechococue elongatus BP-1.";
DNA Res. 9:123-130(2002).
EMBL; AP005377; BAC09988.1; -.
GQ; GQ:0008237; Epeptidase activity; IEA.
GQ; GQ:0004295; F:trypsin activity; IEA.
GQ; GQ:0007242; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 519;
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GO, GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0007422; P:intracellular signaling cascade; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                      protease; Complete proteome 1; SCB8D5F0CC19E428 CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.4%; Score 397.5; DB 1: 34.4%; Pred. No. 7.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 AA
                                                                                                                                                                                  InterPro; IPROU1254; Peptidase S1.
InterPro; IPRO11254; Peptidase_S1C.
Pfam; PRO0595; PDZ; 1.
Pfam; PRO0895; PDZ; 1.
PRINTS; PRO08934; PROTEASES2C.
SMRT; SMO0228; PDZ; 1.
SMART; SMO0229; PDZ; 1.
Hydrolase; Protease; Serine protease; SEQUENCE 519 AA; 50327 MW; 5CBBD5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 VTWQTKSGGTRTGNVTL 324
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Matches 109;
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Hopwood U.A.,

"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3 (2).";

"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3 (2).";

Nature 41:141-147 (2002).

In Nature 41:141-147 (2002).

R MD; A1939122; CAC01350.1; -...ivity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0004295; F:peptidase activity; IEA.

R GO; GO:0004295; F:peptidase activity; IEA.

GO; GO:0006508; P:proteolygis and peptidolygis; IEA.

R GO; GO:0006508; P:proteolygis and peptidolygis; IEA.

InterPro; IPR001940; P2.

R InterPro; IPR001940; Peptidase_S1C.

InterPro; IPR001940; Peptidase_S1C.

R Pfam; PF00089; LYPpsin; 1.

R Pfam; PF00089; PD2; 1.

R RINTS; RN00834; PROTEASES2C.

R RANATIS; PR00834; PROTEASES2C.

R RANATIS; PR00834; PD2; 1.

R PAGOLIES; PS50106; PD2; 1.

R PAGOLIES; PS50106; PD2; 1.

R PGUENCE 542 AA; 53761 WW; G20F7D8899F7212D CRC64;
                                                                         STRAIN=A3(2) / M145;
STRAIN=A3(2) / M145;
MEDLINE=21996410; Pubbled=12000953;
MEDLINE=21996410; Pubbled=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Batceman A., Brown S., Chandra G., Chen C.W., Collins M.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Hopwood D.A.,
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23.2%; Score 393.5; DB 16; Length 542;
Best Local Similarity 32.6%; Pred. No. 1.3e-13;
Matches 112; Conservative 55; Mismatches 132; Indels 45;
Mol. Microbiol. 21:77-96(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 EPVVAMGNSGGOGGTPRAVPGRVVALG--QTVQASDSLTGAEETLNGLIQFDAAIQPGDS 183
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
butative protease.
SC05149 OR SCP8.12.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
NCB1_TaxID=1902;
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23.3%; Score 396; DB 16; Length 379
al Similarity 34.0%; Pred. No. 6.1e-14;
109; Conservative 49; Mismatches 113; Indels
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001940; Peptidase_S1C.
InterPro; IPR001940; Peptidase_S1C.
InterPro; IPR001940; Peptidase_S1C.
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PTVHIGPTAFLGLGV-VDNN--GNGARVQ-----RVVGSAPAASLGISTGDVITAVD 283
               GGPVVNGLGQVVGMNTA-----ASDNFQLSQGQGFAIPIGQAMAIAGQIRSGGGS
9 PPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTN
                                                     NHVI--AGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG--GVAV
                                                                                                          GEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQA-SDSLTGAEETLNGLIQFDDAAIQPGDS
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Last annotation update)
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(TrEMBLrel. 24, I
(TrEMBLrel. 25, I
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SAV4223.
Streptomyces avermitilis.
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01-JUN-2003
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map

STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
Aset of ordered cognids and a detailed genetic and physical m
T.A. Bet of ordered coenics coelicolor A3(2) chromosome.";

STRAIN=A3(2); Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

[2] SEQUENCE FROM N.A.

STRAIN=A3(2); Saunders D., Harris D.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451
                                                                                                                                                                                                                                                                                                                                                                                                          Ikeda H., Ishikawa U., Amamanoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermithis.";

EMBL, Brotosons Streptomyces avermithis.";

EMBL, Aponsons; Freptidase activity; IEA.

GO: GO:0004239; F:trypsin activity; IEA.

GO: GO:0004299; F:trypsin activity; IEA.

GO: GO:0006208; P:intracellular signaling cascade; IEA.

GO: GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPRO09003; Cys Ser_trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 VITGIISAKARPVASSDGSSSSKASYMSALQTDASINPGNSGGPLLDAQGSVIGINSALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 AGVAAKALPSTVTIEAQSSSGEG-GTGTGFVFDKQGHIVTNNHVVAEAVDGGKLTATFPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 GQTYGVDVVGYDRTQDVAVLQLRGA-GGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 ASDNFQLSQGGQ-----GFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFL----GLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| : | | | | : | | | | : | | 334 SSSGGLGSSGQSGIGLGFAIPINQAKYVAQELIKTGKPVYPVIGASVSLEEGTGGAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 VDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 SAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSV--GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                        STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa U., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.6%; Score 384; DB 16; Length 4 32.5%; Pred. No. 3.6e-13; ive 57; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease; Complete proteome.
SEQUENCE 472 AA; 46086 MW; AE04FAA409A3B7E0 CRC64;
                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
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InterPro; IPR001940; Peptidase_S1C.
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452 Y-TRDGKARTTDVTLGE 467
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Q821L8;
01-JUN-2003 (TEMBLrel. 24,
01-JUN-2003 (TEMBLrel. 24,
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Best Local Similarity
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                                                                                         SEQUENCE FROM N.A
                                               NCBI_TaxID=33903;
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--AGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG--GVAVGEPV 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 VILDM-----DYIGDGARVGTKSNDGGSPVTRGGPGBRAGIQAGDVITEVDGQRIHSGEE 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 VAMGNSGGQGGTPRAVPGRVVALGQTVQA-SDSLTGAEETLNGLIQFDAAIQPGDSGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 VAIGAPFDLANT--VTSGIISAKERPITAGGEKGDGSDVSYVDALQTDAPINPGNSGGPL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNGLGQVVGMNTAA----SDNFQLSQGGQ---GFAIPIGQAMAIAGQIRSGGGSPTVHIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 PTAFLGLGVVDNNGNGARV-----QRVVGSAPAASLGISTGDVITAVDGAPINSATA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 SQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Gaps
                                                                                                                                                                                                                                                                                           STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanmoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                         Streptomyces avermitilis.
Bacteria, Actinobacteridae, Actinomycetales, Streptomycincae, Streptomyces.
NCBI_TaxID=33903,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.6%; Score 384; DB 16; Length 619; 34.0%; Pred. No. 4.9e-13; ive 53; Mismatches 126; Indels 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microorganism Streptomyces avermitilis.";
Nat. Blotechnol. 21:526-531(2003).
BMBL, AP006033: BAC70826.1;
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006509; P:intracellular signaling cascade; IEA.
InterPro; IPR009003; Cyg.Ser.trypsin.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase.51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619 AA; 64251 MW; D2D3C72A67D3B3A6 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative serine proteinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
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Best Local Similarity 34.0%
Matches 115; Conservative
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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STRAIN=MA-4680 / A
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SEQUENCE 619 AA
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138 GGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGM 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 SV--GSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG--GGVAVGEPVVAMGNSGGQ 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECUENCE FROM N.A.

SECURENCE FROM N.A.

STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

RAMARIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

RAMARIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

RAMARIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

RAMARIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

RAMARI, SUBUMI, M. Mashima J., Itoh T., Yamagishi A., Nishio Y.,

Usuda Y., Sugimoco S.;

Leo K., Susuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

Ramari, APO05117; BAC17760.1; - Lo the EMBL/GenBank/DDBJ databases.

BMBL, APO0517; BAC17760.1; - Lo the EMBL/GenBank/DDBJ databases.

BMBL, APO0517; BAC17760.1; - Lo the EMBL/GenBank/DDBJ databases.

BMBL, APO0517; BAC17760.1; - RAMARINING CASCAGE; IEA.

GO, GO:0007242; F:heat shock protein activity; IEA.

GO, GO:0007242; F:heat shock protein activity; IEA.

GO, GO:0007242; F:heat shock protein activity; IEA.

GO, GO:0007242; F:heat shock protein activity; IEA.

GO, GO:0007242; F:heat shock proteins and peptidolysis; IEA.

RO, GO:0006509; P:proteins and peptidolysis; IEA.

InterPro; IPR001940; Peptidase_S1.

REAMRY; SM00228; PDZ; 1.

REAMRY; SM00228; PDZ; 1.

REAMRY; SM00228; PDZ; 1.

REAMRY; SM00228; PDZ; 1.

REAMRY; SM00228; PDZ; 1.

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REAMRY; SM00228; PDZ; 1.

REAMRY; SM00228; PDZ; 1.

REAMRY; SM0
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                                                                                                                                                                                                                                                                                                                        Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Q8FR17 PRELIMINARY; PRT; 473 AA. Q8FR17; Q8FR17; Q8FR17; Q8FR17; Q1-MAR-2003 (TFEMBLrel. 23, Last sequence update) 01-MAR-2003 (TFEMBLrel. 23, Last annotation update) Putative serine protease, heat shock protein. CE0950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 QTK-SGGTRTGNVTL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 TAQDTSQTRQVEVTL 470
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Matches 108; Conservative
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Search completed: June 22, 2004, 17:22:46 Job time: 27.9826 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 22, 2004, 16:46:13 ; Search time 5.49204 Seconds (without alignments) 3128.737 Million cell updates/sec

US-09-886-349A-6 1698 1 MHHHHHAPPALSQDRFADF.....QTKSGGTRTGNVTLAEGPPA 330 Title: Perfect score: Sequence:

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	QI	Description	
	323.5	10	145	¦	YVTA BACSU	bacillus s	
1 2	۱ (۲	 . თ	4.1	-	A	lactobaci	
ım	316	ω.	35	Н	DEGS_ECOLI	a)	
4	312	18.4	408	-	1	Q9la06 lactococcus	
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7	02	7.	45	Н	DEGQ_ECOLI	P39099 escherichia	
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11	291.5		47	Н		P09376 escherichia	
12	\sim	۲.	46	Н	HTOA HAEIN	P45129 haemophilus	
13	285.5	9	50	Н			
14	285	ů.	4,	Н	DEGP_CHLTR	chlamydia	
15	284		47	Н	DEGP_BUCAI	P57322 buchnera ap	
16	280.5	ý.	4,	Н	DEGP_CHLMU	chlamydia	
17	279	ė.	48	Н	DEGP_CHLPN	chlamydia	
18	278	é.	43	Н	DEG1_ARATH	arabidopsi	
19	277	Ġ	20	Н	DEGP_RICCN	rickettsi	
20	71	ů.	40	Н	YYXA_BACSU	bacillus	
21	269.5		44	ч	DEG8 ARATH	arabidopsi	
22	67		47		DEGP_BUCAP	085291 buchnera ap	
23	251		51	-	DEGP_RICPR	005942 rickettsia	
24	245.5		45	Н	HRAZ_HUMAN	043464 homo sapien	
25	239		34	Н	DEGS_HAEIN	haemo	
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32	175.5	ö	32	Н	PA	ara	
33	7	ö	63	Н	Y4BJ_RHISN	P55377 rhizobium s	

064761 avian adeno P04985 bos taurus QS0594 wroobacterii QS9372 rattus norv P52320 streptomyce P58877 mycobacterii QS5810 mycobacterii QS5857 troketteia P12021 sus scrofa QS5047 r outer mem Q06653 r outer mem
FIBI ADEGI BLS BOVIN YIATO WYCTU BLS RAT PRIC STRGR Y278 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA21 WYCTU WA21 WYCTU WA22 WYCTU WA21 WYCTU WYCTU WA21 WYCTU WA21 WYCTU WA21 WYCTU WA22 WYCTU WA21 WYCTU WA21 WYCTU WA22 WYCTU WA21 WYCTU WA21 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WA22 WYCTU WYCTU WA22 WYCTU WYC WYCTU WYC WYCTU WYC WYC WYC WYC WYC WYC WYC WYC WYC WYC
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ALIGNMENTS

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AX MEDLINE=20576168; PubMed=11133960;
AN OROTE D., Howell A., Collery R., Devine K.M.;
Noone D., Howell A., Collery R., Devine K.M.;

"Ykda and Ytch, HtrA-like serine proteases in Bacillus subtilis,

"Ykda and Ytch, HtrA-like serine proteases in Bacillus subtilis,

"Ykda and Ytch Gene expression.";

"J. Bacteriol. 183:654-663 (2201).

"J. Bacteriol. 183:654-663 (2201).

"J. Bacteriol. 183:654-663 (2201).

"J. Subclida enzymes.

"J. Subclida enzymes in processing, maturation, or secretion of extracellular enzymes.

"J. Subclida enzymes in processing, maturation, or secretion of extracellular enzymes.

"J. Subclida enzymes in processing, maturation, or secretion of extracellular enzymes in processing operation of heterologous amylases at the transition phase of the growth cycle.

"Negatively requiates its own expression.

"J. Subclida enzymes in compensating overexpression of htrA, especially during stress conditions.

"J. SIMILARITY: Edoings to peptidase family $2C.

"J. SIMILARITY: Contains 1 PDZ/HRR domain.

"J. SIMILARITY: Contains 1 PDZ/HRR domain.

"T. SIMILARITY: Contains 1 PDZ/HRR domain.

"T. SIMILARITY: In positions 87 and 246 that produce two separate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 VI---DPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLP 114
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Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikak K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 458;
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CHARGE RELAY SYSTEM (POTENTIAL),
CHARGE RELAY SYSTEM (POTENTIAL),
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EMBL, 293941; CAB07968.1; ALT FRAME.
EMBL, 293941; CAB07968.1; ALT FRAME.
EMBL, 2939410; CAB07969.1; ALT_FRAME.
EMBL, 299120; CAB12290.1; ALT_FRAME.
Subtilist; BG14155; yvtA.
InterPro; IPR0019035; yvtA.
InterPro; IPR001479; PDZ.
InterPro; IPR001940; Peptidase_S1.
Ffam; PF00595; PDZ; 1.
Pfam; PF00595; PDZ; 1.
Pfam; PF00595; PDZ; 1.
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Serine E
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                                                                                                           Nature 390:249-256(1997).
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PROSITE; PS50106; PDZ;
Hydrolase; Protease; St
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Matches 100; Conserv
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172 IFKKDSDKAYIITNNHVVEGANKLTV-TLYNGETETAKLVGSDTITDLAVLEISGKNVKK 230

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                       230 SGGGSPTVHIGPTAFLGLGVVDNN-------GNGAFVQRVVGSAPAASL 271
                                                                                                                                                                                                                                                                                                        343 QNGKV-----DRPFLGVQMIDMSQVPETYQENTLGLFGDQLGKGVYVKEVQANSPAEKA 396
115 SAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLI 172
                                                                                                                     173 OFDAAIOPGDAGGPVVNGLGQVVGMNTAASDNFQLSQGG---QGFAIPIGQAMAIAGQIR 229
                                                                                                                                                         288 QIDAAINPGNSGGPLINASGQVIGIN----SLKVSESGVESLGFAIPSNDVEPIVDQLL
                                                                                                                                                                                                                                                                                                                                                                      272 GISTGDVITAVDGAPINSATAMADAL-NGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                                                                                                                                                                                                                                                                                                                          CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
BIEBE(77991C88707) CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smeds A., Varmanen P.K., Palva A.M., "Molecular characterization of a stress-inducible gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactobacillus helveticus.";
J. Bacteriol. 180:643-6153 (1998).
-!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
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Pred. No. 8.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
Serine protease do-like htrA (EC 3.4.21.-).
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InterPro: IPR001978; PbZ.
InterPro: IPR001949; Peptidase_S1.
InterPro: IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 1.
Pfan; PF00894; ProTsAsES2C.
SMART; SM00228; PDZ; 1.
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Hydrolase; Serine protease;
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SEQUENCE FROM N.A.
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STRAIN=KIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
MELLOR F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
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Nature 409:529-533(2001).
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Escherichia coli O157.H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Mismatches 121; Indels
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Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
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28-FEB-2003 (Rel. 41, Last annotation update)
Procease degS precursor (EC 3.4.21.-)
DEGS OR HHOB OR HTRH OR B3235 OR Z4594 OR ECS4108
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STRAIN=K12 / W3110;
MEDLINE=96165272; PubMed=8576051;
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STRAIN=K12 / W3110;
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01-FEB-1995 (Rel.
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STRAIN-O157-H7, RIMD 0509952;

STRAIN-O157-H7, RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

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"Structural and catalytic models of trypsin-like viral proteases.";
Semin. Virol. 1:311-322(1990).
-!- SUBCELLULAR LOCATION: Periplasmic (Potential).
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
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PROTEASE DEGS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AE000402; AAC76267.1; EMBL, AE000402; AAC76267.1; EMBL, AE000554; AAC76267.1; EMBL, AE000554; BAB37531.1; EMBL, MAC477; -; NOT ANNOTATED_CDS. PIR, D91142; D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D91142. D9114
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U18997; AAA58037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U15661; AAC43993.1; -.
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Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.9
Matches 108; Conservative
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DEGP_BRUME
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                     QRGYIITNKHVINDADQI-IVALQDGRVFBALLVGSDSLTDLAVLKINATGGLPTIFINA 145
                                                                         :|:|:|| :||:||:
146 RRVPHIGDVVLAIGNP------YNLGQTITQGIISATG-RIGLNPTGRQNFL 190
                                                                                                               -IG 219
PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
                                                                                                                                                                                                  251 DGRVIRGYIGIGGR----EIAPLHAQGGGI--DQLQGIVVNEVSPDGPAANAGIQVNDLI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 QTDASİNHGNSGGALVNSLGELMGİNTLSFDKSNDGETPEĞIĞFAİPFQLATKIMDKLİR
                                                       GVA---VGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV-QASDSLTGAEETLN----GLI
                                                                                                                                                                     220 QAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVI
                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poquet I., Saint V., Seznec E., Simoes N., Bolotin A., Gruss A., "Htrh is the unique surface housekeeping protease in Lactococcus lactis and is required for natural protein processing."; Mol. Microbiol. 35:1042-1051(2000).
                                                                                                                                                                                                                                                        ISVDNKPAISALETMDQVAEIRPGSVIPVV-VMRDDKQLTLQVTIQEYP 352
                                                                                                                                                                                                                              TAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGP
                                                                                                               OFDAAIOPGDAGGPVVNGLGQVVGMNTAASD--NFQLSQGGQGFAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Membrane-bound (Probable).
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease do-like htrA (EC 3.4.21.-) (HtrAL1).
                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                             408 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=1L1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20177820; PubMed=10712686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF155705; AAF61294.1; -. EMBL; AE006442; AAK06234.1; -.
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; H86891; H86891.
MEROPS; S01.273; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                  LL2136.
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InterPro; IPR009003; Cys_Ser_trypsin. InterPro; IPR001478; PDZ. InterPro; IPR001254; Peptidase_S1.

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The Buropean Profit institutions as long as its content is in no way way.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 NA-IQTDAAINPGNSGGALINIEGQVIGITQSKITTTEDGSTSVEGLGFAIPSNDVVNÍI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 NKLEADG-----KISRPA-LGIRMVDLSQLSTNDSSQLKLPSSVTGGVVVYSVQSGLPAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STORINGE FROM N.A.
STRAIN=16M / ATCC 23456 / Biotype 1;
STRAIN=16M / ATCC 23456 / Biotype 1;
STRAIN=20020109; PubMed=11756688;
DelYecchico V.G., Kapatral V., RedKar R.J., Patra G., Mujer C., Los T., Johnova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";

Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAGLKAGDVITKVGDTAVTSSTDLQSALYSHNINDTVKVTYY-RDGKSNTADVKLSK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                         169 NGLIQFDAAIQPGDAGGPVVNGLGQVVGMNTA---ASDNFQLSQGGQGFAIPIGQAMAIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 -AGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQIRSGGGSPTVHIGPTAFLGLGVVD-----NNGN------GARVQRVVGSAPAA
                                                                                                                                                                                                                                                                                                                                                                                                                GTGIVIDPNG---VVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVKDVATFADSSKLTIGEPAIAVGSPLGSQFANTATEGILSATSRQVTLTQE-NGQTTNI
                                                                                                                                                                                                                                                                                                                                                                    34; Gaps
                                                                                                                                                                                                                CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
SALB90BS5A7DF851 CRC64;
                                                                                                                                Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                           Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HTRA OR BMEI1330.
                                                                                                                                                                                                                                                                                                                                                                    52; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
-!- SUBCELLULAR LOCATION: Periplasmic (Potential).
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 2 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                           18.4%; Score 312; DB 1; 31.3%; Pred. No. 3.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  513 AA
                                                                                                                                                  POTENTIAL. CATALYTIC.
InterPro; IPR001940; Peptidase_SIC. Pfam; PP00595; PDZ; 1. Pfam; PF00689; trypsin; 1. PRINTS; PR00884; PROTEASES2C. SWART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                  41648 MW;
                                                                                                                                Hydrolase; Serine protease;
                                                                                                      PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucella melitensis.
                                                                                                                                                                                         302
302
127
157
239
408 AA;
                                                                                                                                                                                                                                                                                                                                                Similarity
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Local S...
93;
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                                                                                                                                                                                                             ACT SITE
ACT SITE
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SEQUENCE
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STITI TITI TELEFORMAN SOLUTION NEW MARKADON

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.2e-10;
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PROBABLE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR009003; Cys_Ser_trypsin.
Interpro; IPR001478; PDZ.
Interpro; IPR001254; Peptidase_S1.
Interpro; IPR001940; Peptidase_S1C.
        MEDLINE=95165990; PubMed=7861951;
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE014368; AAN29540.1; -. PIR; I40060; I40060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53483 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PR0TEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                       EMBL; U07352; AAA70164.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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125
300
414
152
182
182
557
513 AA;
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DOMAIN
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                   238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402
                                                                                                                                                                                                                                                                                                                                                                                                                                    104 VLQIRGAGGLPS-----AAIG--GGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 AIPSSTAKOVVDOLIKKĠSVERĠWIGVOIOPVTKDIAASLĠLA----EEKĠAIVASPQDD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 VLKINA----PKRKFVYVAFGDDNKVRVGDWVVAVGNPFGLGGT--VTSGIVSARGRDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 ASDSLTGAEETLNGLIQFDAAIQPGDAGGPVVNGLGQVVGMNTAASDNFQLSQGGQG--F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 AIPIGQAMAIAGQIRSGG----GSPTVHIGP----TAFLGLGVVDNNGNGARVQRVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLA
                                                                                                                                                                                                                                                                                                                                                                                     46 GYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSV--GSGQTYGVDVVGYDRTQDVA
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                               POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
CATALYTIC.
PDZ 1.
PDZ 2.
                                                                                                                                                                                                                                                                                                                                     ; Score 305.5; DB 1; Length 513; Pred. No. 1e-10; 37; Mismatches 118; Indels 45
                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
                                                               PIR, AD418, AD5418.

InterPro; IPR009003; Cys_Ser_trypsin.

InterPro; IPR001478, PDZ.

InterPro; IPR001479, PDZ; DZ.

InterPro; IPR00154; Peptidase_S1.

InterPro; IPR00154; Peptidase_S1C.

Pfam; PP00089; PDZ; Z.

Pfam; PP00089; PDZ; Z.

PRINTS; PR0084; PROTEASES2C.

SMART; SM00229; PDZ; Z.

PROSITE; PS50106; PDZ; Z.

Hydrolase; Serine protease; Periplasmic; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brucella abortus.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HTRA OR BRO611.
                                                                                                                                                                                                                                                                                                              C472FEF99DFC6268 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   513 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SPECIES=B.abortus; STRAIN=2308;
                                                                                                                                                                                                                                                                         152 CH
182 CH
257 CH
53514 MW;
                                                        EMBL; AE009571; AAL52511.1; -.
                                                                                                                                                                                                                                                                                                                                     18.0%;
34.0%;
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 34.0 Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brucellaceae; Brucella.
                                                                                                                                                                                                                25
299
391
500
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300
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182
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513 AA;
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SIGNAL 1
CHAIN 26
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 VLQLRGAGGLPS----AAIG--GGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQ 156
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                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SPECIES—B suis; STRAIN=1330 / Biovar 1;

MEDLINE=2224741; PubMed=12271122;

MEDLINE=2224741; PubMed=12271122;

Pauleen I.T., Seshadir R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

Read T.D., Dodson R.J., Umayam L., Shetty J., Malen M.J.,

A Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts.";

The Droc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).

--- SUNCELLULAR LOCATION: Periplasmic (Potential).

--- SIMILARITY: Contains 2 PDZ/DHR domains.
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Tatum F.M., Cheville N.F., Morfitt D.; "Cloning, characterization and construction of htrA and htrA-like mutants of Brucella abortus and their survival in BALB/c mice."; Microb. Pathog. 17:23-36(1994).
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PDZ 2.
CHARCE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
DEICEF1959472806 CRC64;
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NCBI_TaxID=602;
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288 AIPSSTAKQVVDQLIKKGSVERGWIGVQIQPVTKDIAASLGLA----EEKGAIVASPQDD 343
                                             266 APAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLA
                                                                                         344 GPAAKAGIKAGDVITAVNGETVQDPRDLARKVANIAPGEKAALTVWRKNKAEEI-NVTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96162272; PubMed=8576051;
Waller P.R., Sauer R.T.;
"Characterization of degQ and degS, Escherichia coli genes encoding homologs of the DegP protease.";
J. Bacteriol. 178:1146-1153[1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97426611; PubMed=9278503;

MEDLINE=97426611; PubMedt G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

Mau B., Shao Y.;

Science 277:1413-1474 (1997).

-I- FUNCTION: PROTEASE WITH A SHARED SPECIFICITY WITH DEGP/DEGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12 / W3110;
Bass S., Gu Q., Goddard A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 2 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DEGQ OR HHOA OR B3234.
                                                                                                                                                                                                                                                                                                 455 AA
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InterPro, IPR001478; PDZ.
InterPro, IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PP00595; PDZ; 2.
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EMBL, AE000402; AAC76266.1; -...
PIR, JC6051, JC6051.
WEROPS; 801.274; -...
SWISS-2DPAGE; P39099; COLI.
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P39099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 QAQKI-SIQLNDGREFDAKLIGSDDQSDIALLQIQNPSKLTQIAIADSDKLRVGDFAVAV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 GNPFGLGQT--ATSGIVSALGR-----SGLNLEGLENFIQTDASINRGNSGGALLNL 221
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MEDLINE=21534948; PubMed=11677669;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 GNSGGGGGTPRAVPGRVVALGOTVQASDSLTGAE-ETLNGLIQFDAAIQPGDAGGPVVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 NGELIGINTAI-----LAPGGGSVGIGFAIPSNMARTLAQQLIDFGEIRRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson K., Charles I., Dougan G., Pickard D., O'Gaora P., Costa G., Ali T., Miller I., Hormaeche C.;
"The role of a stress-response protein in Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                             117.8%; Score 302.5; DB 1; Length 455; 29.4%; Pred. No. 1.4e-10;
                                                                                                                                                                                                                                    PDZ 1.
PDZ 2.
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
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Pfam, PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SW00228; PDZ, 2.
PROSITE; PS50106; PDZ, 2.
Hydrolase; Serine protease; Periplasmic; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                           6A090F93AC021C83 CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Protease do precursor (EC 3.4.21.-).
ENERP OR HTRA OR PTD OR STM0209.
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                                                                                                                                                                                                                                                                                                                                                                                           47205 MW;
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109
139
214
455 AA;
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Best Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 GTGIVID-PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 NFIQTDAAINRGNSGGALVNLNGELIGINTAILAPDGGNI---GIGFAIPSNMVRNLTSQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 MVEYGOVKRG------ELGIMGTELNSELAKAMKVDAORGAFVSOVMPNSSA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 GLIQFDAAIQPGDAGGPVVNGLGQVVGMNTA--ASDNFQLSQGGQGFAIP----IGQA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 MAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGN-------GARVQRVVGSAPA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X54589; CAA38420.1; -

BMBL; AE008704; AAL19173.1; -

BREAD AE008704; AAL19173.1; -

BREAD AE008704; AAL19173.1; -

BREAD AE008704; Cys_Ser_trypsin.

BREAD AE008703; Cys_Ser_trypsin.

BREAD AE00895; PDZ; 2.

BREAD AE00895; PDZ; 2.

BREAD AE00895; LYPSIN; 1.

BRINTS; PRO0895; PDZ; 2.

BRANT; SMO0228; PDZ; 2.

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Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium LTZ.";

Nature 413:852-856(2001).

-!- FUNCTION: SERINE PROTEASE THAT IS REQUIRED AT HIGH TEMPERATURE.

-!- FUNCTION: SERINE PROTEASE THAT IS REQUIRED AT HIGH TEMPERATURE.

-!- SUBCELLITY WITH HHOA/DEGQ.
-!- SUBCELLITY WITH HHOA/DEGQ.
-!- SUBCELLITY BELONGS FAMIC.
-!- INDUCTION: By heat shock.
-!- INDUCTION: By heat shock.
-!- SIMILARITY: Belongs to peptidase family $2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Gaps
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PROTEASE DO.
PDZ 1.
PDZ 2.
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
BY SIMILARITY.
W, 86E685BF3CIA289F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.3%; Score 293; DB 1; Length 475; 31.9%; Pred. No. 5e-10; ive 47; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49315 MW;
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281
378
132
162
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475 AA;
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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
LL -> PV (IN REF. 1).
PSFAUWYDAVSPAVNSVVQARERVSDDESNFTFFFGGRGF
EDLPEDHPLRRFFREFAPRENDRADRWRDRRGPRGBGRLRP RAQGSGFFITEDGYLVTNNHVVSDGSA -> AVSPWMSTPF RRRSSPSACRHVNASATMXATSPSISAAAGSRTCRKTIRCG VSSANSLRVKMTVPIVGATAAVRVAKVVSVRGRKAPASSSP STRAIN=1021;
MEDLINE=96146524; PubMed=8550509;
MEDLINE=96146524; Jichige A., Walker G.C.;
"Genetic analysis of Rhizobium meliloti bacA-phoA fusion results in identification of degP: two loci required for symbiosis are closely J. Bacteriol. 178:745-752(1996). MEDINE=1021;
MEDINE=21395607; PubMed=11481430;
MEDINE=21395607; PubMed=11481430;
Gapela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
Sinorbizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
-! SIMCLARITY: Belongs to peptidase family \$2C.
-! SIMCLARITY: Contains 2 PDZ/DHR domains. EMBL, U31512; AAC43669.1; ALT_INIT.
EMBL, U31512; AAC43669.1; ALT_INIT.
EMBL, ALS9173; -.
InterPro; IPR001273; -.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001540; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1.
Pfam; PP00595; PDZ; 2.
Pfam; PF00699; trypain; 1.
PRINTS; PR00894; PROTEASES2C.
SMART; SM00228; PDZ; 2. SERINE PROTEASE DO-LIKE 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGIT OR DEGPO R ROLO21 OR SMO02365.
EMizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobium.
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCEL_TAXID=382; Periplasmic; Repeat; Signal; 504 AA POTENTIAL. PROBABLE SE CATALYTIC. PRT; PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Pe Complete proteome. 26 PB CHAIN 27 504 P DOMAIN 113 286 C DOMAIN 401 491 PP STANDARD; 26 28 28 28 33 48 49 11 11 11 11 11 11 SEQUENCE FROM N.A. SEQUENCE FROM N.A. 27 28 28 28 28 24 24 24 39 ACT_SITE ACT_SITE ACT_SITE CONFLICT

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Complete proteome.
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12;
                                                                                                                                                                                                                                                                                                                                   343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F., Ogsawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Brotsiser L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Brian K.D., Errington J., Fobret C., Ferrari B., Follger D.,
A Drins C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Guiseppi G., Guy B.J., Haga K., Haiech J., Hawood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Coris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Jones L.,
Joris B., Karamata D., Kasahara S., Mauel C., Madigue C.,
M. Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
M. Medina N., Mallado R.P., Mizuno M., Moesel D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Potherelle D., Porwollik S., Prescott A.M.,
Reger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Rator T., Scanlan E., Schleich S., Schroeter R., Scoffone P.,
                                                                                                                             54 GTGIVIDPNGVVLTNNHVIAGATDINAFSV--GSGQTYGVDVVGYDRTQDVAVLQL--RG 109
                                                                                                                                                                                      110 AGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLN 169
            KSADDVLKVINNAKKDGRSKALFQIEAQEGSRFVALPITQG
-> NRQTTFSR (IN REF. 1).
D7E82BB9981EA23C CRC64;
                                                                                                                                                                                                                                                                          231 DYLQVDAAVNRGNSGGPTFNLSGEVVGINTAI -- - FSPSGGNVGIAFAIPASVAKDVVDS
                                                                                                                                                         124 GSGFFITEDGYLVTNNHVV---SDGSAFTVIMNDGTELDAKLVGKDSRTDLAVLKVDDKR
                                                                                                                                                                                                                181 KFTYVSFADDEKVRVGDWVVAVGNPFGLGGTVTA--GIISARGRDIGSG-----PYD
                                                                                                                                                                                                                                               170 GLIQFDAAIQPGDAGGPVVNGLGQVVGMNTAASDNFQLSQGGQG--FAIPIGQAMAIAGQ
                                                                                                                                                                                                                                                                                                        IRSGG----GSPTVHIGPTA-----FLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDV
                                                                                                                                                                                                                                                                                                                                  288 LIKDGTVSRGWLGVQIQPVTKDIAESLGL----SEANGALVVEPQAGSPGEKAĞİKNGDV
                                                                                                  38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devine K.M.; "Sequence of the Bacillus subtilis genome between xlyA and ykoR."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                344 VTALNGEPVKDPRDLARRVAALRPGSTAEVTLW--RSGKSETVNLEIGTLP 392
                                                                                                                                                                                                                                                                                                                                                                279 ITAVDGAPINSATAMADALNGHHPGDVISVT-WQTKSGGTRTGNVTLAEGP 328
                                                                                                  40; Mismatches 116; Indels
 KTVTSSPTTTSSPTART (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
BerEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable serine protease do-like htrA (EC 3.4.21.-).
                                                                        17.3%; Score 293; DB 1; 33.3%; Pred. No. 5.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98044033; PubMed=9384377;
                                          504 AA; 53035 MW;
                                                                                                  97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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034358;
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SEQUENCE :
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Mol. Microbiol. 41:1159-1172 (2001).

-! FUNCTION: May be involved in processing, maturation, or secretion of extracellular enzymes.

-! SUBCELLULAR LOCATION: Membrane-bound (Potential).

-! INDUCTION: Transcription is css dependent. Induced by heat shock during exponential growth and by heterologous amylases at the transition phase of the growth cycle. Negatively regulates its own expression during exponential growth cycle. Negatively regulates its own expression during exponential growth and during heat shock.

-! MISCELLANEOUS: Inactivation results in compensating overexpression of ytvh, especially during stress conditions.

-! SIMILARITY: Contains 1 PDZ/DHR domain.
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Mipat A., Yamanoco H., Yamane K., Yasumoco K., Yata K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; subtilis "The complete genome sequence of the Gram-positive bacterium Bacillus bubtilis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A novel two-component regulatory system in Bacillus subtilis for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20158875; PubMed=10692364;
Noone D., Howell A., Devine K.M.;
"Expression of ykdA, encoding a Bacillus subtilis homologue of HtrA,
is heat shock inducible and negatively autoregulated.";
J. Bacteriol. 182:1592-1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Noone D., Howell A., Collery R., Devine K.M.; "Ykda and Yvta, Htra-like serine proteases in Bacillus subtilis, engage in negative autoregulation and reciprocal cross-regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hyyrylaeinen H.-L., Bolhuis A., Darmon E., Muukkonen L., Koski P., Vitikainen M., Sarvas M., Pragai Z., Bron S., van Dijl J.M., Kontinen V.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Protease; Serine protease; Heat shock; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A69643; A69643.
MRROPS; S01.273;
Subclifist; B6212609; htra.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ
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J. Bacteriol. 183:654-663(2001).
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EMBL; Z99110; CAB13147.1; -.
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
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                                                                                                                                                                                                                             Markiewicz J., Zurawa D., Tanfani F., Scire A., Wawrzynow A.,
Narkiewicz J., Zurawa D., Tanfani F., Scire A., Wawrzynow A.,
Narkiewicz J., Bertoli E., Lipinska B.;
Narkiewicz J., Bertoli E., Lipinska B.;
The N-terminal region of HtrA heat shock protease from Escherichia
coli is essential for stabilization of HtrA primary structure and
maintaining of its oligomeric structure.";
Elochim. Blophys. Acra 1649:171-182(2003).
INOLVED IN THE DEGRAPATION OF DANAGED PROTEINS. IT CAN DEGRADES
ICIA, ADA, CASEIN AND GLOBIN. SHARED SPECIFICITY WITH DEGQ.
C. SUBCELLULAR LOCATION: Periplasmic.
C. SUBCELLULAR LOCATION: Periplasmic.
C. INDUCTION: By heat shock.
C. INDUCTION: By heat shock.
C. INDUCTION: By Degraphy SECONDERIAL SURVIVAL AT
TEMPERATURES ABOVE 42 DEGRESS CELSIUS.
C. SIMILARITY: Belongs to peptidase family S2C.
C. SIMILARITY: Contains 2 PDZ/DHR domains.
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E -> Q (IN REF. 7).
A -> G (IN REF. 1).
STITING -> RHLPVNAVISLNPFLKTGRGSPYNL (IN REF. 1).
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Hydrolase; Serine protease; Heat shock; Periplasmic; Repeat; Signal;
Seol J.H., Woo S.K., Jung E.M., Yoo S.J., Lee C.S., Kim K.J., Tanaka K., Ichihara A., Ha D.B., Chung C.H.; Procrease Do is essential for survival of Escherichia coli at high temperatures: its identity with the htrA gene product."; Biochem. Biophys. Res. Commun. 176:730-736(1991).
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InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_SI.
InterPro; IPR001940; Peptidase_SIC.
Pfam; PP00595; PDZ; 2.
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PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
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EcoGene; EG10463; degP.
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                                                                                                     54 GTGIVIDPN-GVVLTNNHVIAGAIDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGG 112
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STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Reliachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Pine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

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-!- SUBCELLULAR LOCATION: Periplasmic (Potential).

-!- SIMILARITY: SEEMS TO BE A INTERNEDIATE FORMS BETWEEN E.COLI HTRA

-!- SIMILARITY: Belongs to peptidase family S2C.

-!- SIMILARITY: Contains 2 PDZ/DHR domains.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                  Length 474;
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49354 MW; 5482E596F74B6D5F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 NLVQQILEFGQVRRG------LLGIKGGELNADLAKAFNVSAQQGAFVSEVLPK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 NAVGAGTGIVIDPN-GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 NFRGLGSGVIINASKGYVLTNNHVIDGADKITV-QLQDGREFKAKLVGKDEQSDIALVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 RGAGGLPSA--AIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 EKPSNLTEIKFADSDKLRVGDFTVAIGNPFGLGQT--VTSGIVSALGRS-----TGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 E-TLNGLIQFDAAIQPGDAGGPVVNGLGQVVGMNTAASDNFQLSQGGQG--FAIPIGQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=94299828; PubMed=8027347;
Anderson B., Sims K., Regnery R., Robinson L., Schmidt M.J.,
Anderson B., Hager C., Edwards K.;
"Detection of Rochallmaea henselae DNA in specimens from cat scratch
disease pattents by PCR.";
"Jotton Microbiol. 32:942-948(1994).
-: SUBCELLULAR LOCATION: Periplasmic (Potential).
-: SIMILARITY: Belongs to peptidase family S2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                 PROBABLE PERIPLASMIC SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                DO/HHOA-LIKE.
PDZ 1.
PDZ 2.
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
W, EDOSOA00047B5851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 1; Length 466; 8.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 APAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Mismatches 101; Indels
                                                                                                                                                                                                PROSITE, PS50106, PDZ, 2.
Hydrolase, Serine protease, Periplasmic, Repeat, Signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last annotation update)
Probable periplasmic serine protease DO-like p
DEGP OR HTRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bartonella henselae (Rochalimaea henselae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 289;
Pred. No. 8
                                InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ_
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Ffam; PP00695; PDZ; 2.
PFam; PP00894; Prypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SWART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                            49434 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                        361
458
120
150
                                                                                                                                                                                                                                                                                                                     270
367
120
150
226
466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                           Complete proteome.
SIGNAL 1
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                                                                                                                                                                                                                                                                         30
                     HI1259;
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PS4925;
                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
ACT_SITE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 LKKFFQDFYNRDKPSNKSLQRSHRLRPIAFGSGFFISSDGYIVTNNHVISDGTSY-AVVL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 RAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPVVNGLGQVVGMNTAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 TA--GIVSARGR-----DIGTG---VYDDFIQIDAAVNRGNSGGPTFDLNGKVVGVNTAI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 SDNFQLSQGGQG--FAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRV-----VG----VG-----SAPAASLGISTGDVITAVDGAPINSATAMADALNG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPVTKEISDSIGLKEAKGALITDPLKGPAAKAGIKAGDVIISVNGEKINDVRDLAKRIAN 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | | | | : | : | | | | | : | 47 MQQQGFAD-----IVSQVKPAVVSVQVKSNKKKEWFFSDFFSTPGFDQLPDQHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG--GGVAVGEPVVAMGNSGGQGGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE PERIPLASMIC SERINE PROTEASE
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DEGP CHITR. STANDARD; PRT; 497 AA.
AC P18584; O84830;
DT 01-NOV-1990 (Rel. 16, Created)
DT 30-MAY-2000 (Rel. 15) Last sequence update)
DT 28-FEB-2003 (Rel. 14). Last annotation update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DF Probable serine protease do-like precursor (EC 3.4.21.-) (59 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Mismatches 125; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Periplasmic, Repeat, Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6CD9F4743282AF9E CRC64;
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PDZ 2.
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
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SIMILARITY: Contains 2 PDZ/DHR domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.8%; Score 285.5;
llarity 27.4%; Pred. No. 1.4
Conservative 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ_
InterPro; IPR001284; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 2.
Pfam; PF000894; LTYPSin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54114 MW;
                                                                                                                                                                                                                                                                                                                                       EMBL; L20127; AAA97430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Serine protease;
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CHAIN
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DEGP_BUCAI
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                                                                                                                                                                                                                                                         Marathe R., Aravind L.,
                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis.";
Science 282:754-759(1998).
--- SIMILARITY: Belongs to peptidase family S2C.
--- SIMILARITY: Contains 2 PDZ/DHR domains.
--- SIMILARITY: Contains 2 PDZ/DHR domains.
--- CAUTION: REF.1 SEQUENCE WAS INCORRECT: DUE TO SEQUENCING ERRORS THE AUTHORS TRANSLAIED THEIR PUTATIVE 59 kDa IMMUNGGENIC PROTEIN
ON THE COMPLEMENTARY STRAND TO THAT OF WHAT SEEMS TO BE THE REAL PROTEIN.
                                                                                                                                                  σĘ
                                                                                                                               Kahane S., Weinstein Y., Sarov I.; "Cloning, characterization and sequence of a novel 59-kDa protein Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                     "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                         STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Arav
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
CATALYTIC.
                           Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
66ASE31BB84A38BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.8%; Score 285; DB 1; Length 497; 32.2%; Pred. No. 1.5e-09; ive 46; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Signal; Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; H71465; H71465.
PHC1-2DPAGE; P18884;
InterPro; IPR0000303; Cys.Ser_trypsin.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001255; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1.
                                                                                                       STRAIN=Serovar 112;
MEDLINE=90337348; PubMed=2379836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 PO 497 PR 497 PR 497 CB 683 PD 485 PD 143 CB 1247 CB 53244 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001355; AAC68420.1; -.
EMBL; M31119; AAA23116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0834; PROTEASES2C.
PRINTS; PRO0839; V8PROTEASE.
SMART; SM00228; PDZ; 2.
 (SKS9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
                HTRA OR CT823
 immunogenic protein)
                                                                                                                                                                                 Gene 90:61-67(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                           NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                        Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
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SEQUENCE
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DOMAIN
DOMAIN
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Gaps

40;

Conservative

94;

Matches

à

54 GTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGL

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114 PSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQT----VQASDSLTGAEET 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 DOLISDGOVTRGFLGVT----LQPIDSELATCYKLEKVYGALVTDVVKGSPAEKAGLRQE 344
                                                                                                                                                                                                    LNGLIQFDAAIQPGDAGGPVVNGLGQVVGMNTAASDNFQLSQG--GQGFAIPIGQAMAIA
                                                                                                                                                                                                                                                           235 ---FIQTDAAINPGNSGGPLLNINGQVIGVNTAIVSG---SGGYIGIGFAIPSLMAKRVI
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BDDLINES-20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenome Sequence of the endocellular bacterial symbiont of aphids
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Enterobacteriaceae; Buchnera.
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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modified and this statement is not removed.
entities requires a license agreement (See Por send an email to license@isb-sib.ch).
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InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
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Query Match
Best Local Similarity 30.6%; Pred. No. 1.6e-09;
Matches 88; Conservative 51; Mismatches 109; Indels 40; Gaps 12;
                                              54 GTGIVIDPN-GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGG 112
                                                              113 LPSAAI--GGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAE-ETLN 169
                                                                                                             228 IRSGGGSPTVHIGPTAFLGLGVVD------NNGNGARVQRVVGSAPAASLGISTGDVI 279
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	007175 mycobacteri	Q7u2s9 mycobacteri	Q50320 mycobacteri	Q9ccy9 mycobacteri	Q8vka4 mycobacteri	Q7u0x2 mycobacteri	O53896 mycobacteri	Q9cd67 mycobacteri	Q9z5g6 mycobacteri	Q93j30 streptomyce	Q8dg87 synechococc	Q9fbk9 streptomyce	Q82fm9 streptomyce	Q82il8 streptomyce	Q8fr17 corynebacte	P72780 synechocyst
		QI.	007175	Q7U2S9	050320	Q9CCY9	Q8VKA4	Q7U0X2	053896	Q9CD67	09Z5G6	083530	Q8DG87	Q9FBK9	Q82FM9	Q821L8	Q8FR17	P72780
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		Match Length DB	355	355	361	354	446	464	464	382	452	519	375	542	472	619	473	394
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Q8YTF9 Q8DMV9 Q8G6T3 Q8NS10 O7V5C8	Q89915 Q97GD5 Q8R756 P73354	Q89KP2 Q8PMV4 Q9KJN6 Q7U495 Q8XPT5	Q8DL28 031388 089048 0708K9 087C10	Q70604 Q952R5 Q95QE6 Q8RTK2 Q8PB56 Q81VH0 O83752 Q9RTK4
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MEDLINE=98299; PubMed=982;

MEDLINE=98299; PubMed=982;

MEDLINE=98299; PubMed=9829;

MEDLINE=9835537-544(1998).

MEDLINE=9829597; PubMed=9829;

MEDLINE=9835537-544(1998). SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Obhkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland B., Gwinn M.L., Haft D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nalson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. 01-001-1997 (TrEMBLrel. 04, Created)
01-001-1997 (TrEMBLrel. 04, Last sequence update)
01-001-2003 (TrEMBLrel. 25, Last amnotation update)
Hypothetical protein (Serine protesse, putative).
PEPA OR RV0125 OR MTC1418B.07 OR MT0133. 355 AA. PRT; PRELIMINARY; SEQUENCE FROM N.A. 007175 RESULT 1 007175

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PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
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MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50106; PDZ; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Hypothetical protein; Serine protease; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                          TIGE; WT0133; F'0983;
TIGE; WT0135; --
TUBErculist; Rv0125; --
TUBErculist; Rv0125; --
TUBERCULIST; Rv0125; --
TUBERCULIST; Rv0125; --
TUBERCULIST; Rv0125; --
GO; GO:0006508; P: Errypsin activity; IEA.
GO; GO:0006508; P: Proteolysis and peptidolysis; IEA.
InterPro; IPR001903; Cys. Ser. Lrypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1E.
Fram; PF00089; Lrypsin; 1.
Fram; PF00089; Lrypsin; 1.
FRINTS; PR00839; WBROTEASES2C.
FRINTS; PR00839; PRZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 AA; 34926 MW; 16CE9E21A97BF192 CRC64;
SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable serine protease PEPA (EC 3.4.21.-).
PEPA OR MB0130.
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                EMBL; Z96071; CAB09453.1; -.
EMBL; AE006925; AAK44357.1;
PIR; P70983; F70983.
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Matches 322; Conservative
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SEQUENCE 355 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 VVAMGNSGGOGGTPRAVPGRVVALGOTVQASDSLIGAEETLNGLIQFDAAIQPGDAGGPV
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
34KDa proctein precursor.
Mycobacterium paratuberculosis.
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MEDLINE=95005449; PubMed=7921248;
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Matches 322; Conservative
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us-09-886-349a-6.rspt

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DB 16;
                                                                                                                                                                                                               70.4%; Score 1195; DB 16, 71.7%; Pred. No. 7.8e-57; cive 41; Mismatches 46
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Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; VRDEASESCC.
PRINTS; PR00839; VRPROTEASE.
SWART; SM0228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
Hydrolase; Protease; Serine protes SEQUENCE 354 AA; 35265 MW; 6:
                                                                                                                                                                                                                                       Best Local Similarity 71.79
Matches 231; Conservative
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OBVKA4;
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Q8VKA4
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21128732; PubMed=11234002;
A Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Medeler P.R., Honoze N., Parkhill J., Churcher C., Harris D., Mnegall K., Basham D., Erown D., Chillingworth T., Connor R., A Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Narsive gene decay in the leprosy bacillus.";
I Massive gene decay in the leprosy bacillus.";
I Nature 409:1007-1011(2001).
I SHMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.

EEBEL, ALSS3926; CACS2191.1;
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                                                                                                                                                                                              8 APPALSODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                         NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                                                                                                                                 Gaps
                                                                                                                                               1;
                                                                                                  DB 2; Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Batteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                Query Match 72.3%; Score 1228.5; DB 2; Length Best Local Similarity 72.8%; Pred. No. 1.3e-58; Matches 235; Conservative 39; Mismatches 48; Indels
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DEPLOMA; MA2659; --

GO; GO:0004295; Fitrypsin activity; IEA.

GO; GO:0007242; Fitrypsin activity; IEA.

GO; GO:0007242; Fitrypsin activity; IEA.

GO; GO:0007689; P:intracellular signaling cascade; IEA.

GO; GO:0006809; P:intracellular signaling cascade; IEA.

InterPro; IPR00903; Cys_Ser_trypsin.

InterPro; IPR001254; Peptidase_SI.

InterPro; IPR001254; Peptidase_SI.

InterPro; IPR001940; Peptidase_SIE.
  Protease, Serine protease, Signal.

1 38 POTENTIAL.
361 AA, 35709 MW, 30FEF78FD6F3C411 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Probable secreted serine protease.
ML2659.
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       Hydrolase; Protease;
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                                                   SEQUENCE
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                                GNAL
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       SETOS
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                                                                                                                                                                                                                                                                                                                                                      69 NHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŗ.,
                                                                                                                                                                                                                                                              37 PSTLALDRESNRPPLPLNPAAMVA---PQVVNISTRLGYNSAVGAGTGIVIDSSGVVLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 NSRGQVVGMNTAATDNYKM-LGGQGFAIPIGQAMEVVGAIRSGAGSNTVHIGPTAFFGLG
                                                                                                                                                                                                                         9 PPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTN
                                                                                                                                                            Gaps
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STRAIN=CDC 1551 / Oshkosh;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                               4,
                                                                                           Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
MyCE_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains...;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AE006985, AAK45259.1;
TIGR, MT1011,
GO, GO:0004295; F:trypsin activity, IEA.
GO, GO:0004295; P:trypsin activity, IEA.
GO, GO:000508; P:proteolysis and peptidolysis, IEA.
InterPro; IPR001031, Cys. Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001894; Peptidase_S1.
InterPro; IPR001894; Peptidase_S1.
InterPro; IPR001894; Peptidase_S1.
InterPro; IPR001894; IPR011811, 1.
                                                                                                                                                            46; Indels
protease; Complete proteome 1; 612F23261BC9EA4A CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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242 TAFLGLGVV-DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH 300
                                                                                                                                                                      376 HASLGVQVTNDKDTPGAKIVEVVAGGAAANGVPKGVVVTKVDDRPINSADALVAAVRSK 435
VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 PALPLDPSA---MVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGAT- 76
                     188 VNGLGQVVGMNTA----ASDNFQLSQG--GQGFALPIGQAMAIAGQIRSGGGSPTVHIGP
                                                                                                           322 VNMNAĢLVGVNSAIATLGADSADAQSGSIGLGFAIPVDQAKRIADELISTGKA-----S
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth II., Connor R., Davies R., Devlin K., Keltwell T., Gentles S., Hamin N., Holroy Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.B., Taylor K., Whitchead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
26.9%; Score 456.5; DB 16; Length
Best Local Similarity 37.1%; Pred. No. 5.2e-17;
Matches 121; Conservative 56; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease; Complete proteome.
7; AE93BFCC53E1EC8F CRC64;
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                                                                                                                                                                                                                                                                                                                                                           464
                                                                                                                                                                                                                          HPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                                                                                                                                                                            436 APGATVALIFODPSGGSRÍVQVÍLGK 461
                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                           PRT;
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InterPro; IPR001940; Peptidase S1C.
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Hydrolase; Protease; Serine pr
SEQUENCE 464 AA; 46452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00089; trypsin, 1.
PRINTS, PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative serine protease. RV0983 OR MTV044.11.
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1773;
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 128
                                     265
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053896
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                                                                                                                                                                                            127
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                                                                                                                                                                                                                                                                                                                                                                                               241
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                                                                                                                                                                                                                                                                                                                        128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                     304 VNMNAQLVGVNSAIATLGADSADAQSGSIGLGFAIPVDQAKRIADELISTGKA----S 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
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                                                                                                                                                                                                                                                                                                                                             TAFLGLGVV-DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH
                                                                                                                                                                                                                                                -----DINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGEP
                                                                                                                                                                                                                                                                    187 PPLGSPPPKTTVTFSDGRTAPFTVVGADPTSDIAVVRVQGVSGLTPISLGSSSDLRVGQP
                                                                                                                                                                                                                                                                                                                                                                                               VNGLGQVVGMNTA----ASDNFQLSQG--GQGFAIPIGQAMAIAGQIRSGGGSPTVHIGP
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                                                                                                                                                                      PALPLDPSA---MVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 PALPLDPSA---MVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE AND SECULO SECULO SERVINA PETALOZ/97;
MEDLINE-22709107; PubMed=12788972;
MEDLINE-22709107; PubMed=12788972;
MEDLINE-22709107; PubMed=12788972;
Garnier T., Biglmeier K., Camus J.-C., Medina N., Manscor H., Garnier T., Borndin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
EMBL; BX248337; CAD93870.1; -
Hydrolase; Complete protecome.
                                                                                                                                 31; Gaps
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                                                                                               DB 16; Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Probable serine protease (Serine proteinase) (EC 3.4.21.-).
                                                                                       Query Match
Best Local Similarity 37.1%; Pred. No. 4.4e-17;
Matches 121; Conservative 56; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.9%; Score 457.5; DB 16; Length 37.1%; Pred. No. 4.6e-17; ive 56; Mismatches 118; Indels
                   SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
SEQUENCE 446 AA; 44484 MW; 54170CBEA8FE872B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 AA.
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(TrEMBLrel. 25, Last seq
(TrEMBLrel. 25, Last ann
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   PRINTS; PR00834; PROTEASES2C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium bovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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01-OCT-2003 (
01-OCT-2003 (
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es 121;
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Best Local S:
Matches 121
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59 ASVPAANM-PSGSVEQVAVKVVPSVVMLETDLGRQSE--EGSGVILSADGLILINNHVVA 115
                                                                                                               120 GG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAA 177
                                                                                                                                                                            IQPGDAGGPVVNGLGQVVGNNTAA----SDNFQLSQGGQGFAIPIGQAMAIAGQIRSG 231
                                                                                                                                                                                                             230 INPGNSGGALVNMGGOLVGVNSAIATLGADSGDAOSGSIGLGFAIPVDQAKRIADELIST 289
                                                                                                                                  GA-------TDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG
                                                                     PRELIMINARY;
                                                                                                                                                                                178
                                                                                                                                                                                                                                             232
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KAN DEFINE TO STRAIN=TN:

KAN MEDILINE=21128732; PubMed=11234002;

KAN MEDILINE=21128732; PubMed=11234002;

KAN MEDILINE=21128732; PubMed=11234002;

KAN MERCHER P.R., Honore N., Garnier T., Churcher C., Harris D.,

Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

Andres R.M., Devin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

RA HOLroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Simmonds M., Skelton J., Squares R.,

RA Hutter S., Seeger K., Zimon S., Simmonds M., Skelton J., Squares R.,

RA Barrell B.G.; Gevens K., Taylor K., Whitehead S., Woodward J.R.,

RA Barrell B.G.; Gevens K., Taylor K., Whitehead S., Woodward J.R.,

RA Barrell B.G.; Cavens K., Taylor K., Whitehead S., Moodward J.R.,

RE BERICH B.G.; Gevens K., Taylor K., Whitehead S., Moodward J.R.,

RE BERICH B.G.; Gevens K., Taylor K., Whitehead S., Moodward J.R.,

RE BERICH B.G.; Gevens K., Taylor K., Whitehead S., Moodward J.R.,

RE BERICH B.G.; Gevens K., Taylor K., Whitehead S., Moodward J.R.,

RE BERICH B.G.; Gevens K., Taylor K., Whitehead S., Moodward J.R.,

RE BERICH B.G.; Gevens K., Taylor K., Whitehead S., Moodward J.R.,

RE BERICH B.G.; Gevens K., Taylor K., Whitehead S., Moodward J.R.,

RE PROMOS B.G.; Freptidase activity; IEA.

GO; GO:0004295; Frirypsin activity; IEA.

GO; GO:0004295; Frirypsin activity; IEA.

GO; GO:0004295; Frirypsin activity; IEA.

RO; GO:0004295; Frirypsin activity; IEA.

RO; GO:0004295; PDZ; I.

REPROS PROMOS PROMOS PROTEASESC.

REMEN PROMOS PROMOS PROTEASESC.

REMENT; SMOOLS PROMOS PROTEASESC.

REMENT; SMOOLS PROTEASESC.

ROMER PROMOS PROMOS PROTEASESC.

ROW SMART; SMOOLS PROTEASES SETHER PROTEASES COMPLETE PROTECOME.

SEQUENCE SEQUENCE REMARY SUDBEDBRABSARBARD RECE4;
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      127
                       205 PPLGSPPPKTTVTFSDGRTAPFTVVGADPTSDIAVVRVQGVSGLTPISLGSSSDLRVGQP 264
                                                                                      VNGLGQVVGMNTA----ASDNFQLSQG--GQGFAIPIGQAMAIAGQIRSGGGSPTVHIGP 241
                                                                                                                                                               322 VNWNAQLVGVNSAIATLGADSADAQSGSIGLGFAIPVDQAKRIADELISTGKA----S 375
                                                                                                                                                                                             242 TAFLGLGVV-DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH 300
                                                                                                                                                                                                                  376 HASLGVQVTNDKDTLGAKIVEVVAGGAAANAGVPKGVVVVTKVDDRPINSADALVAAVRSK 435
                                                                   VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV 187
     -----DINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium leprae.
Bacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae; Mycobacteriaceae, Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible secreted serine protease.
                                                                                                                                                                                                                                                                                                                                                                          382 AA
                                                                                                                                                                                                                                                                                436 APGATVALTFQDPSGGSRTVQVTLGK 461
                                                                                                                                                                                                                                                            301 HPGDVISVTWQTKSGGTRTGNVTLAE 326
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                                     290 G--KATH----ASLGVQVATDKGTPGAKVMDVVAGGAAANAAVPKGVVITKVDDKLISSA 343
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MEDLINE=93188700; PubMed=8446027;

MEDLINE=93188700; PubMed=8446027;

MEDLINE=93188700; PubMed=8446027;

MEDLINE=93188700; PubMed=8446027;

Tuse of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae.";

Mol. Microbiol. 7:197-206(1993).

EMBL; AL035500; CA836690.1; ---

BMEL; AL035500; CA836690.1; ---

BMEL; AL035500; CA836690.1; ---

BMEL; AL035500; CA836690.1; ---

BMEL; AL03550; Piprincachlular signaling cascade; IEA.

GO; GO:0004295; Fitrypsin activity; IEA.

GO; GO:0004295; Fitrypsin activity; IEA.

GO; GO:0004295; Piprincachlular signaling cascade; IEA.

InterPro; IPR001254; Peptidase_SI.

RINTERPO; IPR001254; Peptidase_SI.

RINTERPO; IPR001294; Peptidase_SIC.

Pfam; PR00895; trypsin; I.

DR Pfam; PR00895; trypsin; I.

SMART; SM00228; PDZ; I.

SMART; SM00228; PDZ; I.

SMART; SM00228; PDZ; I.

SMART; SM00228; PDZ; I.

SMART; SM00228; PDZ; I.

SMART; SM00228; PDZ; I.

SEQUENCE 452 AA; 45130 MW; 6CA675EB0911F983 CRC64;
GGSPTVHIGPTAFLGLGVVDNNGN-GARVQRVVGSAPAASLGISTGDVITAVDGAPINSA
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MCT-2003 (TrEMBLrel. 25, Last annotation update)
MCCB373.28.
Mycobacterium leprae.
Mycobacterium leprae.
Corynebacterines Mycobacteria; Actinobacteridae; Actinomycetales;
Mycobacterium.
Mycobacterium.
Mycobacterium.
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Mycobacterium.
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Harris D., Taylor K.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                |: |: |: || : || : || : | : || : | 344 DALVAAVRSKAPGDKVSLIYQDQSGSSRIVQVILGK 379
                                                                                                                                       291 TAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
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Best Local Similarity 37.2
Matches 125; Conservative
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18 ADFPALPLDPSAMVAQVG----PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA

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Created)
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497 VTYE-RGGKQHTAEVTL 512
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23,
25,
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                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Redenbach M., Kleser H.M., Denapaite D., Bichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of cordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
ADFPALPLDPSAMVAQVG----PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
              GGSPTVHIGPTAFLGLGVVDNNGN-GARVQRVVGSAPAASLGISTGDVITAVDGAPINSA
                                                                                                                                                                                                                        360 G--KATH----ASLGVQVATDKGTPGAKVMDVVAGGAANAAVPKGVVLTKVDDRLISSA
                                                 -TDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG
                                                                       186 VAAKPGGGPGGGLSPKTTVTFF---DGRTASFTVVGADPTSDIAVVRVQSISGLTPITMG
                                                                                                 GG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAA
                                                                                                                         243 SSADLRVGQPVVAVGSPLGLAGT--VTSGIVSALNRPVSTTGE-SGNQNTVLDAIQTDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21996410; PubMed=12000953; MEDLINE-21996410; PubMed=12000953; MEDLINE-21996410; PubMed=12000953; Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                   291 TAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
                                                                                                                                                                                                                                                                Streptomycineae; Streptomycetaceae, Streptomyces
                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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Nature 417:141-147(2002)
                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collins M., Harris D.;
Submitted (JUL-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                       Putative protease.
SCO3977 OR SCBAC25E3.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ASDNFQLSQGGQ---GFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 STGNGGFGTGQAGSIGLGFAIPVNQAKFVAQQLIKSGKPVYAKIGASVSL----EETTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 GQTYGVDVVGYDRTQDVAVLQLRGA-GGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 AVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPVVNGLGQVVGMNTA--
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MEDLINB=2225144; PubMed=12240834; Ikeuchi M., Katch H., Sasamoto S., Namura 22, Saneko T., Sato S., Ikeuchi M., Kaneko T., Kaneko T., Kaneko T., Kaneko T., Kaneko T., Kishida Y., Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Matanabe A., Iriguchi M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the thermophilic cyanobacterium Thermosymechococcus elongatus BP-1.";

EMBL, AP005377; BAC09988.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 519;
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                                                                                                                                                                                                                                           InterPro; IRRO01254; Peptidase S1.
InterPro; IRRO01254; Peptidase_S1C.
InterPro; IPR001940; Peptidase_S1C.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PR00595; PDZ; 1.
Pfam; PR00599; trypain; 1.
PRNTG; PR00634; PROTEASESCC.
SMART; SM00226; Tryp_SPC; 1.
Hydrolase; Protease; Serine protease; Complete proteome. SEQUENCE 519 AA; 50327 MW; 5CB8D5F0CC19E428 CRC64;
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Bacteria, Cyanobacteria, Chroococcales, Synechococcus.
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EMBL, AL939118; CAC44701.1; -. GO, GO:0008233; F:peptidase activity; IEA. GO; GO:0004295; F:trypsin activity; IEA. GO; GO:0004242; F:intracellular signaling cascade; I GO; GO:0006508; P:proteollysis and peptidolysis; IEA. InterPro; IPR00903; Cys.Ser.trypsin.
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Last annotation update)
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Mol. Microbiol. 21:77-96(1996)
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Q82FM3
ID Q82FM
AC 082FM
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                                                                                                                                                                                                                                                                                     109 AHVVSQADTVNV-RLKDGRVFEGEVRGVDEVSDLAIVKLKGVIEPLPTAPLGDSSEVKVG 167
                                                                                                                                                                                                                                                                                                                        EPVVAMGNSGGCGGTPRAVPGRVVALG--QTVQASDSLTGAEETLNGLIQFDAAIQPGDA 183
                                                                                                                                                                                                                                                                                                                                                 168 DWAIAVGNPLGLDNT-----VTLGIISTLHRSSAQVGIPDKRLDFIQTDAAINPGNS 219
                                                                                                                                                                                                                                                                                                                                                                          GGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIG--P 241
                                                                                                                                                                                                                                                                                                                                                                                                 220 GGPLLNEAGEVIGINTA----IRADAMGIGFAIPINKAKALQARLIRGEKIQHAYIGIQM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                           276 TIFTPAMAKENNANPNSPVILPEVNGVLVLQVLPNTPAAKAGLRWGDVITAVDGEPITSA 335
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                                                                                                                                                                                                                    10 PALSQDRFAD-FPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTN
                                                                                                                                                                                                                                              67 PLLSDPFFRQFFPGLALPPQE------DRLRGQGSGFIIDPSGIVMTN
                                                                                                                                                                                                                                                                                                                                                                                                                           242 TAFLGLGVVDNNG------NGARVQRVVGSAPAASLGISTGDVITAVDGAPINSA
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Ranashi H., Hopwood D.A.; As set of ordered cosmids and a detailed genetic and physical map ithe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
                                                                                                                                                                                            20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                 , Score 393; DB 16; Length 3; Pred. No. 1e-13; 50; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saunders D., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                               Protease; Complete proteome.
SEQUENCE 375 AA; 39724 MW; 0D2602EB534915FS CRC64;
GO; GO:0006508; P:proteolysis and peptidolysis; IBA.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_SI.
InterPro; IPR001254; Peptidase_SI.
InterPro; IPR001940; Peptidase_SI.
Pfam; PF00089; Pp2; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; Pp2; 1.
PROSITE; PS50106; Pp2; 1.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 TAMADALNGHHPGDVISVTWQ 311
                                                                                                                                                                   23.1%;
33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                          Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.
                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative protease.
SCO5149 OR SCP8.12.
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NHVI--AGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG--GVAV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 GEPVVAMGNSGGOGGTPRAVPGRVVALGQTVQA-SDSLTGAEETLNGLIQFDAAIQPGDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 GGPVVNGLGQVVGMNTA-----ASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 PTVHIGPTAFLGLGV-VDNN--GNGARVQ------RVVGSAPAASLGISTGDVITAVD 283
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SEQUENCE FROM N.A.
STRAIN=A3[2] / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harpper D., Bateman A., Brown S., Chandra G., Chen C. W., Collins M.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                               The complete genome sequence of the model actinomycete Streptomyces acolicolor A3(2).",

Complete Genome sequence of the model actinomycete Streptomyces acolicolor A3(2).",

Nature 417:141-147(202).

Nature 417:141-147(202).

REMBL, A4039122, Fortycolor.

RGO; GO:0008233; Fipeptidase activity; IEA.

RGO; GO:0007429; Firtygein activity; IEA.

RGO; GO:0007429; Firtygein activity; IEA.

RGO; GO:0007429; Firtygein activity; IEA.

RGO; GO:0007429; Firtygein activity; IEA.

RINEPPRO; IPRO01247; Piptidase SI.

RINEPPRO; IPRO01254; Peptidase SI.

RINEPPRO; IPRO01254; Peptidase SI.

REFEM: PF00595; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.0%; Score 390.5; DB 16; Length 32.3%; Pred. No. 2.2e-13; ive 56; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 GAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GORVHSGEELIVKTRAHRPGDRLELTLORDGKETKVSLVLGSSG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase, Protease, Serine protease, Complete proteome.
SEQUENCE 542 AA, 53761 MW; 620F7D889DF7212D CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity 32.33
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SAV4223.
Streptomyces avermitilis.
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01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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SMART; SM00228; PDZ; 1.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                             Putative serine proteinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 ĞKKYNAEVVĞHAQĞYDVAVVKLKNAPSDLQPLTLĞDSDKVAVĞDSTIAIĞAPFĞLSNT-- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 VTTGIISAKNRPVASSDGSSSSKASYMSALQTDASINPGNSGGPLLDAQGSVIGINSAIQ 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 AVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPVVNGLGQVVGMNTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 ASDNFQLSQGGO-----GFALPIGOAMAIAGOIRSGGGSPTVHIGPTAFL----GLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 VDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 TEGGASGS--DAITPNGPAKAGIKPGDVITKLDDMVIDSGPTLIGEIWTHRPGATVKLT
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22689306; Pubmed=12692562;
Iteda H ., Ishikawa J ., Danamoco A., Shinose M ., Kikuchi H ., Shiba T ., Sakaki Y ., Hartori M ., Omura S .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 SAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSV--GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531 (2003).
EMBL; APO05038; BAC71935.1; --
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                                                                                                                                                                        Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M., "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.4%; Score 381; DB 16; Length 472; 32.2%; Pred. No. 6.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO, GO:000823; F:peridase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:000742; P:intracellular signaling cascade; IEA.
GO; GO:000788; P:intracellular signaling cascade; IEA.
GO; GO:0006808; P:proteclysis and peptidolysis; IEA.
InterPro; IPR001903; Cys_Ser_trypsin.
InterPro; IPR001249; Peptidase_SI.
InterPro; IPR001249; Peptidase_SIC.
                                                                                                SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46086 MW; AE04FAA409A3B7E0 CRC64;
                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Mismatches 133;
                        Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 Y-TRDGKARTIDVTLGE 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PP00595; PDZ; 1.
Pfam, PP00089; trypsin; 1.
PRINTS; PR00834; PR07EASES2C.
Protease; Complete proteome.
SEQUENCE 472 AA; 46086 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                        metabolites.";
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Matches
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129 VAMGNSGGGGGTPRAVPGRVVALGQTVQA-SDSLTGAEETLNGLIOFDAAIQPGDAGGPV 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 VTLDM-----byrgdgarvgrksndggspytrggpgdragioadvitevdgorihsgee 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tikeda H., Ishikawa U., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";

Nat. Biotechnol. 21:526-531(2003)

Nat. Biotechnol. 21:526-531(2003)

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

InterPro; IPR009003; Cys. Ser_trypsin.

InterPro; IPR009478; PZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 SODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Gaps
                                                                                                                                                            SEQUENCE FROM N.A.
SETAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NREL 8165;
MEDLINE=21477401; PubMed=11572948;
Omuta S., Ikeda H., Ishikawa U., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitiis: deducing the ability of producing secondary
                          Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 22.4%; Score 381; DB 16; Length 619; Best Local Similarity 33.7%; Pred. No. 8.4e-13; Matches 114; Conservative 54; Mismatches 126; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64251 MW; D2D3C72A67D3B3A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 MADALNGHHPGDVISVTWQTKSGGTRTGN---VTLAEG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR001254, Peptidase SI.
InterPro, IPR001940, Peptidase_SIC.
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Pfam; PF00089; trypsin; 1.
PRINTS; PR0083; trypsin; 1.
SWART; SM00228; PDZ; 1.
Streptomyces avermitilis.
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12;

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128 409 467 240

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RESULT Q8FR17

Last sequence update)

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82 SV--GSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG--GGVAVGEPVVAMGNSGGQ 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 SST--VTSGIVSALNRPVRASGD--GGESSLIDAIQTDAAINPGNSGGPLVDMEGNLIGM 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 NTAASDNFQLSQG-----GQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 NSVIA---SISSGIDIGGSIGLGFAIPANFAKRVATQLIETGVATQPMIGVILANGANV- 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXCLORED FROM N.A.

SECURIAL STAINLYS-314 / AJ 12310 / DSM 44549 / JCM 11189;

Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,

Ravarabayasi Y., Sugaiki M., Mashima J., Itch T., Yamagishi A., Nishio Y.,

Usuda Y., Sugaiki M., Mashima J., Itch T., Yamagishi A., Nishio Y.,

Usuda Y., Sugaimoto S.;

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Best Local Similarity 34.0%; Pred. No. 1.1e-12;
Matches 107; Conservative 51; Mismatches 131; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                 Corynebacterium efficiens.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=152794;
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Heat shock; Protease; Complete proteome.
SEQUENCE 473 AA; 47757 MW; 5COCG09561F8C524 CRC64;
                                               Q8FRI7;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative serine protease, heat shock protein.
CE0950.
     473 AA
PRT;
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     PRELIMINARY;
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SMART; SM00228; PDZ;
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     A PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE PACOCO COS SE 
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Search completed: June 22, 2004, 17:22:47 Job time: 27.9826 secs



GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

June 22, 2004, 16:59:04; Search time 9.233 Seconds (without alignments) 3438.018 Million cell updates/sec Run on:

US-09-886-349A-6 1698 1 MHHHHHAPPALSQDRFADF......QTKSGGTRTGNVTLAEGPPA 330

Title: Perfect score: Sequence:

Scoring table:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
2: pir1:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	probable serine or	_	u	u	Už	serine	proteinase hhoA (E	le pro		oteinase	5	le se	serine proteinase	le pe	probable periplasm	serine proteinase	serine proteinase	-like	-like	-like	serine proteinase	d serine	ij	otease	e hhoB	otease	serine endoprotein	ndoprote	
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serine proteinase	htrA-like protein	proteinase DO (EC	trypsin-like prote	serine proteinase	trypsin-like prote	periplasmic serine	proteinase (EC 3.4	probable periplasm	heat shock protein	serine proteinase	serine proteinase	proteinase DO (EC	proteinase DO (EC	proteinase DO (EC	proteinase DO - He
140060	140059	AI3349	JC6051	D69109	AC0909	F72359	AG0433	B81914	815337	C87336	A69643	845229	E85500	E90649	H71936
7	Н	N	0	н	~1	7	7	7	Н	~	~1	7	7	0	7
513	474	474	455	328	356	459	457	499	475	363	449	474	474	474	476
17.9	17.9	17.9	17.8	17.7	17.6	17.6	17.4	17.4	17.3	17.2	17.2	17.2	17.2	17.2	17.1
304.5	303.5	303.5	302.5	301	299.5	298	296	295	293	291.5	291.5	291.5	291.5	291.5	291
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 RESULT 1	
probable serine pr	Troops Properties: Winchbarterium Fubermilosis
C;Date: 17-Jul-1998	.cerium curerionsis 8 #sequence_revision 17-Jul-1998 #text_change 09-Dec-2002 3
C. Cole, S. T., Brosch, R.; I.; Connor, R.; Davies, R.; Brajandream, M.A.; Rogers, R.; Brajandream, M.A.; Rogers, V.	Gracession: Flosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-59 A;Authors: Sqares, A;Title: Decipheri A;Reference number	Nature 393, 537-544, 1998 AAuthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome 1 A;Reference number: A70500; MUID:98295987; PMID:9634230
A,Accession: F70983 A,Status: preliminar A,Molecule type: DNA	A;Accession: F70883 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
 A; Residues: 1-355 < COL> A; Cross-references: GB: A; Experimental source:	A;Residues: 1-355 <col/> A;Cross-references: GB.Z96071; GB:AL123456; NID:g3242254; PIDN:CAB09453.1; PID:g2181967 A;Cross-references: strain H37RV
 C, Senerics: C, Superfamily: Esc	A.Genericas. A.Genericas. C.Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp:
 Query Match Best Local Similarity Matches 322; Conser	96.7%; Score 1642; DB 2; Length 355; larity 99.7%; Pred. No. 7.8e-90; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 œ (APPALSODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLF 67
n (1 6
OY 68 NNHW DD 93 NNHW	NNHVIAGATDINAESVGSGOTYGVDVVGYRRIDDVAVLQLRGAGGLESAAIGGGVAVGEP 127
Qy 128 VVAN Db 153 VVAN	VVAMGNSGGGGTPRAVFGRVVALGGTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV 187
Qy 188 VNGI Db 213 VNGI	VNGLGQVVGMNTAASDNFQLSQGGQFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 247
Qy 248 GWU Db 273 GWU	GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHFGDVIS 307
 2y 308 VIWC Db 333 VIWC	VTWOTKSGGTRTGNVTLAEGPPA 330

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HPGDVISVTWQTKSGGTRTGNVTLAE 326
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C, Genetics:
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Holroyd,
                                                                   A,Residues: 1-361 <CAM>
A,Cross-references: EMBL:223092; NID:g505550; PIDN:CAA80638.1; PID:g505551
C,Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
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Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R. Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Peltwell, T.; Fraser, A.; Hamlin, N.; Holroy eam, M.A.; Rutherford, K.M.
Aduthors: Ruther, 1011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 2011, 20
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A;Residues: 1-354 <STO>
A;Cross-references: GB:AL450380; NID:g13093863; PIDN:CAC32191.1; GSPDB:GN00147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable secreted serine proteinase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: 20-Apr.2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002 C;Accession: A87242
hypothetical protein 34K - Mycobacterium paratuberculosis
C;Species: Mycobacterium paratuberculosis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNSAGOVIGVDTAATDSYKMS-GGGGFAIPIGRAMAVANQIRSGAGSNTVHIGPTAFLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APSGLALDRFADRPLAPIDPSAWVGÓVGÞQVVNIDTKFGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.3%; Score 1228.5; DB 2; Best Local Similarity 72.8%; Pred. No. 1.7e-65; Matches 235; Conservative 39; Mismatches 48;
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Similarity 71.7%; Pred. No. 1.6e-63;
31; Conservative 41; Mismatches 46;
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A;Residues: 1-361 <CAM>
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, C, Connor, R.; Brosch, R.; Peulwell, T.; Genles, S.; Hamlin, N.; Holroyd, Connor, R.; Pajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: C70821
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                             93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable serine proteinase Rv0983 - Mycobacterium tuberculosis (strain H37R)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 VLAIGSPLGLEGT--VTTGIVSALNRPVSTTGE-AGNONTVLDAIGTDAAINPGNSGGAL
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                                                                                NHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPV
                                                                                                                                                                                   VAMGNSGGOGGTPRAVPGRVVALGOTVQASDSLTGAEETLNGLIOFDAAIQPGDAGGPVV
                                                                                                                                                                                                                                                                                   NGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----DINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGEP
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C;Superfamily: Escherichia coli trypsin-like proteinase degS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 NYRSAGGGDLTANVTLAEGPPA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 TWOTKSGGTRIGNVTLAEGPPA 330
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proteinase hhoA (EC 3.4...) - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sll1679
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Dec-2002
C;Accession: S74643
C;Accession: S74643
S;Kaneko, T; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, X.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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to the EMBL Data Library, June 1996
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;Keywords: hydrolase; proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 INPGNSGGALVNMGGQLVGVNSALATLGADSGDAQSGSIGLGFALPVDQAKRIADELIST 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G--KATH----ASLGVQVATDKGTPGAKVMDVVAGGAAANAAVPKGVVLTKVDDRLISSA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 FFQEFFGRSFPVPPRERRIAGGGSGFIIDNSGIILTNAHVVDGASKV-VVTLRDGRTFDG 148
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                                                                                                                                                                                                                                                 74 GA-------TDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG
                                                                                                                                                                                                                                                                                                                                                                                           120 GG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQPGDAGGPVVNGLGQVVGMNTAA----SDNFQLSQGGQGFAIPIGQAMAIAGQIRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGSPTVHIGPTAFLGLGVVDNNGN-GARVQRVVGSAPAASLGISTGDVITAVDGAPINSA
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                                                                                                                                                                                                        18 ADFPALPLDPSAWVAQVG----POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 PPAPVITAQASVPLISESFV-----AAAVSRSGPAVVRIDTETVVTRRIDPILDDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OVRGTDEVTDLAVVKIEPQGSALPVAPLGTSSNLOVGDWAIAVGNPVGLDNT-----
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                                                                                                                                   Gaps
                                                                                                                                       42;
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A;Accession: S74643
A;Accession: S74644
A;Scatus: mucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-394 <KAN>
A;Residues: 1-394 <KAN>
C;Geretics: the nucleotide sequence was submitted to the EMBL Data Line;
                                                                     Length 452;
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21.8%; Score 371; DB 2; Length 39
Best Local Similarity 31.3%; Pred. No. 5.7e-15;
Matches 117; Conservative 50; Mismatches 111; Indels
   F,182,224,305/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449
                                                                                                                                   53; Mismatches 116;
                                                              26.3%; Score 447; DB 2;
larity 37.2%; Pred. No. 2.2e-19;
Conservative 53; Mismatches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 DALVAAVRSKAPGDKVSLTYQDSGSSRTVQVTLGK
                                                                                           Local Similarity
es 125; Conserv
                                                                 Query Match
Best Local S
Matches 125
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Holroyd,
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145448
probable serine proteinase (BC 3.4.21.-) MLCB373.28 [similarity] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium laprae C;Aates : Judan-2000 #text_change 09-Dec-2002 C;Aacession: T45448
R;James, K.D.; Parkhill, J; Barrell, B.G.; Rajandream, M.A.
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                                                                            RESULT 5
H66930
Cyabale secreted serine proteinase [imported] - Mycobacterium leprae
Cyspecies: Mycobacterium leprae
Cyspecies: Mycobacterium leprae
Cybate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002
CyAccession: H86930
Ry Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroeam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-382 <STO>
A;Accession: 1-382 <STO>
A;Accessidues: 1-382 <STO>
A;Cross-references: GB:AL450380; NID:g13092536; PIDN:CAC29684.1; GSPDB:GN00147
C;Genetics:
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Rijames, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, February 1998
A; Reference number: Z2267
A; Reference number: Z2267
A; Reference number: Z2267
A; Reference number: Z2267
A; Reference number: Z2267
A; Reference number: Z2267
A; Reference number: Z2267
A; Reference number: Z2267
A; Reference number: Z2267
A; Residue: T452
A; Residues: 1-452
A; Residues: 1-452
A; Residues: BmBL: AL035500; PIDN: CAB36690.1
A; Residues: BmBL: AL035500; PIDN: CAB36690.1
A; Residues: L452
A; Residues: MCB373.28
A; Note: MCB373.28
C; Generics: A; Note: MCB373.28
C; Repwerfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tC; Keywords: hydrolase; serine proteinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 VAAKPGGGPGGGLSPKTIVTPP---DGRTASFTVVGADPTSDIAVVRVOSISGLTPITMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- TDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 GG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQPGDAGGPVVNGLGQVVGMNTAA----SDNFQLSQGGQGFAIPIGQAMAIAGQIRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 ADFPALPLDPSAMVAQVG----POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 GGSPTVHIGPTAFLGLGVVDNNGN-GARVQRVVGSAPAASLGISTGDVITAVDGAPINSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch
al Similarity 37.2%; Pred. No. 1.8e-19;
125; Conservative 53; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 TAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAE 326
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APGATVALTFQDPSGGSRTVQVTLGK
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Matches 125; Conserv
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Best Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                               Serine proteinase [imported] - Nostoc sp. (strain PCC 7120)

S.Species: Nostoc sp. PCC 7120

A,Note: Nostoc sp. Strain PCC 7120

S,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C,Accession: AG2150

R,Kaneko, T., Nakamura, Y., Wolk, C.P., Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: alr2758
C,Superfamily: Escherichia coli trypsin-like proteinase degS, GLGF domain homology; tryp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
H97199
http-like serine protease (with PDZ domain) [imported] - Clostridium acetobutylicum http-like serine acetobutylicum c;Species: Clostridium acetobutylicum c;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Dec-2002 C;Accession: H97199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                 ----IR
                                                                                         257 ADATGIGFAIPIDQAKAIQNTLAAGGTVPHPYIG-VQMMNITVDQAQQMNRNPNSPFIIP
                                                                                                                                                                 EVDGILVMRVLPGTPAERAGIRRGDVIVAVDGTPISDGARLQRIVEQAGLNKALKLDLLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALG--QTVQASDSLTGAEETLNGLIQFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 VHIGPTAFLGLGV------VDNNG-----NGARVQRVVGSAPAASLGISTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70; Gaps
201 VTLGIISTLGRSAAQAGIPDKRVEFIQTDAAINPGNSGGPLLMARGEVIGINTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VILGVDGQAİTTABQLQNVVENSRLGQALQVRLQ-RGNQTQQLSVRTAE 402
                                                      207 LSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGV---VDNNGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 407;
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                                                                                                                                ---GARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAM-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.5%; Score 365; DB 2; Le
31.2%; Pred. No. 1.3e-14;
iive 52; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 SAMVAQVGPQVVNINTKLGYNNAV-
                                                                                                                                                                                                      GHHPGDVISVTWQT 312
                                                                                                                                                                                                                                         GDRR---LSLTVQT 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Accession: AG2150
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Best Local Simi
Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
Gene: alr2758
                                                                                                                                                                   316
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A;Reference number: 874322; MUID:97061201; PMID:8905231
A;Accession: 877538
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-423 < KAN>
A;Cross-references: EMBL:D90905; GB:AB001339; NID:g1652360; PIDN:BAA17385.1; PID:g165246:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Dec-2002
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Dec-2002
C;Accession: 877538
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; R; Konunra, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain homology; tryps
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                                                                                                         Solvent-Producing Bacterium Clos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                     A).Cross-references: GB:AE001437; PIDN:AAK80387.1; PID:g15025449; GSPDB:GN00168
A).Experimental source: Clostridium acetobutylicum ATCC824
C).Genetics:
A).Gene: CAC2433
C).Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 GPVVNGLGQVVGMNTAASDNFQLSQGGQ---GFALPIGQAMAIAGQIRSGGGSPTVHIGP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPLVNSFGQVVGINSA-----KISENGVEGIGFSIPIDTVKSKIQNLSK-----P 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNHVIAGATDINAFSVGSGOTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGGVA---V 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 TAFLGLG--VVD------NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 ILMLGISGEAVDKSTAEQHNIPQGVYIEQIQDFSSAQKAGMOVGDVITKFDGKKVTSTSD 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDPSAMVAQVGPQVVNINTKL-------GYNNAVGAGTGIVIDPNGVVLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, j. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A.Title: Genome Sequence and Comparative Analysis of the Solvent-Pro A;Reference number: A96900; MUID:21359325; PMID:21359325
A,Accession: H97199
A,Status: preliminary
A,Residues: 1973 «KUR»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
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C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 452,
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20.6%; Score 349; DB 2; Length 45
Best Local Similarity 29.9%; Pred. No. 1.3e-13;
Matches 109; Conservative 60; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine proteinase (EC 3.4.21.-) htrA - Synechocystis sp. N.Alternate names: protein slr1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.6%; Score 350; DB 2; Lu
larity 31.6%; Pred. No. 1.1e-13;
Conservative 51; Mismatches 111;
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us-09-886-349a-6.rpr

Db 113 GQDDEGGIAGRGMGSGFIISKDGYLTNHHVITGASEV-TIKLTDRREFFAKKIIGSDEGY 171 Qy 101 DVAVLQLRGAGGIPBAAIGGGVAVGEPVVAMGNSGGGGTPRAVPGRVVALGGTVQAS 158 172 DVALLKI-DAKNLPTVRIGBSSLKSGQWVVAIGSPFGLDHSVTAGIVSALGRS 224 Qy 159 DSLTGAEETINGLIQFDAAIOPGDAGGPVVGRWTAASDNFGLSGGGGGFAI 216	PRESULT 12 T35287 Probable secreted proteinase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Accession: T35287 R;Seeger, K; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. S;Species: L35287 A;Rocession: T35287 A;Ac	9y 8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTXLGYNNAVGAGTGIVIDPNGVVLT 67	RESULT 13 AB2057 serine proteinase [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 C;Species: Nostoc sp. strain PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
Qy 24 PLDPSAMVAQVGPQVVNINTKLGYNNAV	Oy 274 STGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLABG 327 : : : :	A; Mostecule Type: UNA A; Mostecule Type: UNA A; Mostecule Type: UNA A; Mostecule Type: UNA A; Residues: 1-514 < Calm> A; Residues: 1-514 < Calm> A; Residues: 1-514 < Calm> A; Residues: 1-514 < Calm> A; Cross-references: GB:AE004037; GB:AE003849; NID:g9107394; PIDN:AAF85040.1; GSPDB:GN001 A; Experimental source: Strain 926. A; Simpson, A. G. G. Reinach, F. C.; Arruda, P.; Abreu, F. A.; Camargo, L. E. A; Carraro, D. M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D. M.; Carrer, H. A; Authors: Ferreira, V.C.A.; Ferro, J. A.; Fraga, J. S.; Franca, A.G.; E. E.; Laign Chado, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.C.; Frohm J. D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J. P.; Kitager, J. E.; Kiramae, E.E.; Laign Chado, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. M. A.; Matchisa, M.C.; Ge Oliveira, R. C.; Palmieri, D. Anthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F. M.; Miracca, E.C.; Miyaki, C.Y.; P. F.G.; Numes, L.R.; Oliveira, M.A.; Ge Oliveira, M.C.; Ge Oliveira, R.C.; Palmieri, D. Anthors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.R.; Silva, M.M.; Silva Jr., W.A.; da Silva, A.R.; Silva, M.M.; Silva Jr., W.A.; da Silva, M.; Genetics: A; Contents: annotation C; Genetics: A; Genetics: C; Genetics: C; Genetics: Annotation	QY 23 LPLDPSAMVAQVGPQVVNINTKLGYNNAV

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C;Genetics:
A;Gene: DR1756
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                                  R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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Gene: TP0773
Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
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A, Residues: 1738 <COL>
A, Cross-references: GB:AE001248, GB:AE000520; NID:g3323074; PIDN:AAC65740.1; PID:g332308
A, Experimental source: strain Nichols
C, Genetics: A, Gene: TEO;
A, Gene: TEO;
C, Superfamily: Escherichia coli trypsin-like proteinase degS, GLGF domain homology, tryp
                                                                                                                                                                                                                                                                                                                                                                       Superfamily: Escherichia coli trypsin-like proteinase degs; GLGF domain homology; tryp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                    A;Residues: 1-416 KKIR>
A;Cross-references: GB:BA000019; PIDN:BAB73707.1; PID:g17131098; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPNFVVGVVQKVGGAVVRIDSARIVISRVPNEFNDPFFRRFFGDGVPAQPRQRVERGSGS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 GIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 AAIGGGVAV--GEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 TDAAINPGNSGGPLLNARGQVIGMNTAIIQGAQ----GLGFAIPINTVQKVSQELITQGK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 SPTVHIG-PTAFLGLGVVD--NNGNGARVQ------RVVGSAPAASLGISTGDVIT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDHPYLGVQMATLTPQVKERINERFGDRINITADRGVLLVRIVPGSPAANAGLRPGDIIQ 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation not shown
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable periplasmic serine proteinase DO (htrA-1) - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Dec-2002 C;Accession: B71284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDAALQPGDAGGPVVNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 AVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGP 328
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 416;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
19.4%; Score 330; DB 2; Length 41
Best Local Similarity 28.7%; Pred. No. 1.6e-12;
Matches 100; Conservative 64; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.4%; Score 329; DB 2; Length 39 clarity 32.1%; Pred. No. 1.7e-12; Conservative 43; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: B71284
A; Status: preliminary; nucleic acid sequence not shown; A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 DPS---AMVAQVGPQVVNINTKLGYNNAV-----
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                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                         A; Molecule type: DNA
                       C; Accession: AB2057
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Best Local Simi
Matches 103;
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A;Gene: all2008
C;Superfamily: E
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à d ò q 8 a ð q ò g

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probable periplasmic serine proteinase Do - Deinococcus radiodurans (strain R1) (Species: Deinococcus radiodurans C)Species: Deinococcus radiodurans C)Date: 03.Dec-1999 #sequence_revision 03.Dec-1999 #text_change 09-Dec-2002 C)Accession: 275357 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mas) S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-441 cMH1-A
A;Cross-references: GBLAB002017; GB:AE000513; NID:g6459527; PIDN:AAF11312.1; PID:g645953(
A;Experimental source: strain R1
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A,Reference number: A75250, MUID:20036896; PMID:10567266
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                                                                                                        136
190
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                                                                                                                                                                                                                                                                               191 LART--LTVGVVSALARPIQNKGSI-----IRNMIQTDAAINPGNSGGFLLDTQGRMIG 242
                                                                                                                                                                                                                                                                                                                                                                  247
                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 GVVDNNGNGARVQRVVGSAPASLGIS-------TGDVITAVDGAPIN 288
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INPGNSGGPLLSSAGOVIGVNTQILTGGAGQSAGVGFAIPINTVKRLLPQLQAGKG--- 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAI------GGGVAVGE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 PVVAMG------NSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQPGDAGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --IST-GDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
                                                                                                                                                            131 LSLHDGSQYKATVVGVDRENDLAVLKFVSPPGARLTVIRFGSSRNLDVGQKVLAIGNPFG
                                                                                                        81 FSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG----VAVGEPVVAMGNSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 QDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
                                                                                                                                                                                                                                     137 QGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPVVNGLGQVVG
                                                                                                                                                                                                                                                                                                                                                                     197 MNTAASDNFQLSQGGQGFAIPIGQAMAIA-----GQIRSG---GGSPTVHIGPTAFLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                    243 INTVIYST-SGSSSGVGFAVPVDTAKRIVSELIRYGRVRRGKIDAELVQVNASIAHYAQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Gaps
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C,Superfamily: Bscherichia coli trypsin-like proteinase degS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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19.4%; Score 329; DB 2; Le
Best Local Similarity 29.3%; Pred. No. 1.9e-12;
Matches 106; Conservative 50; Mismatches 110;
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29 AMVAQVGPQVVNINTKL-GYNNAV-----GAGTGIVIDPNGVVLTNNHVIAGATDINA 80

371 LPSAQGTSSISTDGDLITAVNGQPLEDAGSLQEAVLATGEGQPLRLTVR-RGGKTREVEV 429 д ò

323 TL 324 || 430 TL 431

Op

Search completed: June 22, 2004, 17:24:49 Job time: 10.233 secs

Page

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RESULT 1
US-09-886-349A-6
991.5
990.5
989
987
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1698
1 MHHHHHAPPALSQDRFADF.....QTKSGGTRTGNVTLAEGPPA 330
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Perfect score:
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Description	Sequence 6, Appli	Sequence 6, Appli	Sequence 20, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 19, Appl	Sequence 161, App	Seguence 2, Appli	Sequence 80, Appl	Seguence 79, Appl	Sequence 2, Appli	Sequence 18, Appl	Sequence 16, Appl
ΩІ	US-09-886-349A-6	US-10-098-732A-6	US-10-369-983-20	US-10-369-983-2	US-10-369-983-4	US-09-886-349A-4	US-10-098-732A-4	US-10-369-983-19	US-09-712-363-161	US-09-886-349A-2	US-10-193-002-80	US-10-084-843-79	US-10-098-732A-2	US-10-369-983-18	US-10-369-983-16
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Query Match Length DB	330	330	330	723	1010	330	330	330	355	355	355	355	355	1016	1154
Query Match	100.0	100.0	100.0	100.0	100.0	99.8	99.8	99.8	96.7	96.1	96.1	96.1	96.1	58.9	58.4
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Query Match
100.0%; Score 1698; DB 12; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.5e-121;
Matches 330; Conservative 0; Mismatches 0; Indels 0;

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Ra35FLMutSA
US-09-886-349A-6

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equence 14, equence 15, equence 18, equence 18, equence 18,	equence 2 equence 1 quence 26 equence 2 equence 2 equence 2 equence 2 equence 2	equence 2; equence 2; equence 65; equence 65; equence 8; equence 8;	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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ALIGNMENTS

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Sequence 20, Application US/10369983 Publication No. US20030235593A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 330; Conservative
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LENGTH: 330
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10098732A
| Sequence 6, Application US/20030175294A1
| Publication No. US20030175294A1
| GENERAL INFORMATION:
| APPLICANT: Skeiky, Yasir
| APPLICANT: Brannon, Mark
| APPLICANT: Guderian, Jeffrey
| APPLICANT: Guderian, Jeffrey
| APPLICANT: Growation
| TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a TITLE OF INVENTION: Heterologous Fusion Protein Constructs
| TITLE OF INVENTION: Leishmania Antigen |
| TITLE OF INVENTION NUMBER: US 60/275,837 |
| PRIOR APPLICATION NUMBER: US 60/275,837 |
| PRIOR FILING DATE: 2001-03-13 |
| NUMBER OF SED ID NOS: 80 |
| SOFTWARE: PatentIn Ver. 2.1 |
| SEQ ID NO 6 |
| LEMATH. 2001
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ORGANISM: Artificial Sequence
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APPLICANT: Steiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRICR APPLICATION NUMBER: US 60/357,351
PRICR PLICATION DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1698; DB 15;
Pred. No. 1.5e-121;
Mismatches 0;
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APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
TITLE OF INVENTION: Fusion Proteins of Mycob
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR RILING DATE: 2003-02-15
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/10369983; Publication No. US20030235593A1; GENERAL INFORMATION:
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181 GDAGGPVVNGLGQVVGMVTAASDNFQLSQGGGGFAIPIGGAMAIAGQIRSGGGSPTVHIG 240
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  PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
                                                                          61 PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG
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                                                GVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQP
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US-09-886-349A-4

i Sequence 4, Application US/0986349A

i Sequence 4, Application US/0986349A

i Sequence 4, Application US/0986349A

i Sequence 4, Application US/0986349A

i Publication No. US20040086523A1

i GENERAL INFORMATION:

APPLICANT: Reed, Steven

APPLICANT: Action, Mark

APPLICANT: Alderson, Mark

APPLICANT: Alderson, Mark

CONINCENT APPLICANTON NUMBER: US/09/886,349A

CURRENT APPLICATION NUMBER: US/09/886,349A

CURRENT PILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: US 60/265,737

PRIOR APPLICATION NUMBER: US 60/265,737

PRIOR APPLICATION NUMBER: US 60/265,737

PRIOR APPLICATION NUMBER: US 60/265,737

SOFTWARE: PATENT VET. 2.01

SOFTWARE: PATENT VET. 2.1

SEQ ID NOS: 50

LENGTHARE: PATENT VET. 2.1
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Best Local Similarity 99.7%; Pred. No. 2.6e-121;
Matches 329; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                             301 HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
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; OTHER INFORMATION: MTB32A (Ra35 mature)
US-09-886-349A-4
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US-10-369-983-4

| Sequence 4, Application US/10369983
| Publication No. US20030235593A1
| GENERAL INFORMATION:
| APPLICANT: Skeiky, Yasir
| APPLICANT: Reed, Steven
| APPLICANT: Reed, Steven
| APPLICANT: Reed, Steven
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
| FILE REPERENCE: 014058-090301US
| CURRENT FILING DATE: 2002-02-18
| PRIOR PILING DATE: 2002-02-15
| NUMBER: OF SEQ ID NOS: 22
| SEQ ID NO S: 22
| SEQ ID NO S: 22
| SEQ ID NO S: 22
| SEQ ID NO S: 21
| SEQ ID NO S: 21
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100.0%; Score 1698; DB 15; Length 1010;
Best Local Similarity 100.0%; Pred. No. 5.9e-121;
Matches 330; Conservative 0; Mismatches 0; Indels 0;
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; LENGTH: 723
; TYPE: RRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mutated
; OTHER INFORMATION: MTB32-MTB39F fusion protein (MTB32MutSA)
US-10-369-983.
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100.0%; Score 1698; DB 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-121;
Matches 330; Conservative 0; Mismatches 0; 1
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ORGANISM: Artificial Sequence
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TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 99.7%;
Matches 329; Conservative
SOFTWARE: Patentin Ver.
SEQ ID NO 19
LENGTH: 330
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US-10-369-983-19
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                                                                                                                                                          APPLICANT: Skeaky, Yasir
APPLICANT: Skeaky, Yasir
APPLICANT: Skeaky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologous Fusion Protein Constructs
TITLE OF INVENTION: 104058-01201000
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT APPLICATION NUMBER: US 60/275,837
PRICA APPLICATION NUMBER: US 60/275,837
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVID
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Publication No. US20030235593A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014088-03091US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence:Ra35 mature US-10-098-732A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 330;
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Best Local Similarity 99.7%; Pred. No. 2.6e-121;
Matches 329; Conservative 1; Mismatches 0;
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                                                                                           Sequence 4, Application US/10098732A Publication No. US20030175294A1 GENERAL INFORMATION:
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FEATURE:
                                                                             JS-10-098-732A-4
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APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Rotstein, Sergio H.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: DIFFERMINING THE FUNCTIONS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: DIFFERMINING THE FUNCTIONS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: DIFFERMINES: US/09/712,363
CURRENT APPLICATION NUMBER: US/09/712,363
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/119,26
PRIOR PRILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG
                                                                                                                                                                                                                                                                                         1 MHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQP
                                                                                                                                                                                                                       ;
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OTHER INFORMATION: Description of Artificial Sequence:wild-type OTHER INFORMATION: mature MTB32A (Ra35)
                                                                                                                                              Length 330;
                                                                                                                                                                                                                       Indels
                                                                                                                                              Score 1695; DB 15;
Pred. No. 2.6e-121;
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Patent No. US20020164588A1
GENERAL INFORMATION:
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213 VNGLGQVVGMNTAASDNFQLSQGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGFTAFLGL 272
                                      153 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEFTLNGLIQFDAAIQPGDSGGPV 212
                                                                                                                                                                                   248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
                                                                                                                                                                                                                       273 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 332
    128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV 187
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ZIP: 98104-7092
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: OF MAY 100: 80:
SEQUENCE CHARACTERSTICS:
SEQUENCE CHARACTERSTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.1%; Score 1631; DB 14;
99.1%; Pred. No. 2.1e-116;
1ive 1; Mismatches 2;
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Sketky, Yaair A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 80:
                                                                                                                                                                                                                                                                       308 VTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                      333 VNWQTKSGGTRTGNVTLAEGPPA 355
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; Publication No. USC0030135026A1
; GENEAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 355 amino acids
TYPE: amino acid
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Best Local Similarity 99.1:
Matches 320; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-10-193-002-80
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                                                                                                                                                                                                      8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                               33 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                       93 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
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                                                                                                                                                             Gaps
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Sequence 2, Application US/0986349A

Publication No US20040086523A1

GENERAL INFORMATION:
APPLICANT: Reed, Steven

APPLICANT: Reed, Steven

APPLICANT: Alderson, Mark

APPLICANT: Alderson, Mark

APPLICANT: Alderson, Mark

APPLICANT: Alderson Wark

CONTACT APPLICANT: USES 0.0090/086.349A

FILE REFERENCE: 014058-0090/086.349A

CURRENT APPLICATION NUMBER: US 09/597,796

FRIOR APPLICATION NUMBER: US 60/265,737

FRIOR FILING DATE: 2001-06-20

FRIOR FILING DATE: 2001-02-01

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PATENTIN USE: 201-02-01
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99.1%; Pred. No. 2.1e-116;
iive 1; Mismatches 2;
                                                                                                           Query Match
96.7%; Score 1642; DB 9;
Best Local Similarity 99.7%; Pred. No. 3.1e-117;
Matches 322; Conservative 1; Mismatches 0;
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LENGTH: 355
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
; LENGTH: 355
T TYPE: RRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: MTB32A (Ra35FL)
US-09-886-349A-2
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Best Local Similarity 99.1
Matches 320; Conservative
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US-09-886-349A-2
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Gaps

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128 VVAMGNSGGGGGTPRAVPGRVVALGGTVQASDSLTGAEETLNGLIQFDAA1QPGDAGGPV 187
                                                                       96.1%; Score 1631; DB 14; 99.1%; Pred. No. 2.1e-116;
                                                                                                           1; Mismatches
TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-084-843-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 VNWQTKSGGTRTGNVTLAEGPPA 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: MTB32A (Ra35FL) US-10-098-732A-2
                                                                     Query Match
Best Local Similarity 99.19
Matches 320, Conservative
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Matches 320; Conservative
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         APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                          188 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                                                                                                                                                                             213 VNGLGQVVGNNTAASDNFQLSQGGQFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                              68 NNHVIAGAIDINAFSVGSGQIYGVDVVGYDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                                                                                                                                     128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGABETLNGLIQFDAAIQPGDAGGPV
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Dillon, Davin C.
Camoos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:

COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE
COMPATIBLE
CONTROL SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-WAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               VTWOTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 79, Application US/10084843
Publication No. US2030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-6031
MATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 355 amino acids TYPE: amino acid
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STATE: Washington
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US-10-084-843-79
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SEASTAIN TO SEASTAIN
APPLICANT: SREATHON, Mark
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION NUMBER: US/10/098,732A
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT APPLICATION NUMBER: US 60/275,837
PRIOR PRIOR APPLICATION NUMBER: US 60/275,837
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127
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                                                                                                                                                                                                                                                                                                                                                         68 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
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Length 355;
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99.1%; Pred. No. 2.1e-116;
tive 1; Mismatches 2;
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153 VVAMGNSGGGGGTPRAVPGRVVALGGTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 212
                                                                              213 VNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 272
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                                         VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
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                                                                                                                                                                                                                                                                                                      RESULT 14
US-10-369-983-18
Sequence 18, Application US/10369983
Sequence 18, Application US/10369983
Sublication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Gooderian, Jeff
APPLICANT: Coriax Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPREMENCE: 014658-0090841US
CURRENT APPLICATION UNDBER: US/10/369,983
CURRENT PILING DATE: 2003-02-18
PRIOR PAPLICATION UNDBER: US/10/369,983
CURRENT PILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOCTHARE: Patentin Ver: 2.1
SEQ ID NO 18
LENGTH: 1016
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85.5%; Pred. No. 9.5e-68;
tive 7; Mismatches 13; I
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ORGANISM: Artificial Sequence
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Best Local Similarity 85.5
Matches 206; Conservative
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                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: WIB114F (WIB72F-mICC#2)
US-10-369-983-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPI--NSATAMADA 296
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-00081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
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58.4%; Score 992; DB 15;
Best Local Similarity 72.9%; Pred. No. 4.9e-67;
Matches 212; Conservative 14; Mismatches 37;
                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                  SEQ ID NO 16
LENGTH: 1154
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Search completed: June 22, 2004, 18:07:52 Job time : 30.5644 secs

Sequence 16, Application US/10369983; Publication No. US20030235593A1; GENERAL INFORMATION: APPLICANT: Skeiky, Yasir; APPLICANT: Guderian, Jeff

RESULT 15 US-10-369-983-16

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RESULT 1
AAE29703
ID AAE29703 standard; protein; 330 AA.
                                                                                                                          June 22, 2004, 16:44:25; Search time 40.5137 Seconds (without alignments) 2301.458 Million cell updates/sec
                                                                                                                                                                                                            US-09-886-349A-6
1698
1 MHHHHHHAPPALSQDRFADF.....QTKSCGTRTGNVTLAEGPPA 330
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                               1586107 seqs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. A Geneseq 29Jan04:*

1: geneseqp1980s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2001s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2003bs:*

Database :

Aae29703 Mycobacte
Ada26352 Mycobacte
Ada26356 Mycobacte
Ada26356 Mycobacte
Ada26356 Mycobacte
Ada29702 Mycobacte
Ada26371 Mycobacte
Ada020137 Mycobacte
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Ada03010 Mycobacte
Ada23100 Mycobacte
Ada23100 Mycobacte
Ada26370 Mycobacte
Ada26370 Mycobacte
Ada26360 Mycobacte
Ada26366 Mycobacte
Ada26366 Mycobacte
Ada26366 Mycobacte Description SUMMARIES AAE29703 AAE17567 ADA26354 ADA26356 AAE29705 AAE2970500 AAC22137 AAC31110 AAC31110 AAW32435 AAW32435 AAW32435 AAW32435 AAW32435 AAW32435 AAY38972 AAY39109 AAU01890 AAE29701 AAE17565 ADA26370 ADA26368 ADA26368 Query Match Length DB Result No.

Ada26369 Mycobacte	Aae29709 Mycobacte	Aael7573 Mycobacte	4	Ada26365 Mycobacte	Aay32070 Mycobacte	Aae29710 Mycobacte	Aae17574 Mycobacte	Aau74599 Antigenic	Aao22142 Ra12-H9-3	Aae29708 Mycobacte	Aael7572 Mycobacte	Ada26373 Mycobacte	Aae29731 Mycobacte	Ada26364 Mycobacte	Aau74588 Antigenic	Aay32059 Mycobacte	Aae29704 Mycobacte	Aae17568 Mycobacte	Aay32071 Mycobacte	
ú	AAE29709	AAE17573	ADA26374	ADA26365	AAY32070	AAE29710	AAE17574	AAU74599	AA022142	AAE29708	AAE17572	ADA26373	AAE29731	ADA26364	AAU74588	AAY32059	AAE29704	AAE17568	AAY32071	
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26	27	28	29	30	31	32	33	34	35		37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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ΕX	27-JAN-2003 (first entry)
e X	Mycobacterium tuberculosis Ra35FLMutSA mutant antigenic protein.
K K	Vaccine; immunity; diagnostic agent; gene therapy; Ra35FLMutSA; mutant; antigen; mutein.
SS SS	Mycobacterium tuberculosis. Synthetic
XEEE;	Key Misc-difference 183 /note= "Wild type Ser substituted with Ala"
Y II	WO200272792-A2.
¥8;	19-SEP-2002.
X & ;	13-MAR-2002; 2002WO-US008223.
PR	13-MAR-2001; 2001US-0275837P.
X E S	(CORI-) CORIXA CORP.
PI	Skeiky Y, Brannon M, Guderian J;
* # # # #	WPI; 2002-759844/82. N-PSDB; AAD47078.
Y X	New recombinant nucleic acid molecule comprising a Leishmania ISA, LeIF,
댎	M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity
ው ር ር	against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
: X	
g >	Disclosure, Page 81-82; 155pp; English.
Ę	The invention relates to a recombinant nucleic acid molecule encoding a
50	d comprises a heterolog
88	polynucleotide sequence encoding an antigen or an antigenic fragment from
ပ္ပ	otide sequence end
ខ្ល	polypeptide or its fragment. The Leishmania polynucleotide is selected
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are used in methods for eliciting immune response in mammals. They are useful as vacchies to elicit protective immunity against pathogenic microorganisms such as Leishmannia and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis RaisFIMutSA mutant antigenic protein
                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                                                                                                                    GDAGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium species Ra35FL mature protein mutant (S183A), Ra35FLMutSA.
                                                                                                                                                                                                                            PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG
                                                                                                                                                                                                                                                                                                 PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; Ra32FLMutSA protein; mutant; mutein.
                                                                                                                                                                                                            MHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVID
                                                                                                                                                                                                                                                                                                                                                                                       GDAGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIG
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0
                                                                                                                                                  Length 330;
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                                                                                                                                                                               Indels
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                                                                                                                                               Score 1698; DB 5;
Pred. No. 1e-123;
Mismatches 0;
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/note= "Ra35 N-terminal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
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                                                                                                                                                 100.0%;
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01-FEB-2001; 2001US-0265737P.
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Best Local Similarity 100.
Matches 330, Conservative
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sara from individuals infected with cuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, cuseful for eliciting an immune response in a mammal, e.g., human, and prevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human control proteins of the invention are also used as vaccines. MTBJZA animal. Sequences of the invention are useful as in vivo diagnostic againts for intradermal skin test. The present sequence is Mycobacterium species and increase mutant (S183A), Ra35FLMutSA
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                                                                                             Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
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100.0%; Pred. No. 1e-123;
live 0; Mismatches 0;
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                                                                                                                                                           Claim 73, Fig 6, 136pp; English.
Alderson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.'
Matches 330; Conservative
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                                      WPI: 2002-147798/19
Skeiky Y, Reed S,
                                                           N-PSDB; AAD28337
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fusion polypeptide; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
tuberculosis; tuberculostatic; gene therapy; vaccine; mutant; mutein.
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                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                15-FEB-2002; 2002US-0357351P
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Best Local Similarity 100.
Matches 330; Conservative
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                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP
                                                                Mycobacterium sp.
                                                                                                Key
Misc-difference
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                                                                                                                                                                WO2003070187-A2
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB35A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                                                                fusion polypeptide; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
tuberculosis; tuberculostatic; gene therapy; vaccine.
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100.0%; Pred. No. 2.7e-123;
ive 0; Mismatches 0;
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                                                                                                Mycobacterium MTB32-MTB39F fusion protein.
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Matches 330; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-697554/66.
N-PSDB; ADA26353.
                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                                                                                                                    Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 723 AA;
                                                                                                                                                                                                                                  WO2003070187-A2.
                                                              20-NOV-2003
                                                                                                                                                                                                                                                                    28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky Y,
                                ADA26354;
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RESULT 4 ADA26354

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animal. The invention is used in gene therapy. The present sequence is M. tuberculosis mature Ra35 (N-terminus of MTB32A; RA35FL) antigenic protein
New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                Vaccine; immunity; diagnostic agent; gene therapy; Ra35 antigen.
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                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis mature Ra35 antigenic protein.
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                                                                                                      301 HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
                                                                HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by GAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Encoded by GCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 79-80; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guderian J;
                                                                                                                                                                                                                AAE29702 standard; protein; 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity 99.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-759844/82.
N-PSDB; AAD47077.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 182
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Best Local Simi
Matches 329;
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                                                                                                                                                                                                                                                          AAE29702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32B and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB93 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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0
                                                                                                                                                                                                                                                                              fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
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; Pred. No. 4.1e-123;
0; Mismatches 0;
           301 HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                      Mycobacterium MTB-102F fusion protein.
                                                                                                              ADA26356 standard; protein; 1010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reed S;
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100.0%;
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Best Local Similarity 100.
Matches 330; Conservative
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                                                                                                                                                                                                                                                                                                                                              Chimeric.
Mycobacterium sp.
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the real part and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as infection or monitoring of disease progression, as patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species MTB32A (MTB32A) (MTB32A) (MTB32A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
  serological sensitivity of sera from individuals infected with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 330;
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                                                                                                                                                                                                                                                                                                                                                                                                     99.8%; Score 1695; DB 5;
99.7%; Pred. No. 1.7e-123;
ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330
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                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Best Local S
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Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to fusion proteins containing at least tw Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase
                                                                                                                                    GVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEBTLNGLIQFDAAIQP
                                                                                                GVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGABETLNGLIQFDAAIQP
                                                                                                                                                                                    GDAGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIG
                                                                                                                                                                                                                          GDSGGPVVNGLGQVVGMYTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIG
                                                                                                                                                                                                                                                                     PTAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH
               PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serological sensitivity, immune vaccine, MTB32A, Ra32FL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199. .330
/note= "Ra35 C-terminal peptide, Ra12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium sp. MTB32A (Ra35FL) mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide"
                                                                                                                                                                                                                                                                                                                                                        HPGDVISVTWQTKSGGTRIGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                     HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8. .202
/note= "Ra35 N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Encoded by GCG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE17566 standard; protein; 330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70; Fig 6; 136pp; English.
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01-FEB-2001; 2001US-0265737P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; antigen;
losis; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
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N-PSDB; AAD28336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                           The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32B and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polynucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG 120
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                                                                 New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ĠĎŚĠĠPVYNGLĠQVVGMNTAASDNPQLSQGQQGFAIPIGQAMAIAGQIRSGGGSPTVHIG
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MHHHHHAPPALSQDRFADFPALFLDPSAHVAQVGPQVVNINTKLGYNNAVGAGTGIVID
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                 Score 1688; DB 7; Length 330;
Pred. No. 6.1e-123;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 330
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                                                                                                                                                    Disclosure, Fig 19, 112pp; English
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                                                                                                                                                                                                                                                                                                                                                     99.47
Best Local Similarity 99.43
Matches 328, Conservative
             Guderian J,
                                         WPI; 2003-697554/66
                                                                                                                                                                                                                                                                                                                            Sequence 330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium
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              Skeiky
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                                                                                                                                                                                                                 Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serine protease antigen, MTB32A; Mycobacterium tuberculosis;
ne; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVAMGNSGGGGGTPRAVPGRVVALGQTVQASDSLTGARETLNGLIQFDAAIQPGDSGGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 VNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                                                                                                                                                                                                                                                                                                             8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
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                                                                                                                                                                                                                                                                                                                                            Length 355
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                               Guigueno A;
                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 99.7%; Pred. No. 2.5e-119;
Matches 322; Conservative 1; Mismatches 0;
                                                              Pelicic V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis MTB32A protein.
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                                                                                                                                                                                                 Claim 32; Fig 50D; 309pp; French
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97FR-00010404
97FR-00011325
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                                                               Gicquel B, Portnoie D, L
Goguet De La Salmoniere Y;
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                                       (INSP ) INST PASTEUR
                                                                                                      WPI; 1999-181045/15.
N-PSDB; AAX34251.
                                                                                                                                                                       protein expression
                                                                                                                                                                                                                                                                                                                       Sequence 355 AA;
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 14-AUG-1997;
11-SEP-1997;
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Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the sequences.
                                                             Mycobacterium tuberculosis potential drug target protein SEQ
                                                                                                               Drug target; growth; organism viability; characterisation.
                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1999; 99US-0165086P.
12-NOV-1999; 99US-0165124P.
01-FEB-2000; 2000US-0179531P.
                                                                                                                                                                                                                                                                                                                          13-NOV-2000; 2000WO-US031152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eisenberg D, Rotstein SH,
                                                                                                                                                                 Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA
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           04-SEP-2001
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 to 14 t
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                                                                                                                                                                                                                                                                                                                                       Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
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                                                    06-OCT-2000; 2000WO-US027652
                                                                                                      99US-0158585P
                                                                                                                                                                                                             Guderian J;
                                                                                                                                                           (CORI-) CORIXA CORP.
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                                                                                                         07-OCT-1999;
12-APR-2001
                                                                                                                                                                                                             Skeiky Y,
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This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAHS1947 - AAHS2092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characteriaing the function of mucleotic caids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
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Disclosure; Page 157; 207pp; English.
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AAG81110 standard; protein; 355

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Skeiky YAW,
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22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
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                                                                                                                                                               Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection.
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99.7%; Pred. No. 2.7e-119;
Live 1; Mismatches 0;
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                                                                                                                                           Mycobacterium species protein sequence 50F.
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333 VTWQTKSGGTRTGNVTLAEGPPA
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                                                                AAY04830 standard; protein; 379
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N-PSDB; AAX34252.
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                                                                                                                                                                                                          Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                              Gicquel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 APPALSODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic polypeptide (s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                  gen; immunogen; vaccine; tuberculosis; non specific adjuvant;
testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.1%; Score 1631; DB 2;
99.1%; Pred. No. 1.8e-118;
iive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis antigen TbRa35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 124-126; 190pp; English
                                               379
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DR;
                           357 VTWQTKSGGTRTGNVTLAEGPPA
VIWOTKSGGTRIGNVTLAEGPPA
                                                                                                                                                                               protein; 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-00523435.
95US-00532136.
96US-00620280.
96US-00658800.
96US-00688033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US014675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                         (first entry)
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Matches 320; Conservative
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NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP

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272
                                                                               GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
153 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M. tuberculosis antigen, TDRa35. The immunogenic protein, and fusion proteins containing one or more of the proteins pus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                    VNGLGOVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                       GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS
                        188 VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMALAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also diagnosis.
                                                                                                                                                                                                                                                                                                                                               Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
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                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis antigen TbRa35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 114-116; 168pp; English.
                                                                                                                                     VTWOTKSGGTRIGNVTLAEGPPA 330
                                                                                                                                                               VNWOTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon DC,
DR;
                                                                                                                                                                                                                                  AAW32435 standard, protein, 355
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96US-00620874.
96US-00659683.
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                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky YA,
1, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-192903/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT91477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                  WO9709428-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-1996;
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12-JUL-1996;
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Vedvick TH,
                                                                                                                                                                                                                                                                                         08-JAN-1998
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22-MAR-1996
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This polypeptide comprises Mycobacterium tuberculosis soluble antigen tuberculosis strain H37Ra expression library with rabbit anti-sera raised against M. tuberculosis supernatant. No significant homology was found between TbRa35 and Genebank database sequences. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AWK64291-W64379) comprising an antigen; or tip provides soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, or an immunogenic portion of an M. polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for
                                                                212
                                                                                            247
                                                                                                                                                      307
                                                                                                                                                                               GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                     NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                VVAMGNSGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV
                                                                                          VNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                                      213 VNGLGQVVGMNTAASDNFQLSQGGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
                                                                                                                                                  GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuberculosis; infection; diagnosis; antigen; TbRa35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis antigen TbRa35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis; strain H37Ra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 115-116; 250pp; English.
                                                                                                                                                                                                              308 VTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC, Ca
                                                                                                                                                                                                                                                                                                                AAW64307 standard; protein; 355 AA.
                                                                                                                                                                                                                               VNWQTKSGGTRTGNVTLAEGPPA
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97US-00818111.
                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW, Di!
3, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV44355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9816645-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1997;
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09-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-1998
                                  128
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2; Indels

Length 355;

Score 1631; DB 2; Pred. No. 1.8e-118;

96.1%;

1; Mismatches

Matches 320; Conservative

Query Match Best Local Similarity

Sequence 355 AA;

prevention

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                                                                                                                                                                                                                VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEBTLNGLIQFDAAIQPGDAGGPV 187
                                                                                                                                                                                                                                                                                          188 VNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 247
                                                                                                                                                                                                                                                                                                                                                 248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
                                                                                                                                                                                                                                                                                                                                                                                                   273 GVVDNNGNGARVQRVVGSAPASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 332
                                                                                                                                                         detecting M. tuberculosis infection in a patient using the above polypeptides, antibodies or oligonuclectide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                   Gaps
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                                                                                                      Query Match

96.1%; Score 1631; DB 2; Length 355;
Best Local Similarity 99.1%; Pred. No. 1.8e-118;
Matches 320; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              VIWOTKSGGTRIGNVTLAEGPPA 330
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                                                                               Sequence 355 AA;
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3333, 11996, 11996, 1309, 1309, 1309,

Sequence Sequence Sequence

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Seguence

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davis Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Howardzik, Thomas S.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: LAND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPTRE: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FLILNG DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: MAK: DAVIG J: 31,392
REPRENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHRAACTERISTICS:
LENGTH: 355 amino acids
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Pred. No. 3.9e-134;
1; Mismatches 2;
US-09-736-457-1863
US-09-636-215-852
US-09-636-215-852
US-09-620-412C-349
US-09-598-419-333
US-09-598-419-333
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US-09-598-419-333
                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 79, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.1%;
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STATE: Washington
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    STRANDEDNESS:
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Best Local Simi
Matches 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-08-818-112-79
    Sequence 79, Appl
Sequence 80, Appl
Sequence 79, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 67, Appl
Sequence 67, Appl
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                                                                                                                                                                                                                                                                               1 MHHHHHHAPPALSQDRFADF.....QTKSGGTRTGNVTLAEGPPA 330
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-818-111-80
US-09-072-596-80
US-09-072-596-80
US-09-223-040-2
US-09-223-040-2
US-09-223-040-2
US-09-281-849-2
US-09-281-849-2
US-09-072-596-67
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US-09-072-596-67
US-09-072-596-67
US-09-072-596-67
US-09-072-596-67
US-09-072-596-67
US-09-072-596-87
US-09-636-215-848
US-09-636-215-848
US-09-636-215-848
US-09-636-215-848
US-09-636-215-848
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S-09-643-597-352
S-09-666-421B-352
S-09-736-457-1864
S-09-643-597-354
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US-09-636-215-835
US-09-685-166A-835
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                                                                                                                                                                                                                                                                                                                                                                                             389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         - protein search, using sw model
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Maximum DB seq length: 200000000
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1698
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Match Length DB
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Length 355; Indels

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273 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 332
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                                                                           33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDFNGVVLT
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               8 APPALSQDRFADFPALPLDPSAWVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF THE PREVENTION C.
TITLE OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSFFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 VTWQTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 VNWQTKSGGTRTGNVTLAEGPPA 355
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 amino acids
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STATE: Washington
COUNTRY: USA
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US-09-056-556-79
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                                                                                                                                                                                                                                                                              128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV 187
                                                               33 APPALSODRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 92
                                                                                                                                                                                                                                                                                                                       8 APPALSODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                       NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
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Patent No. 638852

GENERAL INPORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Thomas S.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: TWARGEN COMPOUNDS AND METHODS FOR DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS OF DIAGNOSIS O
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96.1%; Score 1631; DB 4; Length 355;
Best Local Similarity 99.1%; Pred. No. 3.9e-134;
Matches 320; Conservative 1; Mismatches 2; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: BEATON GARS.

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/818,111

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Mark, David J.

RESTERENTE/POCKET NUMBER: 21,1392

REFERENCE/DOCKET NUMBER: 21,1312

TELECOMMUNICATION NUMBER: 21,1312

TELECOMMUNICATION NUMBER: 21,1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 VIWOTKSGGTRIGNVTLAEGPPA 330
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INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206) 622-4900
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seattle
Washington
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TOPOLOGY:
US-08-818-111-80
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us-09-886-349a-6.rai

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68 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP 127
                                                                                                                                                                              93 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGGVAVGEP 152
                                                                                                                                                                                                                                                            128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV 187
                                                                                                                                                                                                                                                                                                                                                                        188 VNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 GVVDNNGNGARVORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 GVVDNNGNGARVORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 332
                                                                                 33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 92
                                 8 APPALSQDRFADFPALFLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Campos-Net, Antonio
APPLICANT: Gampos-Net, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Verdick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
NAME: MAKI, DAYIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
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REGISTRATION NUMBER: 31,392
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: Washington
COUNTRY: USA
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TOPOLOGY: lin
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                                                                                                      93 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP 152
                                                                                                                                                                  128 VVAMGNSGGOGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV 187
                                                                                                                                                                                                                              212
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                                                                                                                                                                                                                                                                                                                                                                                                248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 92
                                                                                                                                                                                                         Sequence 80, Application US/09072596
Fatent No. 6458366
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Fatent No. 6458366
Fatent No. 6458366
Fatent No. 6458366
Fatent No. 6458366
Fatent No. 6458366
Fatent No. 645836
Fatent No. 1110n, Davin C.
FAPPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Twardzik, Thomas S.
FAPLICANT: Wedvick, Thomas S.
FAPLICANT: Hendrickson, Ronaiel R.
FAPLICANT: Hendrickson, Ronaiel R.
FAPLICANT: Hendrickson, Ronald C.
TILLE OF INVENTION: COMPCUNDS AND METHODS FOR DIAGNOSIS OF INVENTION: CORRESPONDENCE ADDRESS:
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96.1%; Score 1631; DB 4; Length 355;
Best Local Similarity 99.1%; Pred. No. 3.9e-134;
Matches 320; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/072,596 FILING DATE: US/MAY-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210121.417C9
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
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STREET: 650.
CITY: Seattle
The Washington
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ZIP: 98104-7092
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US-09-072-596-80
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188 UNGLGOUVGMNTAAS 202
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.55
Matches 194; Conservative
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LENGTH: 729
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US-09-287-849-2
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68
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APPLICANT: Campos-Neco, Autonio
APPLICANT: Campos-Neco, Autonio
APPLICANT: Campos-Neco, Autonio
APPLICANT: Campos-Neco, Autonio
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
ITILE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
ITILE OF INVENTION: Fusion Protiens
ITILE OF INVENTION: 1990-002002
ITILE OF INVENTION: 1990-002002
ITILE OF INVENTION NUMBER: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/912,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/023,040
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/023,040
PRIOR FILING DATE: 1998-04-07
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                                                                                                                                                92
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                                                                                                                                                                                                                                                                                                                                                                                                                                     8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                              68 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                                                                                 8 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
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Length 355
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                                                  2; Indels
Score 1631; DB 4;
Pred. No. 3.9e-134;
1; Mismatches 2;
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
  Query Match
Best Local Similarity 99.1%;
Matches 320; Conservative
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Sequence 2, Application US/09223040

Sequence 2, Application US/09223040

Sequence 2, Application US/09223040

GENERAL INFORMATION:
APPLICANT: Sealky, Yasir
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009010US
CURRENT APPLICATION NUMBER: US/09/223,040
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 10

SOFTHARE: Patentin Ver. 2.1
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
FILE REFERENCE: 014058-009020US
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                                                     NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP 521
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99.5%; Pred. No. 2.2e-77;
tive 1; Mismatches 0; Indels
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Patent No. 6627198
GENERAL INFORMATION:
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Gaps

Indels

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258 RVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGT 317
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                                                                                                                                                                                                                                                                                                                                                                                      198 NTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGA
                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion US-09-287-849-28
                                                                                                                                                                                                               4; Length 231;
                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                            Score 676; DB 4;
Pred. No. 3e-51;
1; Mismatches
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Patent No. 6290969
GENERAL INFORMATION:
                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                            39.8%;
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Matches 132, Conservative
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US-08-818-112-66
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US-08-818-112-66
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APPLICANT: Skeiky Yasir A.W.
APPLICANT: Skeiky Yasir A.W.
APPLICANT: Skeiky Yasir A.W.
APPLICANT: Skeiky Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Carixa Corporation
TITLE OF INVENTION: Eusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014059-00902003
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 1999-04-07
CURRENT APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1998-04-07
PRIOR PELING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 VVAMGNSGGGGGTPRAVPGRVVALGQTVQASDSLTGAEETINGLIQFDAAIQPGDAGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 APPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 APPALSQDRFADFPALFLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-2
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58.0%; Score 984; DB 4; Length 729;
Best Local Similarity 99.5%; Pred. No. 2.2e-77;
Matches 194; Conservative 1; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR PELING DATE: 1997-03-13
PRIOR PELING DATE: 1997-10-01
PRIOR FILING DATE: 1998-02-18
PRIOR PELING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR PLING DATE: 1998-12-30
NUMBER OF SEC ID NOS: 46
SOFTHARE: PATENTING DATE: 1998-12-30
NUMBER OF SEC ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 28, Application US/09287849; Patent No. 6627198; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 VNGLGQVVGMNTAAS 202
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LENGIH: 729
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Wedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: G300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washigton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.5%; Score 670; DB 3; Length 132; Best Local Similarity 99.2%; Pred. No. 4.6e-51; Matches 131; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 98104-7092
COMPUTER ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Darby disk
COMPUTER: Darby Compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NAMER: US/88/818,112
FILING DATE: 13-MAR-1997
CLESSIFICATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C6
TELEFANC (206) 622-4900
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TELEFANC (206) 622-4900
TELEFANC (206) 622-4900
TELEFANC (208) 645-6031
SEQUENCE CHARACTERISTICS:
TENGTH: 132 amino acids
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FILING DATE:
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APPLICANT:
APPLICANT:
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APPLICANT:
                                     RESULT 12
US-09-056-556-66
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                                                                                                               61 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR 318
TAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 258
                                                                                     259 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTR 318
                    1 TAASDNFQLSQGGQFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 60
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US-08-818-111-67

Sequence 67, Application US/08818111

Sequence 67, Application US/08818111

SEQUENCY Read, Steven G.

APPLICANT: Read, Steven G.

APPLICANT: Dillon, Davin C.

APPLICANT: Dillon, Davin C.

APPLICANT: Houghton, Raymond

APPLICANT: Vedvick, Thomas S.

APPLICANT: Twandzik, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF T.

CORRESPONDENCE ADDRESS:

STREET: SEED and REPOW ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.5%; Score 670; DB 4; Length 132; 99.2%; Pred. No. 4.6e-51; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-AAR-1997
CLASSIFICATION: 424
ATTONENY/AGENT INPORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REBERENCE/POCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 132 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
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Best Local Similarity 99.2'
Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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199 TAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 258
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Sequence 66, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·
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39.5%; Score 670; DB 4; Length 132;
Best Local Similarity 99.2%; Pred. No. 4.6e-51;
Matches 131; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
                                                                                                                                                                                                                          E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210121.457
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Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Yeatr A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REPRENCE/DOCKET NUMBER: 2101;
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto, Antonia
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                            ADDRESSEE: SEED and
STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUMTRY: USA
ZIP: 98104-7092
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199 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 258
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CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOUTHABLE: FESCISEQ for Windows Version 3.0
SEQ ID NO 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 670; DB 4; Length 132;
Pred. No. 4.6e-51;
0; Mismatches 1; Indels
                                                                                                                                                                                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/072,967

FILING DATE: 05-Max-1998

CLASSIFICATION:

ATTONENY AGENT INFORMATION:

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

REFRENCE/DOCKET NUMBER: 210121.411C9

TELEPHONICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEPAX: (206) 622-631

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHRRACTERISTICS:

LENTH: 132 amino acids
                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 819, Application US/09636215
Patent No. 6620922
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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Henderson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
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99.2%;
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Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 39.5
Best Local Similarity 99.2
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 TGNVTLAEGPPA 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                        TUBERCULOSIS
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APPLICANT: Campos-Neto, Attonio
APPLICANT: Campos-Neto, Attonio
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 670; DB 4; Length 132;
Pred. No. 4.6e-51;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKH, DATA: 31.392
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                           STREET: 6300 Columbia Center, 701
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
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Patent No. 6592877
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio APPLICANT: Houghton, Raymond APPLICANT: Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.2%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 TGNVTLAEGPPA 330
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US-09-072-596-67
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US-09-072-967-66
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CITY: SE
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Gaps

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; LENGTH: 132; Type: PRT | 192 | 192 | 192 | 193 | 193 | 194 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195
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Mycobacte Mycobacte M. tuberc M. tuberc Mycobacte M. tuberc

Mycobacte

Mycobacte M. bovis Mycobacte Mycobacte Mycobacte

Mycobacte

ALIGNMENTS

AAE29708

Mycobacte Mycobacte

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Aae29709 N Aae17573 N Aau01902 N Aau01902 N Aau01903 N Ada26367 N Ada26366 N Ada26366 N Ada26368 N Ada26368 N Ada26368 N Ada26368 N Ada26369 N Ada26369 N

AAO22142 AAE29709 ADA26374 ADA26374 AAU01902 AAU01904 ADA263636 ADA263636 ADA263636 ADA263636 ADA263636 ADA263636 ADA263636 ADA263636 ADA263636 ADA263636 ADA263636 ADA263636

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(first entry)
WPI; 1997-192904/17.
N-PSDB; AAT91432.
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                                                                                                                                                                                                                                                                                                                                            Key
Misc-difference 254
/nc
01-SEP-1995;
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22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
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Vedvick TH,
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Aaw32379 Mycobacte
Aaw2447 Mycobacte
Aaw81680 M. tuberc
Aay32062 Mycobacte
Aay3984 M. tuberc
Aay3984 M. tuberc
Aay39894 M. tuberc
Aae2706 Mycobacte
Aae17570 Mycobacte
Aae17570 Mycobacte
Aaw3281 Mycobacte
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Aaw3281 Mycobacte
Aaw3289 Mycobacte
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Aay39989 M. tuberc
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                                                         June 22, 2004, 16:44:25; Search time 32.2882 Seconds (without alignments) 2301.458 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                           US-09-886-349A-12
1306
1 VAWMSVTAGQAELTAAQVRV......YGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                                                                                               Description
        version 5.1.6 - 2004 Compugen Ltd.
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                      1586107 segs, 282547505 residues
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                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          protein search, using sw model
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AAW648317
AAW648317
AAX32062
AAX32020
AAX32121
AAA239121
AAA29706
AAW81702
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Gapop 10.0 , Gapext 0.5
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3. geneseqp2001s:*
5. geneseqp2002s:*
6. geneseqp2003s:*
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geneseqp2003bs: *
geneseqp2003bs: *
         GenCore (c) 1993
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seq length: 200000000
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Match Length DB
                  Copyright
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Perfect score:
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                                           OM protein
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Maximum DB
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                                                           Run on:
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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                        New immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection.
                                                                                     Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                        Houghton R;
                                                                                                                                                                                                                                                                                                                                                        Campos-Neto A,
                                                                 Mycobacterium tuberculosis antigen TbH-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 138-139; 190pp; English.
                                                                                                                                                                      /note= "Any amino acid"
                                                                                                                                                Location/Qualifiers
AAW32379 standard; protein; 263 AA
                                                                                                                                                                                                                                                                                                                                                      Skeiky YAW, Dillon DC,
4, Twardzik DR;
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95US-00532136.
96US-00620280.
96US-00658800.
                                                                                                                                                                                                                                           96WO-US014675
                                                                                                                          Mycobacterium tuberculosis.
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Aae17571 Mycobacte Aay32070 Mycobacte Aae3710 Mycobacte Aae17574 Mycobacte Aau4559 Antigenic Aay32068 Mycobacte

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(CORI-) CORIXA CORP.
                                                                                                                                                                             Query Match
Best Local Simi
Matches 263;
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13-MAR-1997;
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09-NOV-1998
                                                                                                                                       prevention)
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TbH-9. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis
                                                                                                                                                                    120
                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                          TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
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                                                                                                                                         1 VAWMSVTAGQAELTAAQVRVAAAAXETAYGLTVPPPVIAENRAELMILIATNILGQNTPA
                                                                                                                                                                                  IAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEEAPEMTSAGGLIEQAAAVEEASD
                                                                                                                                                                                                                                                            181 SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA
                                                                                                                                                                     IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                                                                                                             121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
                                                                                                                              1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
skin testing; M.tuberculosis.
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                                                                                        Length 263;
                                                                                                          Indels
                                                                                     99.8%; Score 1304; DB 2; L
100.0%; Pred. No. 3.1e-105;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis antigen TbH-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Any amino acid"
                                                                                                                                                                                                                                                                                                         SVRYGHRDGGKYAXSGRRNGGPA 263
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DR;
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95US-00533634.
96US-00620874.
96US-00659683.
96US-00680574.
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                                                                                                                                                                                                                                                                                                                                                        AAW32447 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
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                                                                                                           Conservative
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I, Twardzik
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N-PSDB; AAT91496.
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                                                                                    Query Match
Best Local Similarity
Matches 263; Conserv
                                                                    Sequence 263 AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
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AAW32447
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                                                                                                                                                                               A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TbH-9. The immunogenic protein, and fusion proteins containing one or more of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.8%; Score 1304; DB 2; 100.0%; Pred. No. 3.1e-105; ive 0; Mismatches 0;
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                                                                                                                                Example 3; Page 126-127; 168pp; English.
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97US-00818111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 263 AA;
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07-0CT-1997;
                                                                  11-0CT-1996;
                                                                             13-MAR-1997;
WO9816646-A2
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                                                                                                                                  TS,
                    23-APR-1998
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                                                                                                                        Reed SG,
Vedvick 7
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AAY32062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises Mycobacterium tuberculosis antigen TbH-9. A DNA sequence (see AAV44371) coding for antigen TbH-9 was isolated from a M. tuberculosis strain H37Rv expression library using sera from patients having pulmonary or pleural tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-0CT-2003 to standardise OS
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and
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                                                                 New isolated Mycobacterium tuberculosis polypeptides and DNA - u develop products for the detection of M. tuberculosis infection diagnosis of tuberculosis.
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  Houghton R;
                                                                                                                                                                                                                                                                                                                               Score 1304; DB 2; Length 263;
Pred. No. 3.1e-105;
0; Mismatches 0; Indels
 Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis immunogenic polypeptide TbH-9
                                                                                                                 Example 3; Page 125-126; 250pp; English
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 Skeiky YAW, Dillon DC, C
;, Twardzik DR, Lodes MJ;
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/label= unknown
                                                                                                                                                                                                                                                                                                                                  99.8%; SCC
100.0%; Pr
tive 0;
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Best Local Similarity 100.4
Matches 263; Conservative
                                   WPI; 1998-251292/22.
N-PSDB; AAV44371.
                                                                                                                                                                                                                                                                                                              Sequence 263 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method inducing protective immunity against tuberculosis (TB). This sequence be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis
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                                                                                                                                                                                                                                                                                                                                      Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used develop products for the detection of M. tuberculosis infection and fidagnosis, treatment and prevention of tuberculosis.
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                                                                                                                                                                                  Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
99.8%; Score 1304; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.1e-105;
Matches 263; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3b; Page 119-120; 230pp; English
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                                                                                                                                                                               Dillon DC, C
DR, Lodes MJ;
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97WO-US018293.
                                                96US-00730510.97US-00818112.
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                                                                                                                                                                                  Skeiky YAW,
                                                                                                                                                                                                                                                                  WPI; 1998-261042/23
N-PSDB; AAV64479.
                                                                                                                               (CORI-) CORIXA CORP
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Wed Jun 23 16:34:25 2004

AAY38984

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Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;

immune response; skin test.

Mycobacterium tuberculosis.

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IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel recombinant antigens and their encod mucleic acids derived from Wycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in biological sample by detecting antibodies which bind with the bolypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as cur vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                              New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                           Dillon DC, Campos-Neto A, Houghton R;
DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.8%; Score 1304; DB 2; L llarity 100.0%; Pred. No. 3.1e-105; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 160-161; 323pp; English
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98US-00072596
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      Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                         Skeiky YAW,
3, Twardzik
                                                                                                                                                                                                                                                                                                                      WPI; 1999-527416/44.
                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
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Best Local Similarity
Matches 263; Conserv
                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ19069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 263 AA;
                                                                                                                    17-FEB-1999;
                                         WO9942118-A2
                                                                                                                                                         18-FEB-1998;
05-MAY-1998;
                                                                                                                                                                                                                                                         Reed SG, S)
Vedvick TS,
                                                                                 26-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the Mycobacterium tuberculosis antigen TbH9. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens such as TbH9. e.g. Mtb32A (see AAY32059) and a TbH9-Tb38-1 fusion. The new fusion proteins are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), and treatment of tuberculosis antibodies), are more effective immunogens than mixtures of the individual protein
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                                                                                                                                                                                                                                                                                                                                                   New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis.
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                    /note= "not identified"
                                                                                                                                                                                                                                                                              Campos-Neto
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                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 4C-D; 83pp; English.
                                                                                                                                                                          98US-00056556
98US-00223040
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Best Local Similarity 100.
Matches 263; Conservative
                                                                                                                                                                                                                                                                            Alderson M,
                                                                                                                                                                                                                                    (CORI-) CORIXA CORP
Misc-difference 254
                                                                                                                                                                                                                                                                                                                   WPI; 1999-601610/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 263 AA;
                                                                                                                                       07-APR-1999;
                                                                                                                                                                          07-APR-1998;
30-DEC-1998;
                                                          WO9951748-A2
                                                                                               14-OCT-1999
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Gaps

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Length 263; Indels 9

Mycobacterium sp

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. Adv39083 to AAV39225 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                             New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
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                                                                                                                                                                                              Houghton R;
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                                                                                                                                                                                            eiky YAW, Dillon DC, Campos-Neto A, Ho
Twardzik DR, Lodes MJ, Hendrickson RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.8%; Score 1304; DB 2; I 100.0%; Pred. No. 3.1e-105; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium sp. TbH9 antigenic protein.
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                                                                                                                                                                                                                                                                                                                              Example 3; Page 115; 299pp; English
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                                                                            99WO-US003268
                                                                                                              98US-00025197
98US-00072967
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Best Local Similarity 100.
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the present invention
                                                                                                                                                                                                Skeiky YAW,
                                                                                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                           WPI; 1999-527409/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 263 AA;
                                                                                                                                                                                                              Vedvick TS,
               WO9942076-A2
                                                                            17-FEB-1999;
                                                                                                                             05-MAY-1998;
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                                               26-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                    New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium
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100.0%; Pred. No. 3.1e-105;
ive 0; Mismatches 0;
                                                                   /note= "Encoded by NAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 84; 155pp; English.
                              Location/Qualifiers
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ID AAE17570 standard; protein; 263
XX
                                                                                                                                                                                                                                                                                     Guderian
                                                                                                                                                                             13-MAR-2002; 2002WO-US008223.
                                                                                                                                                                                                               13-MAR-2001; 2001US-0275837P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                     Brannon M,
                                                                                                                                                                                                                                                                                                                       WPI; 2002-759844/82.
                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP
                                                  Misc-difference 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD47081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 263 AA;
                                                                                                       WO200272792-A2
                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis
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                                                                                                                                         19-SEP-2002
                                                                                                                                                                                                                                                                                     Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
                                            Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB39; TbH9 protein.
                              Mycobacterium species MTB39 (TbH9) protein #1.
                                                                                                /label= Unknown
/note= "Encoded by NAG"
                                                                               ney
Misc-difference 254
                                                                                                                                                                                                                                                                         Claim 83; Page 100; 136pp; English.
                                                                                                                                                       20-JUN-2001; 2001WO-US019959.
                                                                                                                                                                      20-JUN-2000; 2000US-00597796
01-FEB-2001; 2001US-0265737P
                                                                                                                                                                                                                           WPI; 2002-147798/19.
                                                                                                                                                                                             (CORI-) CORIXA CORP
                                                                                                                                                                                                            Skeiky Y, Reed S,
                                                                   Mycobacterium sp
                                                                                                                                                                                                                                   N-PSDB; AAD28340
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 263 AA;
                                                                                                                         WO200198460-A2
              22-APR-2002
                                                                                                                                        27-DEC-2001
AAE17570;
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Alderson M;

The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase exclogical sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. The diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or call-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in an non-human animal. Sequences of the invention are also used as vaccines. MTB32A for intradermal skin test. The present sequence is Mycobacterium species MTB39 (TbH9) protein

Query Match Best Local Similarity Matches 263; Conserv

ö 0; Gaps Length 263; 0; Indels Score 1304; DB 5; L Pred. No. 3.1e-105; 100.0%; Score 1304; Dilarity 100.0%; Pred. No. 3.1 Conservative 0; Mismatches

1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA VAWMSVTAGGAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGGNTPA

à g ò

9 9 61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEWTSAGGLLEQAAAVEEASD 120 120 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAVEEASD

121 TAAANQLMMNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180 181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240 TAAANQIMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA Fusion protein; tuberculosis; Mycobacterium tuberculosis; tuberculostatic; immunogen; vaccine; TbH9-Tb38-1; TbH9; Tb38-1. Campos-Neto A; Alderson M, Antigenic fusion protein TbH9-Tb38-1. SVRYGHRDGGKYAXSGRRNGGPA 263 241 SVRYGHRDGGKYAXSGRRNGGPA 263 Location/Qualifiers AAU74591 standard; protein; 358 AA. Dillon DC, /label= unknown 97US-00818112. 97US-00942578. 98US-00025197. 98US-00056556. 99US-00287849. Mycobacterium tuberculosis (first entry) (revised) CAMPOS-NETO A. Skeiky YA, REED S G. SKEIKY Y A. DILLON D C. ALDERSON M. Misc-difference 254 US2002009459-A1 18-FEB-1998; 07-APR-1998; 30-DEC-1998; 07-APR-1999; 13-MAR-1997; 29-AUG-2003 08-MAY-2002 24-JAN-2002 AAU74591; 181 Reed SG, Chimeric (SKEI/) (DILL/) (ALDE/) (CAMP/) REED/) RESULT 10 AAU74591 ID AAU ద à Db ò d

The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protectin oin animals against the development of tuberculosis. The protectin coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein of the invention. Note: The specification states that this polypeptide is encoded by the polynucleotide shown in ABK14131. (Updated on 29-AUG-2003 New fusion proteins of Mycobacterium tuberculosis antigens, useful for diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis. Claim 1; Fig 4C-D; 62pp; English. WPI; 2002-171134/22.

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Gaps

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133

180 253

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TbH-9FL The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis
                                                                                                                                                                               74 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGQNTPA
                                                                                                                                                                                                       IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                                                                                                         134 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLEPFEEAPEMTSAGGLEGAAAVEEASD
                                                                                                                                                                                                                                                     TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
                                                                                                                                                                                                                                                                      194 TAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWXTVSPHRSPISNMVSMANNHMSMTN
                                                                                                                                                                                                                                                                                                                            254 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA
                                                                                                                                                                                                                                                                                                    SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA
                                                                                                                                                        VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; tuberculosis; non specific adjuvant;
                                                                                                          Length 391;
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                                                                                                                                 0; Indels
                                                                                                        Score 1187; DB 2;
Pred. No. 8.2e-95;
.; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen TbH-9FL
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95US-00533634.
96US-00620874.
96US-00659683.
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DR;
                                                                                                          90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             testing; M.tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US014674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
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                                                                                                                                 Conservative
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I, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen; immunogen;
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                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                   SV 242
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                                                                                   Sequence 391
                                                                                                           Ma.
Local b.
241;
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22-MAR-1996;
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                                                                                                                                                                                           180
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                                                                                                                                                                                                                                                                SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen,
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                                                                                                                                                                   IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; tuberculosis; non specific adjuvant;
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                                              Length 358;
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                                                                       Indels
                                              ; DB 5; L
4.7e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunogenic polypeptide(s) from soluble M. tu.
useful for diagnosis of M. tuberculosis infection
                                                                        ·.
                                       99.8%; Sco. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen TbH-9FL.
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                                                                                                                                                                                                                                                                                        263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC,
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                                                                                                                                                                                                                                                                                                                                                                         AAW32381 standard, protein, 391
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95US-00532136.
96US-00620280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   skin testing; M.tuberculosis
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96US-00680573
                                                                     263; Conservative
  field)
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N-PSDB; AAT91455.
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                                                          Similarity
 standardise OS
                        Sequence 358 AA
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22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
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                                                Query Match
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                                                           Best Local
Matches 26
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This polypeptide comprises Mycobacterium tuberculosis antigen TbH-9FL. It is encoded by genomic DNA (see AAV44395) isolated from a M. tuberculosis strain H37RV genomic library using a probe from clore TbH-9 (see AAV44371). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, or sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonuclectide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 TAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNNVSMANNHMSMTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.9%; Score 1187; DB 2; 99.6%; Pred. No. 8.2e-95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                  Example 3; Page 133-135; 250pp; English.
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S, Twardzik DR, Lodes MJ;
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97US-00818112.
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diagnosis of tuberculosis
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Matches 241; Conservative
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13-MAR-1997;
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Vedvick TS,
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                                               A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TbH-9FL The immunogenic protein, and fusion proteins containing one or more of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAWWSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGGNTPA
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                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.9%; Score 1187; DB 2; Length 391; Best Local Similarity 99.6%; Pred. No. 8.2e-95; Matches 241; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculosis; infection; diagnosis; antigen; TbH-9FL.
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     Example 3; Page 138-139; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon DC, Ca
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97US-00818111.
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Vedvick TS, Twardzik DR,
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N-PSDB; AAV44395.
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WPI; 1999-181045/15.
N-PSDB; AAX34030.
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Best Local Similarity
                                                                                                                                                                              Sequence 391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           SV 242
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                                                                                                        This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
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                                         Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
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                                                                                                                                                                                                            Score 1187; DB 2; Length 391;
Pred. No. 8.2e-95;
1; Mismatches 0; Indels (
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                                                                                      Example 3B; Page 128-129; 230pp; English
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Best Local Similarity 99.6
Matches 241; Conservative
           WPI; 1998-261042/23.
N-PSDB; AAV64503.
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11-SEP-1997;
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wycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
                                                                                                                                                                                                                               Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 VAWMSVIAGQAELIAAQVRVAAAAYETAYGLIVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IAVNEAEYGEMWAQDAAAMFGYAAATATATTLLPFEEAPEMTSAGGLLEQAAAVEEASD
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                                                                                                                                                                    Claim 32; Fig 5R; 309pp; French
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OF TUBERCULOSIS
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ZIP: 98104-702
ZIP: 98104-702
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J
REGISTRATION NUMBER: 210121.411C6
TELECOMMINICATION INFORMATION:
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

LENGTH: 263 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Description, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
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99.8%; Score 1304; DB 3; L
Best Local Similarity 100.0%; Pred. No. 4.8e-116;
Matches 263; Conservative 0; Mismatches .0;
US-09-073-009-142
US-09-073-010-142
US-09-287-849-12
US-09-287-849-12
US-09-477-135A-131
US-08-311-731A-57
US-08-311-731A-508
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Patent No. 6290969
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TOPOLOGY: linear
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Patent No. 6290200
THEORMATION:
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US-08-818-112-91
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CITY: Sea
STATE: Wa
COUNTRY:
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1446.225 Million cell updates/sec
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                                                                                                                                                                                  June 22, 2004, 17:07:54 ; Search time 9.38833 Seconds
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1306
1 VAWMSVTAGQAELTAAQVRV.....YGHRDGGKYAXSGRRNGGPA
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6 >> Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-056-556-91
US-09-072-596-92
US-09-072-596-92
US-09-287-849-8
US-09-072-596-107
US-09-056-556-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext
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Match Length
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Maximum DB
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NAME: Maki, David J.
REGISTRATION NUMBER: 21,392
REFERENCE/DOCKET NUMBER: 211
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 91:
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CITY: Seattle
STATE: Washington
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US-09-056-556-91
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Best Local S:
Matches 263,
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                          1 VAWMSVTAGQABLTAAQVRVAAAAXETAYGLTVPPPVIAENRABLMILIATNLLGQNTPA
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4.8e-116;
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APPLICANT: Campos-Netto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas 8.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/818,111 FILING DATE: 13-MAR-1997 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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Mismatches
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100.0%; Pred. No. 4
:ive 0; Mismatche
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REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                      241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                              Sequence 92, Application US/08818111 Patent No. 6338852 GENERAL INFORMATION:
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Skeiky, Yasir A.W.
Dillon, Davin C.
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
Matches 263; Conservative
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MEDIUM TYPE: Floppy
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121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSWANNHMSMTN 180.
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                                                                                         TAAANQLMNNVVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNWVSMANNHMSMIN
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                                                    TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
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US-05-056-556-91
Squence 91, Application US/09056556
Patent No. 6380456
GENERAL INFORMATION:
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/056,556
FILING DATE: 07-APR-1998
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121 TAAANQLMINVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
               SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
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APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Wedylton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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100.0%; Pred. No. 4.8e-116;
ive 0; Mismatches 0;
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FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                        241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                  241 SVRYGHRDGGKYAXSGRRNGGPA 263
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COMPUTER READABLE FORM:,
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 91, Application US/09072967
: Patent No. 6592877
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ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAYIG J.
REGISTRATION NUMBER: 31,392
REPRENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION:
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                                                                                                                                                                                                                                                                                                                  Reed, Steven G.
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Matches 263; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and E
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STATE: Washington
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APPLICANT: Reed, 8
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                                                                                  181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
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121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
VENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNE: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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Patent No. 6458366
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APPLICANT: Reed, Steven G.
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 263; Conservative
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STREET: 63
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APPLICANT:
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APPLICANT:
TITLE OF II
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STRANDEDNESS:
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RESULT 7
US-08-818-112-107
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANTON: Fusion Prottiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: 1999-04-07
CURRENT APPLICATION NUMBER: US 08/918,112
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,3040
PRIOR APPLICATION NUMBER: US 09/023,040
PRIOR APPLICATION NUMBER: US 09/023,040
PRIOR APPLICATION NUMBER: US 09/023,040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.8%; Score 1304; DB 4; Length 358; Best Local Similarity 100.0%; Pred. No. 7.4e-116; Matches 263; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), OTHER INFORMATION: Xaa = any amino acid US-09-287-849-8
                                                                                                                    241 SVRYGHRDGGKYAXSGRRNGGPA 263
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; Sequence 8, Application US/09287849
; Patent No. 6627198
; GENERAL INFORMATION;
; APPLICANT: Reed, Steven G.
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ORGANISM: Artificial Sequence
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Compounds S.
APPLICANT: Wardzik, Daniel R.
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APPLICANT:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 108/08/818,112
FILING DATE: 108/08/818,112
FILING DATE: 108/08/818,112
FILING DATE: 108/08/818,112
FILING DATE: 108/08/818,112
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J. 392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 107:
SEQUENCE CHRRACTERISTICS:
LENGTH: 391 amino acids
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E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 107, Application US/08818112
Patent No. 6290969
                                                                                                                                                                    Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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amino acid
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STATE: Washington
COUNTRY: USA
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US-09-072-596-102
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                    GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reek, Steven G.
APPLICANT: Brain A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Genos-Neto, Antonia
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF INTMER OF SECUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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90.9%; Score 1187; DB 4; Length 391;
Best Local Similarity 99.6%; Pred. No. 1.1e-104;
Matches 241; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Flopy disk
COMPUTER: Flopy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FLING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REBERBNOCH/DOCKET NUMBER: 210121.417C6
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 102: SEQUENCE CHARACTERISTICS:
LENGTH: 391 mmino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                      3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-056-556-107
; Sequence 107, Application US/09056556
US-08-818-111-102
; Sequence 102, Application US/08818111
; Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 TAAANQLMANVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 253
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                                                                                 COMPOUNDS AND METHODS FOR THE PREVENTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1187; DB 4; Length 391; Pred. No. 1.1e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE PARENTIN Release #1.0, Version #1.30 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556 FILLED DATE: 07-APR-1998 CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J. 31,392 REFERENCE/DOCKET NUMBER: 31,392 REPERENCE/DOCKET NUMBER: 210121.457 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                   3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                               STREEJ:
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPAtible
COMPUTER: IRM PC COMPATIBLE
COMPUTER: OF COMPATIBLE
COMPUTER: OF COMPATIBLE
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// Patent No. 6458366
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Netc, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AN
NUMBER OF SEQUENCES: 241
CORRESPONDENCES: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10'
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 622-4900
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Best Local Similarity 99.69
Matches 241; Conservative
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134 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAVEEASD 193
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                                                                 APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 391;
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APPLICATION NUMBER: US/09/072,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1187; DB 4;
Pred. No. 1.1e-104;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/09/072,967
05-MAY-1998
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Patent No. 6627198
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasır A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky, Yasir A.W.
Dillon, Davin C.
Alderson, Mark
Campos-Neto, Antonio
Corixa Corporation
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INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
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99.68;
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Best Local Similarity 99.6
Matches 241; Conservative
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STREET: 6300
CITY: Seattle
THE: Washington
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US-09-072-967-107
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US-09-287-849-26
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardaik, Daniel R.
APPLICANT: Twardaik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and The SECOND AND METHODS FOR DIAGNOSIS OF
NUMBER OF SECONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1187; DB 4; Length 391;
Pred. No. 1.1e-104;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                               3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J. 31,392
REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 107, Application US/09072967
Select No. 6522877
GENEBAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio APPLICANT: Houghton, Raymond;
APPLICANT: Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.6
Matches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    STREET: 63.0
CITY: Seattle
STATE: Washington
"mov; USA
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TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY:
US-09-072-596-102
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180

Gaps

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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Compos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TILE REPERSONS: 104058-009010US
CURRENT APPLICATION NUMBER: US/09/223,040
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
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                                                                                                                                                                                                                                                      FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-22
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US-09-223-040-2
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                                                                                                                                                                                                                                                                                                                                                                   Length 600,
                                                                                                                                                                                                                                                                                                                                                              Query Match 90.9%; Score 1187; DB 4; Length 6
Best Local Similarity 99.6%; Pred. No. 2e-104;
Matches 241; Conservative 1; Mismatches 0; Indels
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90.5%; Score 1182; DB 4;
Best Local Similarity 99.2%; Pred. No. 8.1e-104;
Matches 240; Conservative 1; Mismatches 1;
                                     09/223,040
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        PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 600
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-223-040-2
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TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens;
TITLE OF INVENTION: and Their Uses
FILE OF INVENTION: and Their Uses
CURRENT APPLICATION NUMBER: 025/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/918,112
PRIOR APPLICATION NUMBER: US 08/918,112
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-02-18
PRIOR PAPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1999-04-07
PRIOR PAPLICATION NUMBER: US 09/025,56
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 46
SECTHARE: PartentIn Ver: 2.1
SEQ ID NO 26
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa coproration
ITILE OF INVENTION: and Their Uses
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ITILE OF INVENTION: and Their Uses
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/918,112
PRIOR APPLICATION NUMBER: US 08/918,112
PRIOR APPLICATION NUMBER: US 08/925,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
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, OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
US-09-287-849-26
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Patent No. 6627198
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-287-849-22
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APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Cariax Corporation
TITLE OF INVENTION: Evision Protisions of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REPERBERGE: 014058-00902008
FILE REPERBERGE: 1999-04-07
FILE REPERBERGE: 1999-04-07
FRICA FILING DATE: 1997-03-13
FRICA FILING DATE: 1997-10-01
FRICA FILING DATE: 1998-02-18
FRICA FILING DATE: 1998-02-18
FRICA FILING DATE: 1998-04-07
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TAAANQIMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                        335 TAAANQLMANVVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 394
                                                                                                                                                        181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSGLGGSGGGVAANLGRAA 240
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; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-2
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90.5%; Score 1182; DB 4; Length 729;
Best Local Similarity 99.2%; Pred. No. 8.1e-104;
Matches 240; Conservative 1; Mismatches 1; Indels
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Patent No. 6627198
GENERAL INFORMATION:
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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455 SV 456
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US-09-287-849-2
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SV 456

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Search completed: June 22, 2004, 17:27:31 Job time: 9.38833 secs
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June 22, 2004, 17:23:10; Search time 24.3589 Seconds (without alignments) 3048.105 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1306
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 12, Appl		Sequence 91, Appl		Sequence 8, Appli	Sequence 8, Appli	Sequence 14, Appl	Sequence 102, App	Sequence 107, App	Sequence 14, Appl	Sequence 26, Appl.	Sequence 20, Appl	Sequence 26, Appl	Sequence 20, Appl	Sequence 22, Appl
QΙ	US-09-886-349A-12	US-10-193-002-92	US-10-084-843-91	US-10-098-732A-12	US-09-287-849-8	US-10-359-460-8	US-09-886-349A-14	US-10-193-002-102	US-10-084-843-107	US-10-098-732A-14	US-09-287-849-26	US-09-886-349A-20	US-10-359-460-26	US-10-098-732A-20	US-09-287-849-22
DB	12	14	14	14	σv	14	12	14	14	14	σ	12	14	14	σ
% Query Match Length DB	263	263	263	263	358	358	391	391	391	391	596	296	596	296	600
% Query Match	99.8	99.8	8.66	99.8	99.8	99.8	90.9	90.9	90.9	90.9	6.06	90.9	6.06	90.9	90.9
Score	1304	1304	1304	1304	1304	1304	1187	1187	1187	1187	1187	1187	1187	1187	1187
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equence 22, Ageneral B. Agener	Sequence 62455, A Sequence 64892, A Sequence 126, App Sequence 62027, A
US-10-359-460-22 US-096-983-2 US-096-983-2 US-10-098-732A-18 US-10-369-983-22 US-10-369-983-12 US-10-369-983-13 US-10-369-983-13 US-10-369-983-13 US-10-369-983-13 US-10-369-983-14 US-10-369-983-14 US-10-369-983-14 US-10-369-983-16 US-10-369-983-16 US-10-369-983-16 US-10-369-983-16 US-10-369-983-16 US-10-369-983-16 US-10-369-983-16 US-10-369-983-16 US-10-369-983-16 US-10-369-983-16 US-10-369-983-16 US-10-369-88-16-16 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	US-10-282-12 US-10-282-12 US-09-073-009 US-09-793-306 US-10-282-12
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ALIGNMENTS

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                                                                                                               JOHNSTON TO SKEIKY, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Red, Steven
APPLICANT: Red, Steven
APPLICANT: Adderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
TITLE OF INVENTION: NUMBER: 05/99/886,349A
CURRENT APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
PEATURE:
COTHER INFORMATION: MTB39 (TbH9)
PEATURE:
NAME/KEY: MOD RES
COTHER INFORMATION: Xaa = any amino acid
US-09-886-349A-12
                                              , Sequence 12, Application US/09886349A
, Publication No. US20040086523A1
, GENERAL INFORMATION:
RESULT 1
US-09-886-349A-12
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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEEAPEMTSAGGILEQAAAVEEASD 120
                                                                                                                                                                                                                                              SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA. 240
                              1 VAWMSVTAGGAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                               TAAANQIMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                             61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHODS FOR IMMUNOTHERAPY OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PATENTIN Release #1.0, Ver
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 91: US-10-084-843-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND ME
                                                                                                                                                                                                                                                                                                                                                                   SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                  241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 91, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 263 amino acids
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STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS
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STATE: Washington
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US-10-084-843-91
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IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAVEEASD 120
                                 IAVNBAEYGEMWAQDAAAMFGYAAATATATATLLPPEBAPEMTSAGGLLEQAAAVEBASD
                                                                                 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
                                                                                                                       121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
                                                                                                                                                                 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.8%; Score 1304; DB 14; Best Local Similarity 100.0%; Pred. No. 1.1e-106; Matches 263; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-0ul-2002
CLASSIFICATION: OUNHOWNDS
PRIOR APPLICATION: AUNHOWNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANI: Skeiky, Yasir A.W.
Dillon, Davin C.
Gampos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPONDS AND ME
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-10-193-002-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                  SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                        241 SVRYGHRDGGKYAXSGRRNGGPA 263
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TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                        US-10-193-002-92
Sequence 92. Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 263 amino acids TYPE: amino acid
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TELEFAX: (206) 682-6
INFORMATION FOR SEQ ID NO: 92:
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COUNTRY: USA
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Matches 263; Conserva
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US-10-098-732A-12

Sequence 12, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir

APPLICANT: Brainon, Mark

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Leishmania Antigen

FILE REFERENCE: 014058-01201003

CURRENT APPLICATION NUMBER: US/10/098,732A

CURRENT PILING DATE: 2003-04-29

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 12

LENGTH: 263
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                                                                                                                                                                                                                         181 SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 240
                                                                                                                                                                                                                                                                                                IAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                              61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEBASD 120
                                                                                                                                                                                                      TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
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                                                                                             1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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                                                                  1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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Query Match 99.8%; Score 1304; DB 14; Length 263; Best Local Similarity 100.0%; Pred. No. 1.1e-106; Matches 263; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
99.8%; Score 1304; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 263; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: MTB39 (TbH9)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (254)
OTHER INFORMATION: Xaa = any amino acid
US-10-098-732A-12
                                                                                                                                                                                                                                                                                                                                             241 SVRYGHRDGGKYAXSGRRNGGPA 263
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ORGANISM: Mycobacterium tuberculosis
FEATURE:
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241 SVRYGHRDGGKYAXSGRRNGGPA 263
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Sequence 8, Application US/09287849
| Sequence 8, Application US/09287849
| Patent No. US2002009459A1
| GENERAL INFORMATION |
| APPLICANT: Skeldy, Yasir A.W. |
| APPLICANT: Skeldy, Yasir A.W. |
| APPLICANT: Skeldy, Yasir A.W. |
| APPLICANT: Skeldy, Yasir A.W. |
| APPLICANT: Skeldy, Yasir A.W. |
| APPLICANT: Alderson, Mark |
| APPLICANT: COTIXA COTPORATION |
| TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens |
| TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens |
| TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens |
| TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens |
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COTHER INFORMATION: Xaa = any amino acid
US-09-287-849-8
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241 SV 242
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                                                                   APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
FILE REPERENCE: 044508-0902008
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
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OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
OTHER INFORMATION: protein TDH9-TD38-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.8%; Score 1304; DB 14; Length 358; Best Local Similarity 100.0%; Pred. No. 1.7e-106; Matches 263; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR PILING DATE: 1999-04-07
PRIOR PELING DATE: 1997-03-13
PRIOR PELING DATE: 1997-03-13
PRIOR PILING DATE: 1997-03-13
PRIOR PILING DATE: 1997-03-13
PRIOR PILING DATE: 1997-10-01
PRIOR PILING DATE: 1997-10-01
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-12-30
NUMBER: PATENT DATE: 1998-12-30
NUMBER: PATENT DATE: 1998-12-30
NUMBER: PATENT DATE: 1998-12-30
NUMBER: PATENT DATE: 1998-12-30
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Sequence 8, Application US/10359460 Publication No. US20030147911A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: MOD RES
LOCATION: (254)
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Sequence 14, Application US/09886349A Publication No. US20040086523A1 GENERAL INFORMATION:

US-09-886-349A-14

RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 313.
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                                                              APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-0090700S
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.9%; Score 1187; DB 12;
99.6%; Pred. No. 3.8e-96;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 102, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: MTB39 (TbH9FL) US-09-886-349A-14
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
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ADDRESSEE: SEED ar
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STATE: Washington
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Best Local Similarity 99.65
Matches 241; Conservative
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; SEQUENCE DESCRIPTION: SEQ ID NO: 107: US-10-084-843-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SV 242
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US-10-098-732A-14
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US.10-084-843-107
Sequence 107, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
Skeiky, Yasia A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
Amd Diagnosis of TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WHERE: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596

FILING DATE: 05-MAY-1998

ATTORNEY/AGENT INFORMATION:
NAME: MAKi, David J.
REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.417C9

TELEPHONE: (206) 622-4900

TELEPAK: (206) 622-4900

TELEFAK: (206) 622-631

INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 391 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.6'
Matches 241; Conservative
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1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.
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COMPUTER READABLE FORM:
COMPUTER: PROBABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: Detentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 25-Feb-2002
CLASSIFICATION: cUnknown>
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PRIOCAMASATALANO.

APPLICATION NUMBER: US/09/072,967

FILING DATE: 05-MAY-1998

ATTORNEY/AGENT INFORMATION.

NAME: Maki, David J.

REGISTRATION NUMBER: 21.392

REFERENCE/DOCKET NUMBER: 210121.411C9

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

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TELEPHONE: (206) 622-4900
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ORGANISM: Artificial Sequence
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APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/912,578
PRIOR PELLING DATE: 1997-10-018
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,297
PRIOR APPLICATION NUMBER: US 09/025,297
PRIOR APPLICATION NUMBER: US 09/025,297
PRIOR APPLICATION NUMBER: US 09/025,207
PRIOR APPLICATION NUMBER: US 09/025,207
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 VAWMSVIAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 133
                                                                                                                                                                                                                                                                                                                                                                                                 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                               1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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A OTHER A PRORMATION: Description of Artificial Sequence:bi-fusion
US-09-287-849-26
                                                                                                                                                                                                  Query Match 90.9%; Score 1187; DB 14; Length 391; Best Local Similarity 99.6%; Pred. No. 3.8e-96; Matches 241; Conservative 1; Mismatches 0; Indels 0
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; SEQ ID NO 14
; LENGTH: 391
; LENGTH: 391
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; CTHER INFORMATION: MTB39 full length (TbH9FL)
US-10-098-732A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/09287849
Patent No. US20020009459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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LENGTH: 596
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82 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGQNTPA 141
                                                                                                                                142 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 201
                                                                                                                                                                                                                                                                                                                                                                    262 SGVSMINITLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 321
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                                                                     IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
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Sequence 20, Application US/08886349A

Publication No. US20040086523A1

GENERAL INCORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Reed, Steven

APPLICANT: Reed, Steven

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

FILE REFERENCE: 014058-009070US

CURRENT APPLICATION NUMBER: US/09/886,349A

CURRENT APPLICATION NUMBER: US 09/597,796

PRIOR APPLICATION NUMBER: US 09/597,796

PRIOR APPLICATION NUMBER: US 00/265,737

PRIOR PILING DATE: 2001-06-20

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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CTHER INFORMATION: Description of Artificial Sequence:bi-fusion:
CTHER INFORMATION: protein TbH9-Ra35 (designated MTB59F)
US-09-886-349A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sv 323
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TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-287-849-22
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Squence 26, Application US/10359460

Squence 26, Application US/10359460

Publication No. US20030147911A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Application Mark

APPLICANT: Campos Aleo, Antonio

APPLICANT: Campos Aleo, Antonio

APPLICANT: Campos Aleo, Antonio

APPLICANT: Campos Aleo, Antonio

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APPLICANT: Campos Aleo, Antonio

APPLICANT: Campos Aleo, Antonio

APPLICANT: Oliver: 2009-02-05

FILE REFERENCE: 014058-009020US

CURRENT FILING DATE: 1997-03-03

PRIOR APPLICATION NUMBER: US 08/9225, 040

PRIOR FILING DATE: 1997-00-01

PRIOR APPLICATION NUMBER: US 09/025, 157

PRIOR PLING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

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PRIOR FILING DATE: 1998-02-19

PRIOR FILING DATE: 1998-02-10

PRIOR FILING DATE: 1998-02-10

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90.9%; Score 1187; DB 14; Length 596;
Best Local Similarity 99.6%; Pred. No. 6.6e-96;
Matches 241; Conservative 1; Mismatches 0; Indels 0
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Publication No. US20030175294A1
SENERAL INPORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brainon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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US-10-098-732A-20
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US-V28/-WAP-ZZ
Sequence 22, Application US/09287849
Fatent No. US2002000945941
Gammar No. US2002000945941
Gammar No. US2002000945941
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Canpos-Neto, Antonio
APPLICANT: Canpos-Neto, Antonio
APPLICANT: Canpos-Neto, Antonio
APPLICANT: Canpos-Neto, Antonio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGGLLEQAAAVEEASD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TAAANQIMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNWVSMANNHMSMTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 TAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 261
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TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a FILE REFERENCE: 014058-01201001 CURRENT APPLICATION: Leishmania Antigen CURRENT APPLICATION NUMBER: US/10/098,732A CURRENT FILING DATE: 2003-04-29 PRIOR PAPLICATION NUMBER: US 60/275,837 PRIOR PAPLICATION NUMBER: US 60/275,837 PRIOR FILING DATE: 2001-03-13 NUMBER OF SEQ ID NOS: 80 SOFTWARE PARENTH Ver. 2.1 SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:bi-fusion OTHER INFORMATION: protein TbH9-Ra35 (designated MTB59F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.9%; Score 1187; DB 14; Length 596;
99.6%; Pred. No. 6.6e-96;
tive 1; Mismatches 0; Indels 0
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) TYPE: PRT CRGANISM: Artificial Sequence ; PEATURE:) OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-22

0 0; Gaps Query Match

Query Match

Best Local Similarity 99.6%; Pred. No. 6.6e-96;

Matches 241; Conservative 1; Mismatches 0; Indels

ò Dp δ QQ à QQ ò qq ò qq

1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 60

121 TAAANQLANNVPPALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180

Search completed: June 22, 2004, 18:07:54 Job time: 24.3589 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

June 22, 2004, 16:59:04; Search time 7.35842 Seconds (without alignments) 3438.018 Million cell updates/sec US-09-886-349A-12 1306 1 VAWMSVTAGQAELTAAQVRV.....YGHRDGGKYAXSGRRNGGPA 263 Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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1 (2)	01.	'n	39	N	74	PPE
m	949	72.7	393	7	9	probable PPE prote
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S		m.	42	7	33	PPE
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00	42	ď.	40	7	33	PPE:
σ	0	Ö	41	7	99	
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11		o.	46	7	93	PPE
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13		φ.	39	N	G70881	PPE
14		σ.	46	7	B70932	PPE prot
15		φ.	38	~	A70646	PPE prot
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22		'n	40	7	5	41
23	255	4.	42	0	C70582	
24		4.	330	7	10	PPE
25	ω,	4.	36	N	990	PPE prot
26		H	96	N	7052	PPE prot
27		o	SS	N	7057	le PPE prot
28	271.5	o	371	~	E70969	prot
29		20.4	H	~	7083	ole PPE p

probable PPE prote	H H H	PPE	PPE	БРЕ	e PPE	PPE	e PPE	PPE	PPE		PPE	PPE	probable PPE prote	probable PPE prote	probable PPE prote
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618	678	1053	615	443	487	346	2523	655	3157	479	204	987	1436	582	645
19.7	19.6	19.2	18.8	18.6	18.6	18.6	18.5	18.3	18.2	18.1	18.0	17.7	17.5	17.4	17.1
257	255.5	250.5	245	243.5	243	242.5	242	239	238	236	235	231.5	229	227	223.5
3.0	31	32	33	3.4	E E	36	3.7	8	6.6	4 0	4	1 2	4.3	4	4.5

ALIGNMENTS

	RESULT 1 B70608 probable C;Species	PPE protein - Mycobacterium tuberculosis (strain H37RV) : Mycobacterium tuberculosis
	C;Date: C;Access R;Cole,	C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Cct-1999 C;Accession: B70608 R;Cole, S.T. Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. - Conor, R.: Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
	Rajandre Nature	am, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares; S. 93. 537-544. 1998
	A; Title:	A.Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.fille: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A.beserand number. A10500: MITD:98295987; PMID::9634430
	A; Access	A) Accession: B70608
	A;Statu: A;Molecu	nucieic acia sequence not snown; cranstation mod
	A, Residu A, Cross	A,Residues: 1-391 <col/> A,Cross.references: GB:293777; GB:AL123456; NID:g3261726; PIDN:CAB07839.1; PID:e311073; F
_	A; Experiment; C; Genetics: A; Gene: PPE	A,Experimental source: strain H3/kv C,Genelics: A,Gene: PPE
	Query Mat Best Loca	Query Match 90.9%; Score 1187; DB 2; Length 391; Best Local Similarity 99.6%; Pred. No. 8.68-74; Matches 241. Concervative 1: Mismatches 0; Indels 0; Gaps 0;
	λō	1 VAWMSVTAGQAELTAAQVR
	qq	
	δ	61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
-	qq	134 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEBAPEMTSAGGLLEGAAAVEEASD 193
	δλ	121 TAAANQLAMANVEQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
	Ωp	194 TAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 253
	δλ	181 SGVSMTNTLSSMLKGFAPAAAQAQVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 240
	q	254 SGVSMINTISSMIKGFRAPAAAAQAVQTAAQNGVRAMSSIGSSIGSSGLGGGGVAANIGRAA 313
	ζ	241 SV 242
	QQ	314 SV 315
	RESULT H70741 probabl C;Speci C;Date:	RESULT 2 H70741 probable PPE protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

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CiSpecies: Mycobacterium tuberculosis
CiSpecies: Mycobacterium tuberculosis
CiSpecies: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
CiAccession: C70568
Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Mature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:99295987; PMID:9634230
                                                                                                                                                                                                                                                               A;Residues: 1-396 <COL>
A;Residues: 1-396 <COL>
A;Cross-references: GB:Z75555; GB:AL123456; NID:g3261608; PIDN:CAA99966.1; PID:e250360; A;Experimental source: strain H37Rv
C;Genetics: A;Gene: PPE
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C;Accession: H70741

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:9829597; PMID:9634230

A;Accession: H70741

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSLGSSGLGGGGVAANL 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                           76.7%; Score 1001.5; DB 2; 84.1%; Pred. No. 3.9e-61; ive 13; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.1%
Matches 207; Conservative
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74 VAWMSVTAGOAQLTAAQVRVAAAAYETAYRLTVPPPVIAENRTELMTLTATNLLGQNTPA 133

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A)Residues: 1-403 <COL>
A)Residues: 1-403 <COL>
A)Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17728.1; PID:e1254616; A)Experimental source: strain H37Rv
C)Genetics:
A,Gene: PPE
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(Species: Mycobacterium tuberculosis
(Species: Mycobacterium tuberculosis
(Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
(SAccession: B70931
(SACCESSION: B70931
(SACCESSION: B70931
(SACCESSION: B70931), T.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwall, T.; Cantles, S.; Hamilin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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(Species: Mycobacterium tuberculosis
(C)Species: Mycobacterium tuberculosis
(C)Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNWVSMANNHMSMTN 180
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                      194 TAAANQLMNNVPQALQQLAQPAQGVVPSSKLGGLWTAVSPHLSPLSNVSSIANNHMSMMG
                                                                                                                                                                                                                                                                                                                                                                                                      181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSS----LGSSLGSSGLGGGVAANL
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Pred. No. 3.4e-24;
5; Mismatches 73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GLGGALVAPLGSAGGLGGTVAAGLGNAATV 330
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43.3%; Pred
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Best Local Similarity 43.3%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 GRAASV 318
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70932
B;Cole, S.T.; Brosch, R.; Parkhill, J.; Carnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devien, R.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitchead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome shaftenene number: A70500; MJID:98295987; PMID:9634230
A;Reference number: A70500; MJID:98295987; PMID:9634230
A;Reterius: preliminary; nucleic acid sequence not shown; translation not shown
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Best Local Similarity 38.8*
Matches 104; Conservative
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R; Connor, R.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davise, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G.
A.Atthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Atthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Atthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Atthors: Communer: A70500; MUID:98295987; PMID:9634230
A.Atthors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A.Accession: G70929
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70931
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-423 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17722.1; PID:e125461
A;Gene: PPE
A;Gene: PPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 IMMTEAQYMEMWAQDAAAMYGYAGSSATA-SRMTAFTEPPQTTNHGQLGAQSSAVAQTAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.8%; Score 441; DB 2; Length 423; Best Local Similarity 41.2%; Pred. No. 7e-23; Matches 117; Conservative 30; Mismatches 67; Indels '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 KIGGKPITGALAPLAEFALHTPILGSEGLGGGSVSAGIGRAGLV 327
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PPE-family protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
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C;Species: Mycobacterium leprae
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Horse,
R;Cole, S.T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: H87056
A;Accession: H87056
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AL450380; NID:g13093150; PIDN:CAC31563.1; GSPDB:GN00147
C;Genetics:
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                    251 ASFFYNTEGLPYFSIGMGNNFIQSAKTL-GLIGSAAPAAVA----AAGDAAKGLPGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 --LEQAAAVEEASDTAAANQLMNN-----VPQALKQ----LAQPTQGTTPSSKLGG--L
                                                                         RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 WMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILLATNILGQNTPAIA
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192 TAQSTLTEMITGLPNALQSLTSPLLQSS-NGPLSWLWQILFGTPNFPTSISALLTDLQPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 EVVEEVVEAEQAISQAALDQAVNEGMEATVVPQVDQQVNVDVATPQTAVPDSSSAAAPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 424.5; DB 2;
; Pred. No. 9.3e-22;
36; Mismatches 99;
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                                                                                                                                                                                                                                                                                            305 MLG----GGPVAAGLGNAASV 321
                                                                                                                                                                                                                     222 SLGSSGLGGGVAANLGRAASV
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Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Authors: Gares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome s. A.Accession: B70625
A.Accession: B70625
A.Accession: B70625
A.Scatus: preliminary; nucleic acid sequence not shown; translation not shown
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A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17723.1; PID:e1254612: A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-391 «COL»
A;Cross-references: GB:292539, GB:AL123456; NID:g3261714; PIDN:CAB06873.1; PID:e304546; E
A;Experimental source: strain H37Rv
C;Genetics:
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: C7031
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davsies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seelen, S.; Seelton, S.; Squares, S.
Natura 393, 537-544, 1998
A;Authoris Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authoris Septence number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70931
A;Accession: C70931
A;Accession: C70931
A;Accession: C70931
A;Andelluminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                        C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 IMATEALYAEMWAQDALAMYGYAAASG-AAGMLQPLSPPSGTTNPGGLAAQSAAVGSAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 TAAVNQVSVADLISSLPNAVSGLASPVTSVLDSTGLSGIIADIDALLATPFVANIINSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHMS-MTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 LAWITYTAEAAAHAGSQAMASAAAYEAAYAMTVPPEVVAANRALLAALVATNVLGINTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TAAANQ-----LMMNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSP--ISNMVSMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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                                                                                                                                                                                                                   probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
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----AAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASV 242
                                    ||| || : | : | || || || EGAKAAGEAAKALPAAVPAIPSAGL-SGVAGAVGQAASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
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; Pred. No. 2.9e-20;
40; Mismatches 99;
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Best Local Similarity 39.6%;
Matches 99; Conservative 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 GASLGEATLV 318
                                                                                                                                                                                                                                                                                                                     C; Accession: B70625
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                       A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17729.1; PID:e125461
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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A;Residues: 1-413 <COL>
A;Cross-references: GB:Z05436; GB:AL123456; NID:G3261770; PIDN:CAB08826.1; PID:e316565; A;Experiental source: strain H37Rv
A;Genetics: A;Gene: PPE
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-011-1999 #sequence_revision 17-011-1999 #text_change 22-oct-1999
C;Accession: F70560
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Perlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70560
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                 73 VAWISVTAGQAEQAGAQAKIAAGVYETAFAATVPPPVIEANRALLMSLVATNIFGQNTPA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 IAATEAHYAEMWAQDAAAMYGYAGSSATA-SQLAPFSEPPQTTNPSATAAQSAVVAQAAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TAAA-----NOLMMNVPQALKQLAQPTQGTTPSSKLGGLWXTVSPHRSPISNMVSMAN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 NHMSMTNSGVS-----MTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSL-GSSLGS-S 226
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                                                                                                                                                                                                                                                                                                                        VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGONTPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.9%; Score 403; DB 2; Length 413; llarity 36.9%; Pred. No. 2.7e-20; Conservative 38; Mismatches 86; Indels
                                                                                                                                                                                                   Length 409
                                                                                                                                                                                                                                                            92; Indels
                                                                                                                                                                                            Query Match 32.3%; Score 422; DB 2; Best Local Similarity 42.2%; Pred. No. 1.3e-21; Matches 108; Conservative 34; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGVSMTNTLSSMLKGFAPAA---AAQAVQT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 GLGGGVAANLGRAASV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 PLGGGATGGIARAIYV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 GAANAQALTDIPKAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 103; Conserv
             A; Residues: 1-409 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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	Query Match Query Match Query Match Best Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Anatches Local Similarity 37.6%; Pred. No. 2.3e-19; Anatches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Anatches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Similarity 37.6%; Pred. No. 2.3e-19; Matches Local Sale Sale Sale Sale Sale Sale Sale Sa	Gaps 11; C;Species: Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: B70932 C;Accession: B709
1 Score 402; DB 2; Length 463; Similarity 35.7%; Pred. No. 3.6e-20; 14; Conservative 37; Mismatches 106; Indels 62; Gaps 104 VAWMSVTAGQAELTAAQVRVAAARTARGGLYOPPVIAENBAELMILIATMLGGNTPA 1 VAWMSVTAGQAELTAAQASAAAAYEAAFAATVPPPVVAANBAELAVLAATNILGGNTPA 1 IAVNEASTGEMARQDAAAMFGYAAATATATTLLPFEEAPEMTSAGGLLEQAAAVEASD 1 IAAAEARYAEMWAQDAAAMFGYAAATATATTLLPFEEAPEMTSAGGLLEQAAAVEASD 1 IAAABARYAEMWAQDAAAMFGYAAATATATTLLPFEEAPEMTSAGGLLEQAAAVEASD 1 IAAABARYAEMWAQDAAAMFGYAAATATATTLLPFEEAPEMTSAGGLLEQAAAVEASD 1 IAAABARYAEMWAQDAAAMFGYAAATATATTLLPFEEAPEMTSAGGLLEQAAAVEASD 1 IAAABARYAEMWAQDAAAMFGYAAAATATATTLLPFEEAPEMTSAGGLLEQAAAVEASD 1 IAAAANQLAMNNVPQALKQLAQGTTPSSKLGGLWKTVS-PHRSPTTNAAGLATGGVAAVQAAG 1 IAAAANQLAMNNVPQALYGGTTPSSKLGGLWKTVS-PHRSPTTNAAGLATGGVAAVQAAGGGGAAANGGAAAA 1 I I I I I I I I I I I I I I I I I	.d 0 .d ed 10 . 0 00 .ed .e. 0.	Query Match Query Match Query Match Query Match Best Local 10, 20.2%; Score 395; DB 2; Length 408; Matches 110; Conservative 31; Mismatches 78; Indels 64; Gaps 1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAERRAELMITATNLLGQNTPA 1 VAWMSTAGGAELGAGQARQAAAAAAYELAFAMTVPPPVVANRALLYALVATNFFGQNTPA 61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEGAAAV 1

Search completed: June 22, 2004, 17:24:51

Job time : 8.35842 secs

us-09-886-349a-12.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 22, 2004, 16:46:13 ; Search time 4.37699 Seconds (without alignments) 3128.737 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-886-349A-12 1306 1 VAWMSVTAGQAELTAAQVRV......YGHRDGGKYAXSGRRNGGPA 263

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	011031 mycobacteri	mycobact	mycobact								O06246 mycobacteri	Q50703 mycobacteri	Q24523 drosophila	P35658 homo sapien		Q10169 schizosacch	Q9fec4 chlamydomon		-					P40472 saccharomyc		mycoba	homod	рошоч	sacche	Q9ul36 homo sapien	herpes	emeric	Q63850 mus musculu
SUMMARIES	ID	YD61 MYCTU	YI02 MYCTU	92	YF48 MYCIU	Y878_MYCTU	Y442_MYCTU	Y096_MYCTU	SRA MYCLE	YU18 MYCTU.	YU21 MYCTU	YY29 MYCTU	YY25_MYCTU	BUN2_DROME	N214_HUMAN	TRG1_ECOLI	YAUG_SCHPO	RAA3_CHLRE	PRY3_YEAST	STFR_ECOLI	FLO1_YEAST	PRY2_YEAST	SFRG HUMAN	YM96_YEAST	SIM1_YEAST	FXC1_MOUSE	YJ83_MYCTU				2236 HUMAN		ď	NU62_MOUSE
	Length DB	1	63	80	678 1	43	87	63	08	34	35	78	9.	11	060	38	354	93	81	20	537	50	on O	40	75	53	60	11	43	75	845	25	416 1	56
a	Query Match I	76.7	0	0	19.6	മ	α	4	4	2	N	ч	ч	8.8	8.6	8.5	8.2	8.1	7.9	7.8	7.7	7.6	7.6	7.6	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5
	Score	1001.5	402	395	255.5	243.5	243	194.5	191.5	158.5	158	156	152	114.5	112	110.5	107.5	106	103.5	102	100.5	66	66	66	98.5	98.5	98.5	98.5	98.5	98.5	98.5	86	97.5	97.5
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P22865 lactococcus O60269 homo sapien	P31503 rattus norv P35827 campylobact	P35828 caulobacter P51610 homo sapien	P51611 mesocricetu P27921 gallus gall	P03764 bacteriopha Q9u6al drosophila	P31368 drosophila P46839 mycobacteri
US45_LACLC Y514_HUMAN	PO21_RAT SLAP_CAMFE	SLAP_CAUCR HFC1_HUMAN	HFC1_MESAU JUND_CHICK	STF LAMBD PROS DROVI	PDM1_DROME CTPA_MYCLE
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461	632 939	1025	323	774 1556	601 780
7.4	7.4	7.4	7.3	 	7.2
96.5 96.5	96.5 96	96 95.5	95.5 95	9 9 0 0	94.5
3.44 5.5	36	8 6 8 7	4 4 1 4	4 4 3 6	4 4 4 5

ALIGNMENTS

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TIGR; MT1851;
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Q10813;
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                                                                                                                                                                                                                                        TAAANQLMINIVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                                                                                                                                                                                                                                        74 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 133
                                                                                                                                                                                                            134 IAVNEAEYGEMWAQDAAAMFGYAATAATATEALLPFEDAPLITNPGGLLEQAVAVEEAID 193
                                                                                                                                                                                                                                                                                                              9
                                                                                                                            1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                             SGVSMINILSSMLKGFAPAAAQAVQTAAQNGVRAMSS----LGSSLGSSGLGGGVAANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES=M. Luberculosis; STRAIN=H37Rv;
SPECIES=M. Luberculosis; STRAIN=H37Rv;
COLE S.T., Brosch R., Pear-6134220;
COLE S.T., Brosch R., Pear-6134220;
COLE S.T., Brosch R., Pear-613420;
COLE S.T., Brosch R., Pear-613420;
COLE S.T., Engine R., Gas S., Barry C.E. III, Tekaia F.,
Davies R., Devlin K., Feltwell T., Centles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Coliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares R.,
Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;
Complete genome sequence.";
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=M.tubercilosis; STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                 'n
                                                                    76.7%; Score 1001.5; DB 1; Length 396; 84.1%; Pred. No. 2.4e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                 21; Indels
Pfam; PF00823; PPE; 1.
Hypothetical protein. Complete proteome.
CONFLICT 158 159 TA -> AT (IN REF. 2).
SEQUENCE 396 AA, 40015 MW, 6AFAE0D785F66B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MXY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical PPB-family protein RV1802/MT1851/Mb1830.
RV1802 OR MT1851 OR MTV049.24 OR MB1830
                                                                                                 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis, and Mycobacterium bovis.
                                                                                                Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                      237 GRAASV 242
                                                                                                                                                                                                                                                                                                                                                                               GRAASV 318
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   X102 MYCTU
053951;
                                                                     Query Match
                                                                                                                                                                                                                                                                                               181
                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEEAPEMTSAGGILEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 IAAAEARYAEMWAQDAAAMYGYAGSSSVAT-QVTPFAAPPPTINAAGLATQGVAVAQAVG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 ASAGN-ARSLVSEVLEFLA--TAGTNYNKTVASLMNAVTGVPYASSVYNSMLGLGFAESK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SMINSGVSMINILSSMLKGFAPAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 MVLPANDTVISTIFGMVQFQKFFNPVTPFNPDLIPKSALGAGLGLRSAISSGLGSTAPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 AAQAVQTAAQNGVR-----AMSSLGSSLGSSCLGGGGVAANLGRA-----ASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Gaps
SPECIES=M.bovis; STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeiner K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeiner K., Camus J.-C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
-! - SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv2892c/MT2959/Mb2916c.
Rv2892C OR WT2959 OR MTCY274.23C OR MB2916c.
Mycobacterium tuberculosis, and
Mycobacterium bovis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterines, Mycobacterium.
NCBI_TAXID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.8%; Score 402; DB 1; Length 46 Best Local Similarity 35.7%; Pred. No. 8.2e-21; Matches 114; Conservative 37; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuberculist; Rv1802; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hyporhetical protein; Complete proteome.
CONFLICT 401 401 S -> L (IN REF. 2).
SEQUENCE 463 AA; 46021 MW; EE64828BF09FA551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AL022021; CAA17723.1; -- EMBL, AA607044; AAK46123.1; -- EMBL; BX246340; CAD94533.1; -- PIR; C70931; C70931.
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192 PPLATTAAVPQLLQQLSSTSLIPWYSALQQWLAENLLGLTPDNRMTIVRLLGISYFDEGL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculist; Rv1548c; -...
InterPro; IPR000030; Microbac PPE.
InterPro; IPR0002899; Mycobac pentapep.
Pfam; PF01469; Pentapeptide_2; 11.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z74020; CAA98335.1; -.
EMBL; AE007026; AAK45866.1; ALT_INIT.
PIR; A70762; A70762.
TIGR; MI1599; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 393:537-544 (1998).
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                              YF48 MYCTU
Q10778;
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YF48 MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.2%; Score 395; DB 1; Length 408;
38.9%; Pred. No. 2.2e-20;
.ive 31; Mismatches 78; Indels 64; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IAVNEABYGEMWAQDAAAMFGYAAATATATATLIPFBEAPEMTSAGGILEQAA----V 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 VAWLSATAGOAEQAGMQARAAAAYELAFAMTVPPPVVVANRALLVALVATNFFGONTPA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 IAATEAQYAEMWAQDAAAMYAYAGSAAIAT-ELTPFTAAPVTTSPAALAGQAAATVSSTV 191
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                                SPECIES=M tuberculosis; STRAIN=H37Rv;

KEDLINE=98295987; PubMed=9634230;

MEDLINE=98295987; PubMed=9634230;

Cole S.T. Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elglmeier K., Barknu D., Erown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holrcyd S., Horisby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A. Hornsby T., Jagels K., Skelton S., Squares S., Squares T., Seeger K., Skelton S., Squares S., Squares T., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;

R. Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                        Harris D.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SPECIES—M. tuberculosis; STRAIN-CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ernolaeva M., Salzberg S.L.,
Bishai W., Jacobs W.R. Tr., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Tr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPECISE=M.bovis; STRAIN=AF2122/97;
SPECISE=M.bovis; STRAIN=AF2122/97;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.",
"The Complete genome sequence of Mycobacterium bovis.",
"The SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculist; Rv2892c; -.
Interpro; IPR000030; Microbac_PPE.
Pfaus PF00823; PPE; Hypothetical protein; Complete proteome.
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EMBL; AE07119; AAK47285.1; -.
EMBL; BX248344; CAD96603.1; -.
PIR; G70925; G70925.
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155 WKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98295987; PubMed=9634230; MEDLINE=98295987; PubMed=9634230; MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Horsby T., Jagels K., Kroph A., McLean J., Mule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares R., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Beciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
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11-0CT-2003 (Rel. 43, Last annotation update)
11-0CT-2003 (Rel. 43, Last annotation update)
11-0CT-2003 (Rel. 43, Last annotation u
                                                                                                                                                                     252 ------LOFEASLAQQAIPGTPGGAG--DSGSSVLDSWGPTIFA
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J. Bacteriol, 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                  215 AMSSL--GSSLGS-----SGLGGGVAANLGRAAS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 ASPSVAGGGAVGGVQTPQPYWYWALDRESIGGSVSAALGKGSS 333
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TRANSMEM 14 34 POTENTIAL.
TRANSMEM 180 200 POTENTIAL.
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EMBL, Z73101; CAA97385.1; --
EMBL, ZA00697; AAK45143.1; ALT_INIT.
PIN. C.70780; C70780.
TIGR, MT0901, --
TUBETCHIST, RV0878C; --
INTERPO, IPR000030; Microbac PPE.
INTERPO, IPR002989; Mycobac Perapep.
Pfam, PF01469; Pentapeptide_2; 4.
Pfam, PF01463; PPE, Hypothetical protein; Transmembrane; Rep
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POTENTIAL.
POTENTIAL.
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ALA-RICH.
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MEDLINE=87137260; PubMed=3029018;
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29.3%;
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79
79
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STRAIN=H37RV;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                       181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANL---- 236
                                                                                                                                                                                               75 WLTTAAAQAEQAAGQAQAAVSAFEAALAATVHPGAVSANRGRLRSLVASNLLGQNAPAIA 134
                                                                                                                                                                                                                                            63 VNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGGLLEQAAAVEEASDTA 122
                                                                                                                                                                                                                                                                                    135 AVEAVYEOMWAADVAAMLGYHGEASAVALSLTPFTPSP-----SAAATPGGAVII 184
                                                                                                                                                     3 WMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 LG------SFNPGSANTGSVNLGNANIGDLNLGSGNIGSYNLGGGNTGDLNPDS
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                                                                                                                                                                                                                                                                                                                                                               Cole S.T., Broad, F. Marchall J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Ellilingworth T., Connor B., Davies R., Deviln D., Ellilingworth T., Connor B., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Squares S., Squares R., Schlon S., Squares S., Squares R., "Deciphering the blology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Deloher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Lr., Veneer J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 184:5479-5490(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                 19.6%; Score 255.5; DB 1; Length 678; 27.3%; Pred. No. 1.7e-10; tive 34; Mismatches 97; Indels 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 258 D -> G (IN REF. 2).
678 AA; 66736 MW; 209F1593D52533A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 GRAASVRYGHRDGGKYAXSGRRNG 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98295987; PubMed=9634230;
                                                                                      Local Similarity 27.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Q10540;
CONFLICT
                                                                                                                                                                                                                                                                                                                                   123
                                                                   Query Match
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DAC OLOCTI

DT 01-0CTI

DT 01-0CTI

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OC Bactel

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 IAATEASYEQLWAQDVAAWVGYHGGASTVASQLTPWQQ------LLSVLPPVVTAAP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 AGAV-----GVPAA---LAIPALGV---ENIG------VGNFLGIGNIGNNNVG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 MTNSG-----VSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGS-----SL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 SGNTGDYNFGIGNIGNAN-LGNGNIGNANLGSGNAGFFNFGNGNDGNTNFGSGNAGFLNI 282
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                                   restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMV---SMANNHMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Repeat; Complete proteome.
the European Bioinformatics Institute. There are no restrict
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Bacteriol. 169:1080-1088(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 X 10 AA APPROXIMATE REPEATS.
C58BEC607F0675E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 GSSGLGGGVAANLGRAASVRYGHR--DGGKYAXSGRRNGG 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 243.5; DB 1
; Pred. No. 7.2e-10;
38; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y442_MYCTU STANDARD; PRT; 487 AA. P42611, 053.72; 2. P42611, 053.72; 3. Created) 16-0CT-2001 (Rel. 40, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) 110-0CT-2003 (Rel. 42, Last annotation update) RV0442C OR MT0458 OR MTV037.06C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAG-----GLLEQAAA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 NTGSGNIGNNNIGNNNIGSGNTGTGNIGSGNTGSGNIGLGNLGDGNIGFGNTGSGNIGFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VAWMSVTAGGAELTAAGVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Bacham D., Erown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Selston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Melschmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nalson W.C., Umayam L.A., Ernouri H., Gill J., Mikula A., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 GSLNSGIGTSGT---INAGLGSAGSLNTSFWNAGMQNAALGSAAGSEA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 18.6%; Score 243; DB 1; Length 487 Similarity 28.8%; Pred. No. 8.6e-10; 83; Conservative 30; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 SSLGSSLGSSGLGGGVAANLGRAASVRYGHRDGG-KYAXSGRRNGGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.

CONFLICT 40 40 E -> K (IN REF. 1).

CONFLICT 96 96 I -> T (IN REF. 1).

SEQUENCE 21 211 G -> GNNNIG (IN REF. 1).

SEQUENCE 487 AA, 47247 MW, 97234D5B316CBC7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, M15467; AAA88235.1; ALT_INIT.
EMBL, AL021932; CAA17399.1;
EMBL, AE006948; AAK44681.1; -.
EMBL, MT04580; C70830.
TIGR, MT0458; -.
Tuberculist; Rv0442c; -.
InterPro; IPR0000030; Microbac_PPE.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF01469; Pentapeptide_2; S.
Pfam; PF01823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160
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MEDLINE=22206494; PubMed=12218036;
Relischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains...;
Whole-genome Location Integral membrane protein (Potential).
-: SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95/RV;
MEDLINE=95/RV;
MEDLINE=95/RV;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III. Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd & Horneby T., Jagels K., Krogh A., Mchean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Complete genome sequence.

"Nature 393:537-544(1998)."
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                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
Bacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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23 POTENTIAL.
08 POTENTIAL.
32 POTENTIAL.
65 POTENTIAL.
665 POTENTIAL.
966 POTENTIAL.
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Pred. No. 1.8e-06;
Y096_MYCTU

Y096_MYCTU

ID Y096_MYCTU

TO 10082,

DT 01-0CT-1996 (Rel. 34, Created)

DT 01-0CT-2003 (Rel. 34, Last sequence update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DE Hypothetical PPE-family protein RV0096/MY0105,

GN RV0096 OR MT0105 OR MTCX251.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIĞR; MT0105; -.
Tuberculist; Rv0096; -.
Tuberro: IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Transmembranë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
112
1132
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296
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7C
46894 MW; 4
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EMBL, AE006922, AAK44327.1; -.
PIR, H70750, H70750.
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36.3%;
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216
245
276
323
419
463 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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Gaps

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Indels

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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 VAALEADYDLMWVQNSTAMTTYRDTVLRETGKMENFEPAPQLVSR-YCMDRRDSVNSFHS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 LSATSLTQQLGGL-----DSIISSASASLLTTNS--ISSSTASSIM----PIVA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 --GTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAA 201
                                                                                                                                                                                                                                                                                                                                                                                                 1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TAAANQLMINIVPQALKQLAQ------PTQ------PTQ-----
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.B., Taylor K., Mitchead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                               POLY-SER.
2 X 6 AA REPEATS OF S-V-A-Q-S-E.
                                                                                                                                                                                                                                                                                                                           14.7%; Score 191.5; DB 1; Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 AQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAAN----LGRAASV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42466 MW; 5C0C2BE0D6E6A9D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YU18_MYCTU STANDARD; PRT; 434 AA.
P31506; 053265; 26.
01-UUL-1933 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
12-0CT-2003 (Rel. 42, Last annotation update)
13-0CT-2003 (Rel. 42, Last annotation update)
14-ypochetical PPB-family protein Rv3018c/WT3098/WT3101.
RV3018C OR MT3098/WT3101 OR MTV012.32C.
                                                                                                                                                                                                                   T -> S (IN REF. 2).
S -> L (IN REF. 2).
H -> D (IN REF. 2).
P -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                            24.5%; Pred. No. 2.6e-06; ative 49; Mismatches 104;
 Antigen, Repeat; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 24.59
Matches 70; Conservative
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                                                                                                                                                                                                                                                   191
292
408 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
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                                                                                                    61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                70 LAWLEQTAINSAVTAAQHVAAAAAYCSALAAMPTPAELAANHAIHGVLIATNFFGINTVP 129
                                   1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=3323928; Pubmed=8478104;
MED-LOPEZ F., Brooks L.A., Dockrell H.M., de Smet K.A.L.,
Thompson J.K., Hussain R., Stoker N.G.;
"Sequence and immunological characterization of a serine-rich antigen
   17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Holroyd S., Hornsby T., Duthoy S., Feltwell T., Fraser A., Hamlin N., Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M., Rutherter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95020554; PubMed=7934845,
Rinke de Wit T.F., Clark-Curtiss J.E., Abebe F., Kolkon A.H.J.,
Jonson A.A.M., Thole J.E.R.;
"A Mycobacterium leprae-specific gene encoding an immunologically
                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine-rich antigen (25L) 45 kDa protein).
SPA OR ML0411 OR MLCL383.14.
Mycobacterium leprae.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corresponded to the Actinomycetales.
   55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
21; Mismatches
                                                                                                                                                                           121 T----AAANQLMNNVPQALKQLAQP 141
                                                                                                                                                                                                  181 TRLDVLSSIGQLIRDI---LDFIANP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from Mycobacterium leprae.";
Infect. Immun. 61:2145-2153(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recognized 45 kDa protein.";
Mol. Microbiol. 10:829-838(1993).
                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U00015; AAC43220.1; -. EMBL; X68431; CAA48480.1; -. EMBL; Z21952; CAA79950.1; -. EMBL; Z97179; CAB09938.1; -.
53; Conservative
                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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007297;
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us-09-886-349a-12.rsp

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Mycobacterium tuberculosis.
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Best Local Similarity 21.9%
Matches 67, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TAAAN------QLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPH---RSPIS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAWLVQASADSAAAAGEHEAAAAGYVCALAEMPTLPELAANHLTHAVLVATNFFGINTIP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 NMVSMANNHMSMTNSGVS------197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 FIITLASNAQLLTEFAINASYVAVGLLYAIAGVIDIVVEWVIGNLFGVVPLLGGPLLGAL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reductase.
-!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 294; 337 and 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGQNTPA
STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleischmann R.D., Hand D., Eisen J.A., Eaft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman U.A., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Isolate 50410;
Backi A.H., Dale U.W.;
Submitted (MPR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
-!- CAUTION: In strain Oshkosh the gene for this protein is interrupted in position 307 by an IS6110 element.
-!- CAUTION: Was originally (Ref.3) thought to be a dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55,
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Best Local Similarity 23.4%; Pred. No. 0.00053;
Matches 67; Conservative 34; Mismatches 130; Indels 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAPAAQAVQ-TAAQNGVRAMSSLGSSLGS-SGLGGGGVAANLGRAAS 241
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EMBL; AE007129; AAK47427.1; ALT SEQ.
EMBL; X50771; CAA41961.1; ALT SEQ.
EMBL; X59271; CAA41961.1; ALT FRAME.
PIR; E70857; F70857.
TIGR; MT3098; -...
TIGR; MT3098; -...
TUBErculise; RV3018c; -..
Tuberculise; RV3018c; -..
TuberPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PEF. 1.
Hypothetical protein; Complete proteome SEQUENCE 434 AA; 43029 NW; 41D673C5
                                                                                                                                                                                                                                                                                                              Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 160-374 FROM N.A.
                                                                                                                                                                                                                                                                                 laboratory strains."
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YU21 MYCTU
ID YU21 MYCTU ST
AC 053268; 053269;
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                                                                                                                                                                                                                                                                                                                          PSEQUENCE FROM N.A.

PSEQUENCE FROM N.A.

STRAIN-HJ7Rv;

MEDJINE=89295987; PubMed=9634230;

MEDJINE=89295987; PubMed=9634230;

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

A Gordon S.V., Eiglmeier K., Gas S., Hamin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Nutter S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

A Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

I "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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STRAIN=CDC 1551 / Obhkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Peterson J., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
--- SIMILMENTY: Belongs to the mycobacterial PPE family.
--- CAUTION: Ref. 1 sequence differs from that shown due to a frameshift in position 82.
                                                                                                                                                                                                           Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.1%; Score 158; DB 1; Length 435; 21.9%; Pred. No. 0.00057; Live 32; Mismatches 113; Indels
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LAGV -> VTGL (IN REF. 2).
L -> V (IN REF. 2).
3B157643EAA8484A CRC64;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
14ypothetical PPE-family protein Rv3021c/Rv3022c/MT3106.
RV3021C/RV3022C OR MT3106 OR MTV012.35C/MTV012.36C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IAVNEAEYGEMWAQDAAAMFGYAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, ALO21287; CAA16106.1; ALT_FRAME.
EMBL, ALO21287; CAA16107.1; ALT_FRAME.
EMBL, AE007129; AAK47435.1; -._
TIGR; WT3106; -.
TUBerculist; Rv3021c; -.
TUBerculist; Rv3022c; -.
InterPro, IPR000030; Microbac_PPE.
Pfam, PR00823; PPE; 1.
Hypotherical protein; Complete proteome.
CONFLICT 299 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 299 G
317 320 LA
326 326 L
435 AA; 42876 MW;
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us-09-886-349a-12.rsp

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Pfam; PF00823; PPE; 1.

Hypothetical protein; Complete proteome.
SEQUENCE 178 AA; 19811 MW; 8BEIFC025ABFBEA6 CRC64;
InterPro; IPR000030; Microbac_PPE.
                                                                                                                                                                                                                                                                                                                                                                             RV3425 OR MTCY78.04C.
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                    YY25 MYCTU
Q50703:
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SO WW.
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                                           243
                                                                     183
                                                                                                                                             LLPFEE------APEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALKQLAQPTQG 144
                                                                                               244 ------WLV-----LTGMIDMFPATVGFALGVFVLVPLLEFAVVLELAILSIGW 286
                                      196 PFPFGELAKFLEMAAQAFTEVGELIMKSAEAWAVGFVELITGLVNFEP------
                                                                                                                            184 SMINILSS------MLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGS-SGLGGGVAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., Mchean J., Moule S., Murphy L., Oliver S., Ceeger K., Kredh A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CDC 1551 / Oshkosh,
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Fatt D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J.A., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
RV3429 OR MT3533 OR MTCY77.01.
                                                                                                                                                                                                                                                                                       178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
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                                                                                                                                                                                   236 LGRAAS 241
                                                                                                                                                                                                              347 SĠGVVS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   _TaxID=1773;
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                                                                                                                                                                                                                                                         3 WMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILIGQNTPAIA 62
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"Destphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
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                                                                                                                                   Gaps
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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11.6%; Score 152; DB 1; Length 176;
Best Local Similarity 36.5%; Pred. No. 0.00054;
Matches 38; Conservative 17; Mismatches 49; Indels
      Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 VNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 107
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                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; F70738; F70738.

Tuberculist; Rv3425; -.
InterPro; IRR00030; Microbac_PPE.

Pfam; PF00623; PPE; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 176 AA; 19855 MW; BGCEF2E9463B87B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterineae; Mycobacteriaceae; Mycobacterium
11.9%; Score 156; DB 1; 37.1%; Pred. No. 0.00029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 35, Last sequence update) (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical PPE-family protein Rv3425.
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MEDLINE=98295987; PubMed=9634230;
                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
16-OCT-2001 (Rel. 40, Last ann
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                                                                                                                                   39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 393:537-544(1998).
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63 VNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAG 106

Tuberculist; Rv3429; -.

TIGR; MT3533;

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C STEANUE-BEYER 1979.

Adams M D. Celniker S.E., Hölt R.A., Evens C.A., Gocayne J.D., Adams M D. Celniker S.E., Hölt R.A., Hökkins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Ici He, Holkins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Isile P.W., Höskins R.A., Galle R.F., Sutton G.G., Mortnan J.R., Yandell M.D., Zhang Q., Chen L.X., Abradon R.C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G., Abril M. Beaul A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beanden R.C., Bench M.R., Bench W.P., Bench P.V., Bernan B.P., Bhandari D., Bolankov S., Borkova D.A., Butler H., Cadieu E., Center A., Chardra I., R. Borkova D.A., Butler H., Cadieu E., Center A., Chardra I., R. Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R. Durbin K.J., Evanglaista C.C., Ferraz C., Ferriera S., Pleischman W., R.A. Bouch W., Gabriellan A.E., Garg N.S., Gelbart M.M., Glasser K., Gong F., Gorrell J.H., Wallsh P., Houston K.J., Browsen M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Houston K.J., Brownes M., Dugan-Rocha S., Dunkov B.C., Dun P., Harris N.L., Harvey D.A., Heiman T.J., Hermandez J.R., Houck J., Alali M., Kalush P., Karlen G. M., Gabriellan A.E., Garg N.S., Gelbart M.M., Glasser K., Jasko P., Lei Y., Levitsky A.A., Liu J.H., Liegwam C., Lasko P., Lei Y., Levitsky A.A., Liu J.H., Lia Z., Liang Y., Liu X., Mattei B., McIntoeh T.C., McIecod M.P., Morint S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L., Nelson D.L., Nertei B., Mount S.M., Wolskern D.Y., Weissern D.Y., Shin H., Shin E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., Shin B. S., Spier E., Spradling A.C., Narak C., Wan G., Shin E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O., Ableng Z.Y., Wassarman D.A., Wanskern D.Y., Wan G., Chan C., Stapleton M., Stupski M.P., Smith H.O., Ableng Z.Y., Wassarman D.A., Wan Stone E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O., Ableng Z.W., Wassarman D.A., Wang G.Y., Wassarman D.A., Wang G.W., Shin B., Shin B., Shin B., Shin B., Shin B., Shin B., Shin B., Shin B., Shin B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB=Eye-antennal disk;
MEDLINE=96038094; PubMed=7555710;
Treisman J.E., Lai Z.-C., Rubin G.M.;
"Shortsighted acts in the decapentaplegic pathway in Drosophila eye development and has homology to a mouse TGF-beta-responsive gene.";
Development 121:2835-2845(1995).
                                                                                                                                                                                                                                                                                                                  Q24523; Q9VK78; Q9VK79; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 41, Last annotation update) Bunched protein, class 2/class 3 isoforms (Shortsighted protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM CLASS 2), SUBCELLULAR LOCATION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BUN OR SHS OR CG5461.

Drosophila melanogaster (Fruit fly).

Bukaryota; Mttaroa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
SEQUENCE FROM N.A. (ISOFORMS CLASS 2 AND CLASS 3)
                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
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                                                                                                                                                 Name=class 3;
IsoAe=224523-2; Sequence=VSP 006670;
SIMILARITY: Belongs to the TSC-22/Dip/Bun family.
CAUTION: Ref.2 sequence differs from that shown due to erroneous
           of
the second optic lobe relative to the first. Plays a role in determining proper dorsal cell fates leading to the formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; Alternative splicing. GLN.
                                                           Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1211;
                                                                                                                                                                                                                                                                                                                                                                           HSSP; P80220; IDIP.
Flybase; F8p0010460; bun.
GGO; GO:0007422; P:peripheral nervous system development; NAS.
InterPro; IPR000580; TSC-22_Dip_Bun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (in isoform Class 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FIId=VSP 006670.

K -> E (IN REF. 1).

MISSING (IN REF. 1).

Q -> QQO (IN REF. 1).

QQVTSAA -> TS (IN REF. 2).

MW; 9925A9159A7051B0 CRC64;
                                   SUBCELLULAR LOCATION: Nuclear and cytoplasmic. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 114.5;
Pred. No. 1.8;
28; Mismatches
                                                                                                  Name=Class 2;
IsoId=Q24523-1; Sequence=Displayed;
                                                                                                                           Name=Class 1;
IsoId=Q24522-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLN.
POLY-SER.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALA-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01166; TSC22; 1.
ProDom; PD007152; TSC-22 Dip_Bun; 1.
PROSITE; PS01289; TSC22; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing
                                                                                                                                                                                                                                                                                                                         EMBL; L42512; AAC41608.1; -.
EMBL; AE003636; AAF53200.1; ALT_SEQ.
EMBL; AE003636; AAF53201.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
328
1801
1195
125299 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulation; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%;
               determining proper dori
the dorsal appendages.
                                                                                                                                                                                                   gene model prediction.
                                                                                                                                                                                                                                                                                                                                                             PIR; T13804; T13804.
                                                                                          isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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DOMAIN
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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13;

Gaps

81;

Indels

80;

Conservative

99

Matches

14

à

Similarity

Local

70

TAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIA----VNBAEYGE

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967 TNTNVVATGEATTNALTLTDEQATAALAAAFATGAAAAATGATGAAAAATQQQIQQLQQQQP 1026
                                                                                                                                                                           996
MNNVPQAL-----KQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMA--NNHMSM 178
                                                                                                                                                                                                               213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DOMAIN: Contains F-G repeats.
-!- PIM: Probably glycosylated as it reacts with wheat germ agglutinin
                                                        MWAQDAAAMFGYAAATATATATLLP -- FEEAPEMTSAGGLLEQAAAVEEASDTAAANQL
                                                                                                                                                                         -----LPPANIASASANNSNLNL
                                                                                                                                                                                                             179 TN----SGVSMTNTL-----SSMLKGFAPAAAAAAV-QTAA-----QNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Von Lindern M., Fornerod M., Van Baal S., Jaegle M., De Wit T., Buijs A., Grosveld G.;

"The translocation (6;9), associated with a specific subtype of acute myeloid leukemia, results in the fusion of two genes, dek and can, and the expression of a chimeric, leukemia-specific dek-can mRNA.";

Mol. Cell. Biol. 12:1687-1697(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 91:1519-1523(1994).

-!- FUNCTION: May serve as a docking site in the receptor-mediated import of substrates across the nuclear pore complex.
-!- SUBGNIT: Homodimer. Interacts with DDX19 and NUP88.
-!- SUBCELLULAR LOCATION: Nuclear pore complex. Cytoplasmic filaments.
-!- TISSUE SPECIFICITY: Expressed in thymus, splean, bone marrow, kidney, brain and testis, but hardly in all other tissues or in whole embryos during development.
-!- DOMAIN: Contains F-G repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myeloid leukemogenesis, is a nuclear pore complex protein that faces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
CHARACTERIZATION.
MEDLINE=9113161; PubMed=8108440;
MEDLINE=9151361; PubMed=8108440;
Kraemer D., Wozniak R.W., Blobel G., Radu A.;
Kraemer D., Wozniak R.W., a putative oncogene product associated with
"The human CAN protein, a putative oncogene product associated with
"The human CAN protein, a nuclear pore complex protein that faces
"In whemogenesis, is a nuclear pore complex protein that faces
"In whemogenesis, is a nuclear pore complex protein that faces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Nuclear pore complex protein Nup214 (Nucleoporin Nup214)
Nucleoporin) (CAN protein).
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 2090 AA.
                                                                                              LGAAAAAAAGGTAATSVAAPQAIPTLQLQSAP
                                                                                                                                                                         M--VPOOQQQQHQEEQQQQPQQQQQP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Testis;
MEDLINE=92195315; PubMed=1549122;
                                                                                                                                                                                                                                                                                                                | | | : |:| :
1027 NAESETESASGTSAV 1041
                                                                                                                                                                                                                                                                                      214 RAMSSLGSSLGSSGL 228
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       N214 HUMAN
P35658;
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(AUL) through a chromosomal translocation t(6;9) (q21;q34:1) that involves MPE14/CAM and SET.
DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infoblogen.fr/services/chromcancer/Genes/CAN.html".

DISEASE: Implicated in a subset of acute myeloid leukemia (acute nonlymphocytic leukemia) (AML) carrying a chromosomal transfocation t(6;9) [p23;q34) that results in the formation of a DEK-CAM fusion gene. Both some cases of acute undifferentiated leukemia

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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1652 SSSS-----AFNQLTNNTATAPSATPVFGQVAASTAPSLFGQQTGSTASTAAATPQVS 1704
                                                                                                                                                                   MIM; 114350; -.

GO; GO:0005643; C:nuclear pore; TAS.

GO; GO:0005515; F:transporter activity; TAS.

InterPro; IPR004325; Nucleoporin_FG.

InterPro; IPR001680; WD40.

Pfam; PF03093; Nucleoporin_FG; 22.

SMART; SM00320; WD40; 2.

Nuclear protein; Transport; Proto-oncogene; Chromosomal translocation; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AAAYET---AYGLTVPPPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1592 GQTAVTAAAISSAGPVAVETSSTPIASSTTSIVAPGPSAEAAAFGTVTSGSSVFAQPPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1705 SSGFSSPAFGTTAPGVFGQTTFGQASVFGQSASSAASVFSFSQPGFSSVPAFGQPA-SST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1764 PTSTSGSVFGAASSTSS--SSSFSFG---QSSPNTGGGLFGQSNAPAFGQSPGFGQGGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 - AAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGG--GVAANLGRAASVRYGHRDGGKYAXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1819 FGGTSAATTTAATSGFSFCQA---SGFGSSNTGSVFGQAASTGGIVFGQQSSSSSGSVFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 ---FEEAPEMTSAGGLLEQA----AAVEEASDTAAANQLMNNVP--QALKQLAQPTQGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 AENRAELMILIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10,
                                                                                                                                                                                                                                                                                                                    11 X 5 AA APPROXIMATE REPEATS.
18 X 4 AA APPROXIMATE REPEATS.
11 X 3 AA APPROXIMATE REPEATS.
PRO/SER/THR-RICH.
LEUCINE-ZIPPER 1.
LEUCINE-ZIPPER 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.6%; Score 112; DB 1; Length 2090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       6DBE767FDD857F8F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                       BREAKPOINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
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ID TRG1_ECOLI

AC P33790.

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence up

DT 16-OCT-2001 (Rel. 40, Last annotation "
                                                                                                                                                                                                                                                                                                                                                                                                                                       213766 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 GQAELTAAQVRVA------
                                                                                                                      EMBL; X64228; CAA45535.1; -. PIR; S26058; S26058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.1%;
                                                                                                                                                  Genew, HGNC:8064; NUP214.
MIM, 114350; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNTGRGGG 1884
                                                                                                                                                                                                                                                                                                                                                                                                    861 88
812 81
2090 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GR--RNGG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Irag protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid F.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGILEQAAAVEEASDTAAANQLM-----NNVPQALKQLAQPTQGTTPSSKLGGLWKTVS- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAMSRLPVGINATRQIAAAQQEMAREASNRAESALHGF------SSSIASAWNTLSQ 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : : | : : | : : | 395 SELSQIQLKYSNLASTAGYLSAMIPPLSWMMVKGLGAGFSSVYSHFASSSISPIASAGS 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IAVNEAEYGEM------WAQDAAAMFGY-----AAATATATLLPFEEAPEMTSA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 --PHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPA---AAAQAVQTAAQNGVR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AELTAAQVRVAAAAYETAYGLTVPPPV-----IAENRAELMILIATNLLGQNTPA--- 60
                                                                                                                                                                                                                                                                                                                                                                                                                INTERACT WITH TRAN.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- PTM: TRAG* PROBABLY ARISES FROM THE POST-TRANSLATIONAL CLEAVAGE OF
                                                                                                        [2]
SEQUENCE FROM N.A.
MEDLINE=94359430; PubMed=7915817;
MEDLINE=94359430; PubMed=7915817;
Frost L.S., Ippen-Thler K., Skurray R.A.;
"Analysis of the sequence and gene products of the transfer region of the F sex factor.";
the F sex factor.";
Microbiol. Rev. 58:162-210(1994).
                                                                                                                                                                                                                                    [3]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Shimizu H., Saitch Y., Suda Y., Uehara K., Sampei G., Mizobuchi K.;
Shimizu H., Saitch Y., Suda Y., Uehara K., Sampei G., Mizobuchi K.;
"Complete nucleotide sequence of the F plasmid; its implications for organization and diversification of plasmid genomes.";
Submitted (APR-2000) to the EMBL/GenBank/DbBJ databases.
-!- FUNCTION: PLASTA A RUGIAL ROLE IN DONNY-RECIPIENT CELL
INTERACTIONS. REQUIRED FOR TWO STAGES OF THE CONUUGATION PROCESS:
PILUS BIOSYNTHESIS AND MATING AGGREGATE STABILIZATION. MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CAUTION: TRAG IS NOT RESPONSIBLE FOR THE N-TERMINAL ACETYLATION OF F PILIN AS STATED BY SOME AUTHORS.
                                  Firth N., Skurray R.A.; "Characterization of the F plasmid bifunctional conjugation gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 950 POTENTIAL. (FOLIATION).
412 CYTOPLASMIC (POTENTIAL).
433 POTENTIALSMIC (POTENTIAL).
102471 MW; 9E09C8402ACDFDDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRAG* PROTEIN.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; MS9763; AAA98081.1; -.
EMBL; U01159; AAC44184.1; -.
EMBL; AP001218; BAA97969.1; -.
PIR; S20480.
ECOGENE; EG40114; traG.
Plasmid; Conjugation; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 110.5; D 22.8%; Pred. No. 2.6;
                                                                                      . Gen. Genet. 232:145-153(1992)
                 MEDLINE=92204127; PubMed=1348105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 22.8
les 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434
938 AA;
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TRANSMEM
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SEQUENCE
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Db 561 FGSNRGSSDSVTGGADSTMSAQDS--MMASRMRSAVESYAKAHNISNEQATRELASRSTN 618

Qy 215 AMSSLG------SSLGSS--GLGGGVAANLGRAASVRYGHRDGGKVAXSGRR 258

Db 619 A--SLGLYGDAYAKGHLGISVLGNGGGVGLQAGAKASIDGSDLDSHE-ASSGSR 669
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Search completed: June 22, 2004, 17:16:53 Job time: 7.4679 secs

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Maximum Match 100%
Listing first 45 summaries
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	Description	O05298 mycobacteri	Q7u0e9 mycobacteri	Q7u071 mycobacteri	Q8viz3 mycobacteri	006341 mycobacteri		Q7tzh8 mycobacteri		O53950 mycobacteri		Q7tzj3 mycobacteri		Q9z5k0 mycobacteri	O53957 mycobacteri	Q7tzh7 mycobacteri	Q99qil mycobacteri
SUMMARIES	ID	005298	Q7U0E9	Q7U071	QBVIZ3	006341	Q7TWFS	Q7TZH8	053956	053950	Q7TZI4	Q7TZJ3	053939	Q9Z5K0	053957	Q7TZH7	099011
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ж	Query Match	6.06	88.7	85.9	77.2	72.7	72.7	35.5	35.2	33.8	33.8	33.1	33.1	32.5	32.3	32.2	32.2
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11 01-0UL-1997 (TERMELFEL) 04, Created)

12 01-0UL-1997 (TERMELFEL) 04, Last sequence update)

13 01-0UL-1997 (TERMELFEL) 04, Last sequence update)

14 01-0UL-1997 (TERMELFEL) 04, Last sequence update)

15 01-0UL-1997 (TERMELFEL) 04, Last sequence update)

16 NV195 OR WT01364, OR NVT01364.

17 01-0UL-1997 (TERMELFEL) 04, Last sequence update)

18 NV195 OR NVT01364.

18 NV195 OR NVT01364.

19 NVC0bacterium tuberculosis.

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11 Nature 1931:377-544(1998).

12 SECUENCE FROW N.D.

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11 Nature 1931:377-544(1998).

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                                  134 IAVNEAEYGEMWAQDAAAMFGYAAATATATLIPFEEAPEMTSAGGLIEQAAVEEASD 193
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TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
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STRAIN=AF2129:97;

MEDLINE=22709107; PubMed=12788972;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,

Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Harris B., Atkin R., Doggett J., Maeler P.R.,

Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,

"The complete genome sequence of Mycobacterium bovis.";

"The Acad. Sci. U.S.A. 100:7877-7882(2003).
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium bovis.
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0
                                                                                                                                                                                                                                                                              Length 391;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                       Indels
   EMBL, AE007000, AAK5491.1; -.
PIR, B70668; B70608.
TIGR, MT1281; R1196; -.
InterPro, IPR000030; Microbac_PPE.
Pfam, PR00823; PE; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 391 AA; 39158 MW; E409396B3ABDC0F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 AA; 39013 MW; 42788276BAB0B436 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                           Score 1187; DB 16;
Pred. No. 4.5e-73;
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STRAIN-AF2122/97;
MEDLINE-22709107; PubMed=12788972;
                                                                                                                                                                                                                                                                              90.9%;
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Q7U0E9;
01-0CT-2003 (TEMBLEE1. 25,
01-0CT-2003 (TEMBLEE1. 25,
01-0CT-2003 (TEMBLEE1. 25,
                                                                                                                                                                                                                                                                                                           99.68;
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Matches 241; Conservative
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PPB18 OR MB1228.
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121 TAAANQLAMNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
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STRAIN=AF2122/97;
STRAIN=AF2122/97;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
EMBL; BX248346; CAD95692.1; -.
A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Sulton S., Seager K., Skelton S., Squares R., Sulton J.E., Taylor K., Whitehead S., Barrell B.G.;

T. Complete genome sequence.";

Complete genome sequence.";

In Nature 393:537-544(1999)

R. PEBB; 293:590; CAB08702.1; -.

R. PIR, C70568; C70568.

R. Tuberculist; RV378; -.

R. Tuberculist; RV378; -.

R. Tuberculist; RV378; -.

R. Fram; PR000030.:Microbac_PPE.

R. Fram; PR00030.:Microbac_PPE.

R. Fypothetical protein; Complete proteome.

W. Hypothetical protein; A33-413 MW; AF4C20C95DAE7DD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                 72.7%; Score 949.5; DB 16; Length 393; 79.7%; Pred. No. 7e-57; Live 14; Mismatches 31; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Post Local Similarity 79.7%; Pred. No. 7e-57;
Matches 196; Conservative 14; Mismatches 31; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence-2003 (TrEMBLrel. 25, Last anno
PE family protein.
PPE (Emily protein.
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Matches 196; Conservative
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Best Local 9
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Q7TWF5
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                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
                                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 17.2%; Score 1008.5; DB 16; Length 393; Local Similarity 84.6%; Pred. No. 6.6e-61; es 208; Conservative 14; Mismatches 19; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-2003 (TrEMBLrel. 04, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Rv3478.
RV3478 OR MTCY13E12.31.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria; Actinobacteridae, Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                            Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AE007161, AAK47941.1; -.
TIGR; MT3582; -.
                                                                                                                                                                                                                                                                                                                                                                                                                GO: 00:0016020; C:membrane; IEA.
GO: 00:008033; F:peptidase activity; IEA.
GO: 00:006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000030; Microbac PPE.
InterPro; IPR000508; Peptidase_S26.
Pfam; PP00823; PPE; 1.
SEQUENCE 393 AA; 39688 II; 1.
SEQUENCE 393 AA; 39688 WW; 86F0B67798855511 CRC64;
                                                          Mycobacterium tuberculosis.
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                    family protein
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                                                                                                                       NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                           Bishai W.;
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01-JUN-1998 (
01-JUN-1998 (
01-JUN-2003 (
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VAWMSVTAGQAQLTAAQVRVAAAAYETAYRLTVPPPVIAENRTELMTLTATNLLGQNTPA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                      254 TGVSMTNTLHSMLKGLAP-AAAQAVETAAENGVWAMSSLGSQLGSSLGSSGLGAGVAANL 312
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                                                                                                   IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                          134 IEANQAAYSQWWGQDAEAMYGYATAATATEALLPFEDAPLITNPGGLLEQAVAVEEAID
                                                                                                                                                                                                                                          TAAANQLMINIVPQALKQLAQPTQGTTPSSKLGGLWXTVSPHRSPISINWVSMANNHMSMTN
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Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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SEQUENCE 399 AA; 38840 MW; 1A0F4377318E74F2 CRC64;
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MEDLINE=22709107; PubMed=12788972;
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STRAIN=CDC 1551 / Oshkosh;
Fleistenmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleistenmann T.D., Alland D., Eisen J.A., Eaft D., Hickey E.,
Kolonay J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III. Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy D., Oliver S., Seeger K., Skelton S., Rajandream M.A., Ragers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Toociphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                          PPE-family protein.
RV1807 OR MT1856 OR MTV049.29.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ALO22021; CAAJ7728.1; -.
EMBL, AE007044; AAK46128.1; -.
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238 V -> L (IN REF. 2).
39243.MW; DCE18880FD15CBFE CRC64;
                                         Last sequence update)
Last annotation update)
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(TrEMBLrel. 06, Created)
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TIGR: WT1856; -
TUB-cculist; Rv1807; -
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
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                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=AF1122/97;
MEDINE=22709107; PubMed=12788972;
MEDINE=22709107; PubMed=12788972;
MEDINE=22709107; PubMed=12788972;
Pror M., Dithoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Dogget U., Mayes R., Keating L., Wheeler P.R., Parkhil J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobaccerium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
EMBL; BX248340; CAD94532.1; -.
Complete proteome.
SEQUENCE 423 AA, 41477 MW; 26E52CC271FBBF57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.8%; Score 441; DB 16; Length 423; 41.2%; Pred. No. 3.5e-22; ive 30; Mismatches 67; Indels 70
                                                                                                                                                                                                                                                                                                             Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1765;
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterinee, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1765,
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MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor
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284 KIGGKPITGALAPLAEFALHTPILGSEGLGGGSVSAGIGRAGLV 327
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01-0CT-2003 (TrEMBLrel. 25,
01-0CT-2003 (TrEMBLrel. 25,
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PPE26 OR MB1817.
                                                                                                                                                                                                                                           PPE family protein.
PPE29 OR MB1829.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO22021; CRA17722.1; -..
EMBL; AE007044; AAK46122.1; -..
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                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
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InterPro; IPR000030; Microbac_PPE.
Pfam; PF000031; PPE; 1.
Complete proteome.
SEQUENCE 423 AA; 41477 MM; 26E
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MEDLINE=98295987; PubMed=9634230;
                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Cre 01-JUN-1998 (TrEMBLrel. 06, Las 01-CT-2003 (TrEMBLrel. 25, Las PPE-family protein. RV1801 OR MTV049.23 OR MT1850.
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les 117; Conservative
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TIGR; MT1850; -.
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32.5%; Score 424.5; DB 16; Length 421;
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EMBL, AE007043; AAK46108.1; -.
PIR, G70229; G70929.
TIGR, MT1838; -.
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Harris B., Atkin R., Dogget U., Macroix C., Monsempe C., Simon S., Harris B., Atkin R., Dogget U., Mace R., Keating L., Wheeler P.R., Parkhill U., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G., The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

EMBL, BX48340; CAD94520.1; -. Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglaneier K., Gas S., Barry C.E. III, Texaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

Complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                           33.1%; Score 432.5; DB 16; Length 393; 41.0%; Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                           Best Local Similarity 41.0%
Matches 107; Conservative
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91 VAWMSAAAAQAEQAATQARAAAAFEAAFAATVPPPLIAANRASLMQLISTNVFGQNTSA 150
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garkhill T., Churcher C., Harris D.,

Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

Squares S., Stevens K., Taylor K., Whitehead S., Moodward J.R.,
                                                                                                                                                                                                                                                                    31; Gaps
                                                                                                                                                                                                 33.1%; Score 432.5; DB 16; Length 411; 41.0%; Pred. No. 1.3e-21; ive 38; Mismatches 85; Indels 31;
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Corymebacterinees; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                     411 AA; 40557 MW; 03C90B5E0590B7DA CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Putative PPE protein (PPE-family protein).
M11182 OR MLCB1701.08C.
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Nature 409:1007-1011(2001).
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Pfam; PF00823; PPE; 1.
Complete proteome.
SEQUENCE 421 AA; 43119 MW: 680
Tuberculist; Rv1789; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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ŝ 108 135 EKEAEÝTEMWIÓDAAMTSYQASVLEAVGATKAFTAPPLGVNEVGLAQEVVEEVVE 194 254 WKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVR 214 255 WGGFAQHLSPINDTLSMINNHAGMANAGLSLVNGMGSAMKSLAP-TTTKAAESAFKAMGS 313 62 --LEQAAAVEEASDTAAANQLMMN-----VPQALKQ----LAQPTQGTTPSSKLGG--L WMSVTAGOAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIA Gaps 29; Indels 63 VNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL-4.6e-21; thes 99; Best Local Similarity 38.8%; Pred. No. 4.6e Matches 104; Conservative 36; Mismatches AMSSLGSSLGSSGLGGGVAANLGRAASV 242 155 215 g 9 g ò ò ò

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Length

32.3%; Score 422; DB 16; 42.2%; Pred. No. 6.6e-21; iive 34; Mismatches 92;

Conservative

108;

Similarity

Query Match Local Best Loca Matches

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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGGLLEQAAAVEEASD 120

73 VAWISVTAGQAEQAGAQAKIAAGVYETAFAATVPPFVIEANRALLMSLVATNIFGQNIPA

1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGQNTPA

121 TAAA-----NOLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMAN 173

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245 GPYŠIIGLGAIPGGWWLIFGQILGLAQNAPGVAALLGPKAAAGALSPLAPLRGGYIGDIT

174 NHMSMTNSGVS-----MTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSL-GSSLGS-S

> SEQUENCE FROM N.A.
> STRANG-CD [155] / Oshkosh;
> STRANG-CD [155] / Oshkosh;
> Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
> Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
> Rolonay J.F., Nalson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
> Bishai W., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., MEDLINE=9829587; PubMed=9634230;
> Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Erown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Krelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."; Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium. NCBI_TaxID=1773; Last sequence update) Last annotation update) 409 Created) 01-JUN-1998 (TrEMBLrel. 06, Creat 01-JUN-1998 (TrEMBLrel. 06, Last 01-JUN-2003 (TrEMBLrel. 24, Last PPE-family protein. RV1808 OR MT1856.1 OR MTV049.30. Mycobacterium tuberculosis. PRELIMINARY; FROM N.A SEQUENCE 053957 053957 0.850

"Whole genome comparison of Mycobacterium tuberculosis clinical and

laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; ALO22021; CAA17729.1; -. EMBL; AE007044; AAK46129.1; ALT_INIT.

39917 MW; IE15202BACF36379 CRC64;

Tuberculist, Rv1808, ...
InterPro, IPR00030; Microbac_PPE.
Pfam, PF00823, PPE, 1.
Complete proteome.
SEQUENCE 409 AA, 39917 MM, IE1

PIR, A70932; A70932. TIGR; MT1856.1; -.

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Harris

61 IAVNEABYGEMWAQDAAAMFGYAAATATATILIPFEBAPEMTSAGGLLEQAAAVEEASD 120 121 TAAA-----NOLMMNVPQALKOLAOPTOGTTPSSKLGGLWKTVSPHRSPISNMVSMAN 173 245 GPYSIIGLGAIPGGWWLTFGQIL-GLAQNAPGVAALLGPKAAAGALSPLAPLRGGYIADI 303 133 IAATEAHYAEMWAQDAAAMYGYAGSSATA-SQLAPFSEPPQTINPSATAAQSAVVAQAAG 174 NHMSMTNSGV---SMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGS----1 VAWMSVTAGGAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003). 24; / Match 12.2%; Score 420; DB 16; Length 409; Local Similarity 41.6%; Pred. No. 9.1e-21; les 107; Conservative 32; Mismatches 94; Indels 24 Mycobacterium bovis. Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corymebacterinee, Mycobacteriaceae, Mycobacterium. 39931 MW; D57892628B131A9E CRC64; Last sequence update) Last annotation update) Created) (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 25, 226 SGLGGGVAANLGRAASV PRELIMINARY; 409 AA; protein. FROM N.A. Complete proteome. SEQUENCE 409 AA; PPE family prot PPE32 OR MB1837 01-OCT-2003 (01-OCT-2003 (01-OCT-2003 (Query Match Best Local S: Matches 107, SEQUENCE Q7TZH7 RESULT 15 Q7TZH7 g g g ò ö à ò

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Search completed: June 22, 2004, 17:22:50 Job time: 22:5043 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES	;	ID	AAW32381	AAW32449	AAW64335	AAW81702	AAY04778	AAY38989	AAY39132	AAU01888	AAE29707	AAE17571	AAY32070	AAE29710	AAE17574	AAU74599	AAY32068	AAU74597	ADA26354	AA022142	AAE29709	AAE17573	ADA26374	AAU01902	ADA26367	AAU01904	ADA26366
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ALIGNMENTS

Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis. Houghton R; Campos-Neto A, Mycobacterium tuberculosis antigen TbH-9FL Skeiky YAW, Dillon DC, I, Twardzik DR; AAW32381 standard; protein; 391 AA 95US-00523435. 95US-00532136. 96US-00620280. 96US-00658800. 96WO-US014675. Mycobacterium tuberculosis. (first entry) CORI-) CORIXA CORP. WO9709429-A2. 22-SEP-1995; 22-MAR-1996; 05-JUN-1996; 30-AUG-1996; 12-JUL-1996; Reed SG, Sk Vedvick TH, 13-JAN-1998 01-SEP-1995; 13-MAR-1997. AAW32381

WPI; 1997-192904/17. N-PSDB; AAT91455.

New immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection.

Example 3; Page 150-152; 190pp; English.

A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TbH-9FL The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen,

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especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis
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                                                                                                                          0; Mismatches
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DR;
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95US-00533634.
96US-00620874.
96US-00659683.
                                                                                         100.0%;
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testing; M.tuberculosis.
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1, Twardzik
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N-PSDB; AAT91521.
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                                                      Sequence 391 AA
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22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
                                                                                         Query Match
Best Local Simi
Matches 391;
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Vedvick TH,
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                                                                                                                                           A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TbH-9FL The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 100.0%; Score 1949; DB 2; Local Similarity 100.0%; Pred. No. 1.2e-142; nes 391; Conservative 0; Mismatches 0;
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                                                                                                    English.
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                                                                                                    Page 138-139; 168pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW64335 standard; protein; 391
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 391 AA;
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                                                                                                                                                                                                                                                                                                                                             prevention)
                                                                                                    Example 3;
                                                        diagnosis
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96US-00729622.

m

M. tuberculosis immunogenic polypeptide TbH-9FL

to

Houghton

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This polypeptide comprises Mycobacterium tuberculosis antigen TbH-9FL. It is encoded by genomic DNA (see AAV44395) isolated from a M. tuberculosis strain H37Ry genomic library using a probe from colone TbH-9 (see AAV44371). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigent portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to
                                                                                                                                                        New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 1949; DB 2; Length 391; Best Local Similarity 100.0%; Pred. No. 1.2e-142; Matches 391; Conservative 0; Mismatches 0; Indels 0
                                                              Dillon DC, Campos-Neto A, DR, Lodes MJ;
                                                                                                                                                                                                                                Example 3; Page 133-135; 250pp; English
97US-0081B111
                                                                Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       primers, for the diag
standardise OS field)
                                                                                                              WPI; 1998-251292/22.
N-PSDB; AAV44395.
                                (CORI-) CORIXA CORP
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Vedvick TS,
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                   1 MYDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                     LIATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
                                                                                                                                     MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                          SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                     SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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RESULT

AAW81702 standard; protein; 391

(first entry)

27-JAN-1999

AAW81702 ID AAW XX AC AAW XX DT 27-XX

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                                                                                                                                                                                                                                                                                                                                                     Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
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                    Tuberculosis, immunogenic; soluble, antigen, protective immunity, vaccine, pharmaceutical; infection; diagnosis.
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100.0%; Pred. No. 1.2e-142;
tive 0; Mismatches 0;
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)R, Lodes MJ;
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13-MAR-1997; 97US-00818112.
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Matches 391; Conservative
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3, Twardzik
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N-PSDB; AAV64503.
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Vedvick TS,
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                             standard; protein; 391 AA
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97FR-00011325
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Best Local Simi:
Matches 391;
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LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEEAPEMTSAGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; diagnosis; detection; infection; antibody; immunisation; vaccine; immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide comprising antigenic portions of M. tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eiky YAW, Dillon DC, Campos-Neto A, Ho
Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                         M. tuberculosis recombinant antigen protein TbH-9FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.2e-142;
Matches 391; Conservative. 0; Mismatches 0:
                                           361 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
   GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 168-169; 323pp; English.
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                                                                                                                                                                                                                   AAY38989 standard; protein; 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US003265
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98US-00072596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                              05-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-527416/44.
N-PSDB; AAZ19093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed SG, Ske
Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-1999;
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LGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
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                                                                                                                                                     241 MVSMANNHMSMINSGVSMINILSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                                                                                                                                                          LIATNILGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATLILPFEEAPEMTSAGG
                                                   LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                          TbH9; Mtb39A; antigen; vaccine; tuberculosis; AIDS; acquired immunodeficiency disease.
                                                                                                                                                                                                                                              361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                             GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis antigen TbH9 (Mtb39A)
                                                                                                                                                                                                                                                                                                               AAU01888 standard; protein; 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0158338P.
99US-0158425P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2000; 2000WO-US028095
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                              (first entry)
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N-PSDB; AAS03779.
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07-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. M. operations and part of them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of
     360
                                                      New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                         LGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campos-Neto A, Houghton J, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                            M. tuberculosis antigen TbH-9FL amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1949; DB 2;
100.0%; Pred. No. 1.2e-142;
tive 0; Mismatches 0;
                                                                                                      361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                        GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 123-124; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC, Car
R, Lodes MJ,
                                                                                                                                                                        AAY39132 standard; protein; 391 AA
                                                                                                                                                                                                                                                                                                                                                                                         99WO-US003268
                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00025197
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                                                                                                                                                                                                                                                                                  immunotherapy; diagnosis; i
immune response; skin test.
                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                        (first entry)
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Best Local Similarity 100.
Matches 391; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed SG, Skeiky YAW,
Vedvick TS, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention
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N-PSDB; AAZ19305.
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05-MAY-1998;
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The sequence represents Mycobacterium tuberculosis TbH9 (also known as Mtb39A), an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
Lodes ML;
                                                                                                                                                                                                                 fusion
                                                                                                                                                                                                            Vaccinating against Mycobacteria infections in mammals using proteins comprising combinations of heterologous antigens.
    Dillon DC,
    Mcneill PD,
                                                                                                                                                                                                                                                                                                                                             Example 2; Page 151-152; 168pp; English
    Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 391 AA;
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Length 391;

4, DB

Query Match

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SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120

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1 MVDFGALPPEINSARMYAGPGSASIVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIG 60

1 MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG

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Length 391; Indels 180 180 240

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from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishannia and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as animal. The invention is used in gene therapy. The present sequence is Mycobacterium sp. TBH9FL antigenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV.360
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                                                                                                                                                                                                                                                                                                  1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                     1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                            SSAGLMVAAASPYVAWMSVTAGOAELTAAOVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LIATNLLGONTPAIAVNEAEYGEMWAQDAAMFGYAAATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                                                                                                                                                                                                                                                                                                                                                                                                                 61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein, antigen, serological sensitivity, immune response, losis, infection, vaccine, MTB19; TbH9 protein.
                                                                                                                                                                                                                    100.0%; Score 1949; DB 5; 100.0%; Pred. No. 1.2e-142;
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                                                                                                                                                                                                                                                           Mismatches
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01-FEB-2001; 2001US-0265737P
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                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                 Sequence 391 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant nucleic acid molecule encoding a billiaion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antispen or an antispenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected
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                                                                                                                                                                                                                                            LIATNILIGONTPAIAVNEAEYGEMMAQDAAMFGYAAATATATATLIPFEEAPENTSAGG
                                                         MVDFGALPPEINSARMYAGPGSASIVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                              MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                   SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                        SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                               LIAINLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                            LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                 181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                      MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                           241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                        Gaps
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                    Indels
    1.2e-142;
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                    Mismatches
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  Pred. No.
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100.08;
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                    Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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tuberculosis.
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                Matches 391;
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RESULT 9 AAE29707

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with increase the serological sensitivity of sera from individuals infected with the tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis to generate or ellicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB3ZA fusion proteins (The present sequence is Mycobacterium species MTB3ZA ThEUB33 (ThB39 (ThB3) protein.
                                               Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject
                                                                                                                              Claim 83; Page 102-103; 136pp; English.
                                                                           Mycobacterium species,
N-PSDB; AAD28341.
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Sequence 391 AA;

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                                                                                                      1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                               1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                   SSAGIMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIABNRAELMI
                                                                                                                                                                                                                                       LIATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                           121 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLILPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                  MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                         Gaps
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100.0%; Score 1949; DB 5; Length 391; 100.0%; Pred. No. 1.2e-142; ive 0; Mismatches 0; Indels 0
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Query Match
Best Local Similarity 100.
Matches 391; Conservative
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AAY32070 standard; protein; 596 AA
                                     AAY32070;
RESULT 11
       AAY32070
ID AAY3
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AC AAY3
XX
DT 17-J
XX
DE MYCC
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129 LIAINLLGONIPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG 188 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240

LIATNILLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG

121

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MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300 249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 308

189 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN

181

Mycobacterium tuberculosis antigen fusion protein Mtb59f.

(first entry)

17-JAN-2000

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128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a recombinant Mycobacterium tuberculosis biantigen fusion protein, termed Mtb59f, composed of the antigens TbH9 and Ra35. The fusion protein is expressed in host cells using a vector carrying a polymucleotide (see AAZ20205) comprising the coding sequences for the 2 antigens. The invention provides fusion proteins (see AAX32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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                        Puberculosis; antigen; fusion protein; Mtb59f; TbH9; Ra35; diagnosis;
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/note= "Met/His tag"
                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                        /note= "Ra12"
                                                                                                                                                                                                                                                                                                                                                        143. .596
/note= "TbH9"
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98US-00223040.
                                                           therapy; vaccine; immunogen.
                                                                                                                           Mycobacterium tuberculosis.
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N-PSDB; AAZ20205.
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, Leff, MIS, and 6H polymucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mysobacterium tuberculosis and TDH9 protein from Mycobacterium sp.

(Updated on 29-AUG-2003 to standardise OS field)
                            LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 368
LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLISLISAAERGPGOMLGGLPV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                              Vaccine; immunity; diagnostic agent; gene therapy; TbH9; antigen; Ra35;
                                                                                            GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                          Mycobacterium sp. MTB59F fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 98-99; 155pp; English.
                                                                                                                                                                                               AAE29710 standard; protein; 596 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2002; 2002WO-US008223
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium sp.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                MTB59F; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-759844/82.
N-PSDB; AAD47086.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200272792-A2.
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27-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject
MVDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                  189 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                    SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                        LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                       129 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                             241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                         249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSLGSSC
                                                                                                                                                                                                                                                                                                                                 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                309 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                    69 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                            LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB59F; TbH9-Ra35 protein.
                                                                                                                                                                                                                                                                                                                                                                                                     391
                                                                                                                                                                                                                                                                                                                                                                                                                                    369 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium species MTB59F fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                     GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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Query Match Best Local Similarity 100.0 Matches 391; Conservative

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immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species MTB59F (TbH9-Ra35) fusion protein
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/note= "OTHER= Xaa. Xaa= In frame stop codon"
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tuberculostatic; immunogen; vaccine; Tb59-Ra35; Mtb59f.
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Misc-difference
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The invention relates to a purified polypeptide which induces an immune response of Myobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion proteins of Mycobacterium tuberculosis antigens, used diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
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100.0%; Pred. No. 2.1e-142;
ive 0; Mismatches 0;
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                                            97US-00818112.
97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
99US-00287849
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Matches 391; Conservative
                                                                                                                                                                                                     REED S G.
SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A.
                                                                                                                                                                                                                                                                                                                                                                    Reed SG, Skeiky YA,
                                                                                                                                                                                                                                                                                                                                                                                                                   2002-171134/22
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                                                                        01-OCT-1997;
18-FEB-1998;
07-APR-1998;
30-DEC-1998;
  07-APR-1999;
                                                  13-MAR-1997;
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                                                                                                                                                                                                                                 (SKEI/)
(DILL/)
(ALDE/)
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This sequence represents a recombinant Mycobacterium tuberculosis triantigen fusion protein, termed Mtb61f, composed of the antigens TbH9, DPV and MTI. The fusion protein is expressed in host cells using a vector carrying a polymuclectide (see AAZ20203) comprising the coding sequences for the 3 antigens. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or preventing tuberculosis (or detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
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                                                                                                                                                         Tuberculosis; antigen; fusion protein; Mtb61f; TbH9; DPV; MTI; diagnosis;
therapy; vaccine; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis.
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                                                                                                                       Mycobacterium tuberculosis antigen fusion protein Mtb61f.
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                  AAY32068 standard; protein; 600 AA.
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98US-00223040.
                                                                                                                                                                                                             Mycobacterium tuberculosis.
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Best Local Similarity
Matches 391; Conserv
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OY 301 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360

Db 309 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 368

Qy 361 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391

Db 369 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
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Search completed: June 22, 2004, 17:15:29 Job time : 49.0027 secs

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June 22, 2004, 17:07:54; Search time 13.9576 Seconds (without alignments) 1446.225 Million cell updates/sec
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1949
1 WVDFGALPPEINSARMYAGP......SGVLRVPFRPYVMPHSPAAG 391
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence:
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Total number of hits satisfying chosen parameters:

389414 seqs, 51625971 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep;*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep;* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMEDIES

	Description	Sequence 107, App	e 102	equence 107	equence 102	e 107	26,	e 22,	7	7	111	907 6	딤	106	9 111	100	104	e 109	104	103	8	e 91,	92,	91,	92,	91,	e 126	12
SUMMARIES	Д	18-112-10	-818-111-10	-056-556-10	-09-072-596-1	-072-967-10	-849-2	-09-287-849-2	23-040-	-287-849-	-08-818-112-11	8-111-10	-09-056-556-11	-09-072-596-10	-09-072-967-11	08-818-112-1	-08-818-111-10	-09-056-556-10	-09-072-596-10	-09-072-967-10	-09-287-	-08-818-112-9	S-08-818-1	-056-556-9	-09-072-596-9	-09-072-967-9	9-073-00	-09-073-010-12
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Query Match 100.0%; Score 1949; DB 3; Length 391; Best Local Similarity 100.0%; Pred. No. 2.9e-154; Matches 391; Conservative 0; Mismatches 0; Indels 0

	Sequence 12, Appl	Ñ		131,	15,	15,	57,	208	92,	114,	109	114,	109	114,	2, 7	Sequence 2, Appli	Sequence 2, Appli	
US-09-287-849-16	US-09-287-849-12	US-09-073-009-142	US-09-073-010-142	US-09-477-135A-131	US-09-073-009-15	US-09-073-010-15	US-08-311-731A-57	US-08-311-731A-208	US-09-050-739-92	US-08-818-112-114	US-08-818-111-109	US-09-056-556-114	US-09-072-596-109	US-09-072-967-114	US-08-095-734-2	22	US-08-471-869-2	
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Sequence 107, Application US/08818112

Sequence 107, Application US/08818112

Patent No. 6290869

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Dillon, Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Wardzik, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: G300 Columbia Center, 701 Fifth Avenue
CITY: Seattle SEED and BERRY LLP
STREET: G300 Columbia Center, 701 Fifth Avenue
CITY: Seattle Mashington
COUNTRY: USA

ZIP: 98104-7092

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMP FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: 11,397

ATTORNEY APPLICANTION NUMBER: 13,1392

CLASSIFICATION NUMBER: 13,1392

RESTERRATION: 434
ATTORNEY APPLICANTION NUMBER: 13,130

RESTERRATION: 434
ATTORNEY APPLICANTION NUMBER: 13,130

RESTERRATION: 434
ATTORNEY APPLICANTION NUMBER: 13,130

TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
TENGTH: 391 amino acids
TYPE: amino acid
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// TOPOLOGY: linear
US-08-818-112-107
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100.0%; Scc...
100.0%; Pred. No. 2...
... 0; Mismatches
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NAME: Maki, David J.
REGISTRATION WUMBER: 31,392
REFRENCE/DOCKET WUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031
INFORMATION POS ESQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
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             Query Match
Best Local Similarity 100.0
Matches 391; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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CITY: Seattle
STATE: Washington
COUNTRY: USA
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                                   1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60
 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                          SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 102, Application US/08818111

Patent No. 6338622

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Transcript Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOTTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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amino acid
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STATE: Washing
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                                                                                                                                        1 MVDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIG
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
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  Length 391;
                                                 Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
Score 1949; DB 4;
Pred. No. 2.9e-154;
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6300 Columbia Center, 701 Fifth Avenue
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COMPUTRY: USA
ZIP: 98104-7092
COMPUTRY READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/072,967
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INFORMATION FOR EEQ ID NO: 1
SEQUENCE CHARACTERICS: SEQUENCE CHARACTERICS: LENGTH: 391 amino acids
                                                                              single
                                                             TYPE: amino acid;
STRANDEDNESS: sir;
TOPOLOGY: linear
US-09-072-596-102
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APPLICANT: Reed, Steven G.
APPLICANT: Rest, Yasair A.W.
APPLICANT: Dillon Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                             ;
0
                                Length 391;
                                                             Indels
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Pred. No. 2.9e-154;
0; Mismatches 0;
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6300 Columbia Center, 701 Fifth Avenue
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSULT 4
5.09-072-596-102
Sequence 102, Application US/09072596
Patent No. 6458366
                            Query Match
Best Local Similarity 100.0%;
Matches 391; Conservative 0
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STATE: Washing
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STREET: 63
US-09-056-556-107
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                                                             Gaps
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Sequence 107, Application US/09072967

Patent No. 6592877

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.A.W.

APPLICANT: Houghton, Raymond

APPLICANT: Wedvick, Thomas S.

APPLICANT: Wedvick, Thomas S.

APPLICANT: Hendrich, Daniel R.

APPLICANT: Hendrick, Daniel R.

APPLICANT: Hendrickson, Ronald C.

TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 355

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSES: SEED and BERRY LLP

STREET: Washington

CONTRY: USA
                                                             ·.
                                                          Indels
Query Match
100.0%; Score 1949; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.9e-154;
Matches 391; Conservative 0; Mismatches 0;
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neco, Autonio
APPLICANT: Campos-Neco, Autonio
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Davis Davis Davis Dillon Corporation
APPLICANT: DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAVIS DAV
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                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 596;
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100.0%; Score 1949; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.2e-154;
Matches 391; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09,
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SCOFWARE PATENTIN Ver. 2.1
SEQ ID NO 26
LENGTH: 596
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORM
US-09-287-849-26
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US-09-287-849-22
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Wasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Osiona Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014025-03038
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US/09/25,197
PRIOR APPLICATION NUMBER: US/09/25,197
PRIOR APPLICATION NUMBER: US/09/25,197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSAGLMVAAASPYVAWMSVTAGQAELITAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1949; DB 4; 100.0%; Pred. No. 2.9e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/09287849
Patent No. 6627198
                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEPAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acids
STRANDEDNESS: single
                 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 391; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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RESULT 9

US 09-287-849-2

US 09-287-849-2

Sequence 2, Application US/09287849

Patent No. 6627198

APPLICANT: Need, Steven G.
APPLICANT: Skerky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Netch, Antonio
APPLICANT: Campos Netch Antonio
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APPLICANT: Campos Netch Antonio
APPLICANT: Campos Netch Antonio
APPLICANT: Dillon NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,197
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PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION US 05/025,197
PRIOR APPLICATION US 05/025,197
PRIOR APPLICATION US 05/025,1
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202 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261
                                                                                                                                                                                                                                                                              LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                                                                                                                                                                                                                       241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLFV 501
                                                                                                                                                                                                        262 LIAINLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 321
                                                                      202 SSAGLMVAAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261
                                                                                                                                                                                                                                                                                                                   322 LLEQAAAVEEASDIAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                          SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
18-09-287-849-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 729;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
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US-09-223-040-2
; Sequence 2, Application US/09223040
; Patent No. 6544522
; GENERAL INFORMATION:
; APPLICANT: Skelky, Yasir
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and Their Uses
; FILE REFERENCE: 014058-009010US
; CURRENT FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
: LENGTH: 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 LIATNILGGNTPALAVNEAEYGEMWAQDAAAMFGYAAATATATTLLPFEEAPEMTSAGG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAQYQTAAQNGVRAMSSLGSSLGSSG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 368
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                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-223-040-2
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                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 1949; DB 4; Length
Best Local Similarity 100.0%; Pred. No. 5.2e-154;
Matches 391; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 99.7%; Pred. No. 1.8e-153;
Matches 390; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 GOMGARAGGGLSGVLRVPPRRPYVMPHSPAAG 399
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                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
PatentIn Ver. 2.1
                       SEQ ID NO 22
LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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SOFTWARE:
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Wed Jun 23 16:34:27 2004

LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG 180

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SEQUENCE CHARACTERISTICS
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STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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US-08-818-111-106
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TOPOLOGY:
US-08-818-111-106
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262 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60
                                                                                                                                                                                                                                                                                                                                                                                   442 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                      LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                      MVSMANNHMSMINSGVSMINILSSMLKGFAPAAARQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence | 11, Application US/08818112 |
| Patent No. 6290869 |
| Patent No. 6290869 |
| GENERAL INFORMATION: |
| APPLICANT: Read, Steven G. |
| APPLICANT: Skeiky, Yasir A.W. |
| APPLICANT: Campos.Neto, Antonio |
| APPLICANT: Houghton, Raymond |
| APPLICANT: Padrick, Thomas S. |
| APPLICANT: Tradzik, Daniel R. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS |
| NUMBER OF SEQUENCES: 153 |
| APPLICANT: CORRESPONDENCES: 153 |
| APPLICANT: Tradzik, Daniel R. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY |
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| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY |
| TITLE OF INVENTION: COMPOUNDS AND METHO
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84.9%; Pred. No. 1.4e-129;
tive 19; Mismatches 34; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.97
Matches 337; Conservative
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US-08-818-112-111
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61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neco, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Campos: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 391
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 396 amino acids amino acids
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181 LLEGAAAVEEASDIAAANQLMNNVPQALQQLAQPIQGTTPSSKLGGLWKTVSPHRSPISN 240
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US-09-072-586-106

US-09-072-596-106

Sequence 106, Application US/09072596

Patent No. 645836

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Wardzik, Daniel R.
APPLICANT: Ucdes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TOWNER OF SEQUENCES: 350

NUMBER OF SEQUENCES: 350

CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and RPPDY ...
                                                      7:
           Length 396;
                                                      34; Indels
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COUNTRY: Washington
COUNTRY: USA
ZIF: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Par PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
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             84.8%; Score 1652.5; DB 4; 84.9%; Pred. No. 1.4e-129; iive 19; Mismatches 34;
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NAME: MARI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
               Query Match
Best Local Similarity 84.9
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 356
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                                                                                      1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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Sequence 111, Application US/09056556

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
DB 4; Length 396;
                                        34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: COUNTRY: COUNTRY: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: PACENTRY PC-DOS/MS-DOS
SOFTWARE: PACENTR Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
84.9%; Score 1652.5; DB 4.84.9%; Pred. No. 1.4e-129; iive 19; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REBERBENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-490
TELEPHONE: (206) 682-693
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 84.99
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
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US-09-056-556-111
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US-09-056-556-111
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Sequence 109, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
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                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                            Similarity
      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6300 Cc
CITY: Seattle
STATE: Washingt
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                                                                                                                                                                                             STRANDEDNESS
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US-08-818-112-109
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Best Local Simi
Matches 337;
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                                                                                                                                                              Gaps
                                                                                                                                                              7 ;
                                                                                                                                Length 396;
                                                                                                                                                              34; Indels
                                                                                                                              DB 4;
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|GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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OF TUBERCULOSIS
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                           84.8%; Score 1652.5; DB 4; 84.9%; Pred. No. 1.4e-129; iive 19; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
ITILE OF INVENTION: COMPOUNDS AND ME
ITILE OF INVENTION: AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 111, Application US/09072967
Patent No. 6592877
                                : 396 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G.
                                                                                                                                            Best Local Similarity 84.9%
Matches 337; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
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                                                                               linear
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GENERAL INFORMATION:
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STATE: Washingt
COUNTRY: USA
                                                            STRANDEDNESS
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                                                                                            US-09-072-596-106
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US-09-072-967-111
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                                                                                                                                                                                                                                                                                                                                                            84.8%; Score 1652.5; DB 4; Length 396;
84.9%; Pred. No. 1.4e-129;
ive 19; Mismatches 34; Indels 7;
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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6300 Columbia Center, 701 Fifth Avenue
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPAK: (206) 622-4900
TELEPAK: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acids
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us-09-886-349a-14.rai
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61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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CCMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Mak!, David J.
REGISTRATION NUMBER: 210121.411C6
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPPAN: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acid
STRANDEDNESS:
TPOPOLOGY: linear
US-08-818-112-109
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US-09-886-349A-14 1949 1 MVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 1163542 segs, 282313646 residues Searched:

1163542

Minimum DB seq length; 0 Maximum DB seq length; 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_pep:*
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| cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 14, Appl	Sequence 102, App	Sequence 107, App	Sequence 14, Appl	Sequence 26, Appl	~	Sequence 26, Appl	Sequence 20, Appl			~	Seguence 18, Appl	18,	Sequence 21, Appl	22,
SUMMARIES			DI.	US-09-886-349A-14	US-10-193-002-102	US-10-084-843-107	US-10-098-732A-14	US-09-287-849-26	US-09-886-349A-20	US-10-359-460-26	US-10-098-732A-20	US-09-287-849-22	US-10-359-460-22	US-10-369-983-2	US-09-886-349A-18	US-10-098-732A-18	US-10-369-983-21	US-10-369-983-22
			ВВ	12	14	14	14	σ	12	14	14	σ	14	15	12	14	15	15
		Query	Length	391	391	391	391	596	596	596	596	009	600	723	729	729	729	729
	æ	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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9-983-1	10-369-9	US-10-369-983	US-10-098-7	US-10-369-9	US-10-369-9	369-983-1	US-10-3	US-10-3	-09-28	8-60-	-10-3	US-10-0	-10 - 3	US-09-8	-10-1	-10-0	-10-282-122A-62	-282-122A-6489	US-10-193-0	3-10-084-843-10	-09-287-849-	9-460-8	US-09-886-349A-	US-10-193-0	US-10-084-843-9	US-10-098-732A-	073-009-12	S-09-793-306-1	2 US-10-282-122A-62027
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1949	1949	1949	1949	1949	1949	1949	1949	1949	1944	1944	1944	1944	1944	1934	1652.5	1652.5	1583	1583	1486.5	1486.5	1187.5	1187.5	1187	1187	1187	1187	766.5	766.5	742.5
16	.17	18	13	20	21	22	23	24	25	26	27	78	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ö 9 1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60 1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG Gaps APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Adderson, Mark
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/597,796
PRIOR FILING DATE: 2000-06-20
PRIOR PRIOR DATE: 2001-02-01
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
ILENGINE DATE: 2001-02-01
SEQ ID NO 14 0 Query Match
Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0; TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
FEATURE: Sequence 14, Application US/0986349A Publication No. US20040086523A1 GENERAL INFORMATION: ; OTHER INFORMATION: MTB39 (TDH9FL) US-09-886-349A-14 US-09-886-349A-14 à 9 ò qq

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Query Match
Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0;
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APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Reb-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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                                                                                  LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 210121.417C9 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 102: US-10-193-002-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, Steven G.
APPLICANT: Reed, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Rorald C.
TITLE OF INVENTION: COMPOUNDS AND ME.
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 102, Application US/10193002 Publication No. US20030135026A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 102:
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TYPE: amino acid
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INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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Squence 26, Application US/09287849

| Squence 26, Application US/09287849
| Patent No. US20020009459A1
| GENERAL INFORMATION:
| APPLICANT: Read, Steven G. APPLICANT: Read, Steven G. APPLICANT: Dillon, Davin C. APPLICANT: Alderson, Mark
| APPLICANT: Campos-Neto, Antonio APPLICANT: Corixa Corporation
| TITLE OF INVENTION: Taxion Proteins of Mycobacterium tuberculosis Antigens | TITLE OF INVENTION: and Their Uses | TITLE OF INVENTION: and Their Uses | TITLE OF INVENTION: and Their Uses | CURRENT APPLICATION NUMBER: US 08/818,112 |
| PRIOR FILING DATE: 1999-04-07 | PRIOR PILING DATE: 1997-10-01 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-02-04 |
| PRIOR FILING DATE: 1998-02-04 |
| PRIOR FILING DATE: 1998-02-04 |
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OTHER THORMATION: Description of Artificial Sequence:bi-fusion
US-09-287-849-26
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100.0%; Score 1949; DB 9; Length 596;
Best Local Similarity 100.0%; Pred. No. 1.8e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0
                                         Indels
      Local Similarity 100.0%; Pred. No. 1e-145; les 391; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Seguence
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US-09-287-849-26
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Sequence 14, Application US/10098732A

Sequence 14, Application US/10098732A

Publication No. US20030175294A1

APPLICANT: Skeiky, Yasir

APPLICANT: Skeiky, Wark

APPLICANT: Guderian, Jeffrey

APPLICANT: Graporation,

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

FILE REFERENCE: 014058-0121010 S

CURRENT APPLICATION NUMBER: US/10/098,732A

CURRENT APPLICATION NUMBER: US 60/275,837

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFFWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENDRYH: 391
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Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0;
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REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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; OTHER INFORMATION: MTB39 full length (TbH9FL)
US-10-098-732A-14
                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-10-084-843-107
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                                                                                                                                                                                                 LENGTH: 391 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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ò 1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60

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APPLICANT: Reed, 1900.

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Beeky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: and Their Uses
FILE REFRENCE: 014068-00902003
FILE OF INVENTION: and Their Uses
FILE OF INVENTION: and Their Uses
FILE OF INVENTION: 01408-00902003
FILE OF INVENTION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-00
PRIOR APPLICATION NUMBER: US 08/912,578
PRIOR APPLICATION NUMBER: US 08/912,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PELING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
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241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                      249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
US-10-359-460-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                         GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                                                                                                                                               361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 26, Application US/10359460; Publication No. US20030147911A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-10-359-460-26
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                                                                                                                                                                                                                                               LIAINLIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLEFFEAPEMTSAGG 188
                                                                                                                                                                                                                                                                                                                                                 189 ILEQAAAVEBASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHKSPISN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 LGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
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                                                                                                                                                                                                                                                                                                       LLEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
           61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                              SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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APPLICANT: Skeiky. Yasir
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 01408-00907005
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 00/265,737
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
CHER INFORMATION: protein TbH9-Ra35 (designated MTB59F)
US-09-886-349A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
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ORGANISM: Artificial Sequence
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SEQ ID NO 20
LENGTH: 596
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Sequence 22, Application US/09287849 Patent No. US20020009459A1
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ORGANISM: Artificial Sequence
                                                                                                                   Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                  Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 391; Conservative
                                                          020009459A1
RESULT 9
US-09-287-849-22
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Fublication No. US20030175294A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Brannon, Mark

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Leishmania Antigen

FILE REFRENCE: 014058-01201005

CURRENT APPLICATION NUMBER: US 60/275,837

PRIOR APPLICATION NUMBER: US 60/275,837

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1
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  241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1949; DB 14; Length 596; 100.0%; Pred. No. 1.8e-145; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                               361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 391, Conservative
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LENGTH: 596
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APPLICANT: DILIGH, Dark
APPLICANT: Campos-Neco, Autonio
APPLICANT: Campos-Neco, Autonio
APPLICANT: Campos-Neco, Autonio
APPLICANT: Corriva Corporation
TITLE OF INVENTION: Eusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE REFERENCE: 014058-009020/S
FULE REFERENCE: 1999-04-07
FURBUT FILING DATE: 1999-04-07
FRICA APPLICATION NUMBER: US 08/912,578
FRICA FILING DATE: 1999-02-18
FRICA FILING DATE: 1999-02-18
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FRICA FILING DATE: 1998-04-07
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100.0%; Pred. No. 1.8e-145;
ive 0; Mismatches 0;
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US-10-359-460-22
; Sequence 22, Application US/10359460
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RESULT 12
US-09-886-349A-18
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                                    GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Discourant of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the st
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Publication No. US20030147911A1
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RESULT 11
US-10-369-983-2
Sequence 2, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:

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APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Strong Proteins
APPLICANT: Corixa Corporation
TITLE OF INVENTION Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO : 22
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OTHER INFORMATION: Description of Artificial Sequence:mutated
OTHER INFORMATION: MTB32-MTB39F fusion protein (MTB32MutSA)
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100.0%; Score 1949; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-145;
Matches 391; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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US-10-369-983-21
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Best Local Si
Matches 391;
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Sequence 18, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasix

APPLICANT: Graitan, Jeffrey

APPLICANT: Graitan, Jeffrey

APPLICANT: Graitan Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: MUMBER: US 0/10/098,732A

CURRENT APPLICATION NUMBER: US 60/275,837

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SSQ ID NO 18

LENGTH: 729
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OTHER INFORMATION: Description of Artificial Sequence:MTB72FMutSA
OTHER INFORMATION: (Ra12-TbH9-Ra35MutSA)
                                                                                Description of Artificial Sequence:MTB72FMutSA (Ra12-TbHp-Ra35MutSA)
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100.0%; Score 1949; DB 12; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-145;
Matches 391; Conservative 0; Mismatches 0; Indels 0;
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100.0%; Score 1949; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-145;
Matches 391; Conservative 0; Mismatches 0;
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                      LENGTH: 729
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                    ) OTHER INFORMATION:

) OTHER INFORMATION:

US-09-886-349A-18
     SEQ ID NO 18
LENGTH: 729
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                                                                    SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
                                                                                                                                                                                                        LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                                                                                                                                               322 LLEGAAAVEEASDTAAANOLMNNVPOALOOLAOPTOGTTPSSKLGGLWKTVSPHRSPISN 381
                                                                                                                                                                                                                                                                                                                                                                                241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
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9
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                                                                                                                   SSAGIMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAEIMI
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APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Gorixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009031US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT PILING DATE: 2003-02-18
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 21
LENGTH: 729
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US-10-369-983-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 21, Application US/10369983; Publication No. US20030235593A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                   241 MVSMANNHMSMINSGVSMINILSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                               382 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                              **Sequence 22, Application US/10369983
**Publication No. US20030235593A1
**Publication No. US20030235593A1
**Sequence 22, Application No. US20030235593A1
**Septence 1 No. US20030235593A1
**APPLICANT: Skeiky, Yasir
**APPLICANT: Goderian, Jeff
**APPLICANT: Corixa Corporation
**TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
**TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
**TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
**TITLE OF INVENTION NUMBER: US/10/369,983.
**CURRENT FILING DATE: 2003-02-18
**NUMBER OF SEQ ID NOS: 22
**SEQ ID NO SEQ ID NOS: 22
**SEQ ID NO 22
**SEQ ID NO 22
**LENGTH: 729
***COFUMARRE: PatentIN Ver. 2.1
**SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 1949; DB 15; Length 729; Best Local Similarity 100.0%; Pred. No. 2.3e-145; Matches 391; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:mutated
US-10-369-983-22
                                                                                                                                                                                                                  361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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Search completed: June 22, 2004, 18:07:55 Job time: 37.2142 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 22, 2004, 16:59:04; Search time 10.9397 Seconds (without alignments) 3438.018 Million cell updates/sec

US-09-886-349A-14 1949 1 WVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG 391

Title: Perfect score: Sequence: Scoring table:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

W	Description	probable PPE prote	PPE prot	PPE prot	PPE prot	PPE	PPE pro	PPE	ly prote	PPE	: PPE prot	PPE prot	PPE prot	PPE prot	PPE	PPE prot	PPE prot	PPE	PPE prot	PPE prot	PPE	PPE prot	PPE	PPE prot	PPE prot	PPE prot	PPE prot	PP.	PPE prot	PPE prot
SUMMARIES		. 0	4	9	2	3	H70931	33	5	2	22	9	33	33	54	38	20	092	092	088	058	D70922	067	020	7066	7057	7083	96	7057	7087
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	Result No.		N	m	4	Ŋ	φ	7	8	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

361 GQMGARAGGELSGVLRVPPRPYVMPHSPAAG 391

probable PPE prote	e PPE	PE prote	PPE		PPE	PPE	e PPE	е РРЕ	probable PPE prote		probable PPE prote	ø	e PPE	probable PPE prote
B70524	A70931	D70676	B70987	C70780	F70846	E70663	A70762	B70969	H70552	F70675	E70808	E70946	F70825	A70647
00	1 (1	0	~	0	N	N	N	N	N	N	N	2	N	71
963	655	479	1053	443	2523	615	678	3157	618	582	987	590	645	409
22.7	22.6	22.0	22.0	21.9	21.7	21.7	21.4	21.4	21.3	21.3	21.3	21.1	21.1	21.0
443	439,5	429.5	428.5	426.5	423.5	422.5	418	418	415.5	415	414.5	412	412	409.5
30	3 7	33	34	32	36	37	38	9	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1		
	probable PPE protein	PPE prot	B70808 Probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
	C,Date: 1	7-Jul-15	C.)Species: Mycobaccerium tubercurors C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
	C;Accession: B/0608 R;Cole, S.T.; Brosc! ; Connor, R.; Davie: Rajandream, M.A.; R	on: B/or T.; Bro R.; Dav m, M.A.;	C.Accession: B.Vovo R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hanris, D.; Gordon, S.; ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
	Nature 35 A;Authors A;Title: A;Referer	3, 537-! s: Sgares Deciphes ce numbe	Nature 393, 537-544, 1998 Ayuthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MUID:98295987; PMID:9634230
	A; Accession: B70608 A; Status: preliminar	on: B70: prelim:	A,Accession: B70608 A,Status: preliminary, nucleic acid sequence not shown, translation not shown
	A) Residues: 1-391 <col/> A) Cross-references: GB:	s: 1-39 eference	A.Resides: 1-391 <col/> A.Resides: 1-392 <col/> A.Resides: 1-391 <col/> A.Cross-references: GB:Z93777; GB:AL123456; NID:g3261726; PIDN:CAB07839.1; PID:e311073; I
t*	A; Experimen C; Genetics: A; Gene: PPE	lental Si SS:	Akaypermental source: strain n3/kv C;Genetics: A;Gene: PPE
	Query Match Best Local Matches 39	fatch scal Simi s 391;	Query Match Best Local Similarity 100.0%; Score 1949; DB 2; Length 391; Best Local Similarity 100.0%; Pred. No. 3.5e-108; Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
-	λõ	1 MV	WUDEGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60
	QC	1 MVi	
	δ	61 53	SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
	qq	61 88	SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
	ð	121 111	LIATNILGGNTPALAVNEAEYGEMWAQDAAMFGYAAATATATELPFEEAPEWTSAGG 180
	q C	121 LI	LIATNILIGGNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLILPFEEAPEWTSAGG 180
	ζ	181 LL	LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
	qq	181 [[LIEGAAAVEEASDTAAANQIMMVVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
	ò	241 MV8	NVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
	q	241 MV	NVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
	δ	301 LG	LGGGVAANLGRAASVGSLSVPQAMAAANQAVTPAARALFLTSLTSAAERGFGQMLGGLPV 360
_	qq	301 LG	LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
	δ	361 GQI	GQMGARAGGGLSGVLRVPPRPYWPHSPAAG 391

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A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17711.1; PID:e1254600
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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40.0%; Score 779.5; DB 2;
Best Local Similarity 43.7%; Pred. No. 4.3e-39;
Matches 179; Conservative 65; Mismatches 129;
                                                                                                                                                                                                                                81.2%; Score 1583; DB 2; ilarity 81.5%; Pred. No. 1.5e-86; Conservative 20; Mismatches 47;
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|GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
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Matches 322; Conser
Molecule type: DNA
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                                                                                                                                                     probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

(Species: Mycobacterium tuberculosis

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: H70741
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A;Cross-references: GB:Z75555; GB:AL123456; NID:g3261608; PIDN:CAA99966.1; PID:e250360;
A;Experimental source: strain H37Rv
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-011-1998 #sequence_revision 17-011-1998 #text_change 22-Oct-1999
C;Accession: C70568
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Pevlin, K.; Feltwell, T.; Gentles, S.; Hamlin, M.; Holroyd, S;Connor, R.; Davies, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: A70500; MUID:98295987; PMID:9634230
A;Accession: C70568
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Best Local Similarity
Matches 338; Conserv
361
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A, Gene: PPE
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: : : :	RESULT 6 H70931 probable PPE protein - Mycobacterium tuberculogis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis	C,Accession: H70931 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Peorlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Pasiandream M. P. Roners, J.; Ritter, S.; Seeger, K.; Skelton, S.; Squares, S.	Nature 393, 737-544, 1998 A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Title: Deciphering the bloolegy of Mycobacterium tuberculosis from the complete genome ?	AjAccession: H70314 AjAccession: H70314 AjAccession: H70314 AjAccession: H70314 AjAccession: H70314 AjAccession: H70314 AjAccession: H70314 AjAccession: H70314015 AjAccession: H703140	Ajtross-reletences: GB:Allozzozzi GB:Allozzozzo, NID:BJ:ZJ:COZJ; FICH.COTZ: COZZOZZOZZOZZOZZOZZOZZOZZOZZOZZOZZOZZOZZ	Query Match 37.8%; Score 737.5; DB 2; Length 403; Best Local Similarity 42.6%; Pred. No. 1.4e-36; Matches 181; Conservative 60; Mismatches 123; Indels 61; Gaps 12;	2 VDFGALPPEIN	5 LDFATLFFEINSAKMISGAGSAFMLAFASAMRGLSAELBYSAFLBISSSVLSILDGSEBMISS 62 SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPVIAENRAELMIL 63 SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPVIAENRAELMIL 64 SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPVIARNAELMIL 65 SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPVIARNAELMIL			Db 184 AAQSAAIAHATGASAGAQQTTLSQLIAAIPSVLQGLSSSTAATFASGPSGLLGIVGSGSS 243 Qy 223 KLGGLWKTVSPHRSPISNNVSMANNHMSMTNSGVSM-TNTLSSMLKGFAPAAAAQAV 278	Db 244 WLDXLWALLDPNSNFWNTIASGLFLPSNTIAPFLGLLGGVAADAADAAGDV 293 Qy 279 QTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAANQAVFP 333	Db 294 LGERTSGGLGGALVAPLGSAGGLGGTVAAACLGNAATVGTLSVPPSWTALAAPLASP 348 Qy 334 AARALPLTSLTSAAERGPGQMLGGLYQQMGARAGGLSGVLRVPPRPYVMPH 386	PGMPFGTMGG		REGULT 7 B70931 probable PPE protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis	
122 IATNLLGONTPALAVNEAEYGEMWAQDAAANFGYAAATATATLLPFEEAPEMTSAGGL 18	DB 121 ISTRVFGQNTSALAAAEAQYGEMMAQUSAAMYATAGSSASASA-VIFFSIFFQLANFIAQ 1/9 QY 182 LEQAAAVEEASDTAAANQLMNNVPQALQOEAQPTQGTTPSSKLGGLWK 229	Qy 230TVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAÞAAAQAVQTAA 282 Db 239 SISALLTDLQPYASFFYNTEGLPYFSIGMGNNFIQSAKTL-GLIGSAAFAAVAAA 292	QY 283 QNGVRAMSSLGSSGLGGGGVAANLGRAASVGSLSVPQAWAA-ANQAVTPAARALPLT 341 : :	OY 342 SLTSAAERGPGOMLGGLPVGCMGARAGGGLSGVLRVPPRPYWPHSPAAG 391 ::::	RESULT 5 A70932 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)	C;Species: Mycobacterium tuberculosis C;Date: 17-Uul-1998 #sequence_revision 17-Uul-1998 #text_change 22-Oct-1999 C;Accession: A70932 P:Cole S T * Prosch R * Parkhill II.* Garnier T : Churcher C.: Harris, D.; Gordon, S	; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998	A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Decighering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Accession: A70932	A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-409 <col- a;crors-references:="" a;exper-references:="" gb:al022021;="" gb:al123456;="" h37rv<="" nid:g3250699;="" pid:e125461="" pidn:caa17729.1;="" strain="" td=""><td>C,Genetics: A,Gene: PPE</td><td>Query Match 38.5%; Score 751; DB 2; Length 409; Best Local Similarity 44.7%; Pred. No. 2.2e-37; Matches 177; Conservative 53; Mismatches 138; Indels 28; Gaps 10;</td><td>QY 2 VDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIGS 61 </td><td>OY 62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121 </td><td>QY 122 IATNLIGQNTPAIAVNEAEYGEMMAQDAAAMFGYAAATATATLIPFEEAPEMTSAGGL 181 </td><td>QY 182 LEQABAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH 234 </td><td>235</td><td>OY 290 SSL-GSSLGS-SGLGGGVAANLGRAASVGSLSVPQAMAAANQAVTPAARALPLTSLTSA-346 </td></col->	C,Genetics: A,Gene: PPE	Query Match 38.5%; Score 751; DB 2; Length 409; Best Local Similarity 44.7%; Pred. No. 2.2e-37; Matches 177; Conservative 53; Mismatches 138; Indels 28; Gaps 10;	QY 2 VDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIGS 61	OY 62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121	QY 122 IATNLIGQNTPAIAVNEAEYGEMMAQDAAAMFGYAAATATATLIPFEEAPEMTSAGGL 181 	QY 182 LEQABAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH 234	235	OY 290 SSL-GSSLGS-SGLGGGVAANLGRAASVGSLSVPQAMAAANQAVTPAARALPLTSLTSA-346

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A,Residues: 1408 -CCL>
A,Cross-references: GB:Z74024, GB:AL123456, NID:g3250700, PIDN:CAA98377.1, PID:e1301025,
A,Experimental source: strain H37Rv
C,Genetics:
A,Gene: PPE
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C;Species Mycobacterium tuberculosis
C;Species Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G70925
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlini, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL 181
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                                                               MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                      1 MFDFAALSPETNSTRMYLGPGSSPILTAAAAWVVLAKELTAAAQGLQSAVEAL-LTTFEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 AATRALSPARVAVATESESAPLIGGGLPWAPWVPGGGSGTGGVNTALRLQPRAFVMPRNP
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llarity 41.8%; Pred. No. 1.1e-34;
Conservative 47; Mismatches 134;
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Best Local Similarity
Matches 182; Conserv
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Status: B70931
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-423 <COL>
A;Coss-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17722.1; PID:e125461
A;Gene: PPE
A;Gene: PPE
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C;Species: Mycobacterium leprae
C;Species: Wycobacterium leprae
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87056
B;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HGen, M.A.; Rutherford, K.M.
am, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter S.S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq.
A;Authors: Rutter S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq.
A;Reference number: A86909; MUID:21128732; PMID:11234002
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Cross-references: GB:AL450380; NID:g13093150; PIDN:CAC31563.1; GSPDB:GN00147
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37.5%; Score 731; DB 2; Length 421;
Best Local Similarity 41.1%; Pred. No. 3.5e-36;
Matches 174; Conservative 55; Mismatches 160; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                          37.8%; Score 736; DB 2; Length 42 41.8%; Pred. No. 1.8e-36; ive 50; Mismatches 123; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 182; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-421 <STO>
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: C70931

R;Conlos S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 333, 537-544, 1998
A;Authors: Squares, R.; Suleton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Squares, R.; Suleton, Mycobacterium tuberculosis from the complete genome &
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Uil-1998 #sequence_revision 17-Uil-1998 #text_change 22-Oct-1999
C;Accession: B70625
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70625
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275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355
                                                                                                                                                                                                                                                                                                                                                 339 VPPDWAARARWANPAAWRLPGDDVTALRGTAENA---LLRGFPWASAGOSTGGGF--VHK 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121
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                                                                                                           240 RLLGISYFDEGL------LQFEASLAQQAIPGTPGGAG--DSGSSVLDSWGPTIFA
                                                                                                                                                                                                                       182 LEQAAAVEEASDIAAANQ----LMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRS
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                                                                            -----GGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 IATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGGL
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42.3%; Pred. No. 1.6e-34;
ive 62; Mismatches 150; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 YGFRLAVMORPPFAG 408
                                                                                                                                                                                                                                                                                                                                                                                                    377 VPPRPYVMPHSPAAG 391
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Best Local Similarity 42.3%
Matches 166; Conservative
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70560
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
R;Conor, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Ritle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MulD:98295987; PMID:9634230
A;Accession: F70560
A;Accession: F70560
A;Accession: F70560
A;Accession: GB:Z95436; GB:AL123456; NID:G3261770; PIDN:CAB08826.1; PID:e316565; EA;Cross-references: strain H37RV
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 YFGLAHDLPKWASEGAKAAGEAAKALPAAVPAIPSAGL-SGVAGAVGQAASVGGLKVPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 36.0%; Score 702; DB 2; Length 41 Best Local Similarity 39.1%; Pred. No. 1.7e-34; Matches 168; Conservative 61; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAA---AAQAVQT----
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276 291

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Avobable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revigion 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70646
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Ramlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Natuce 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Ritle: Deoribhering the biology of Mycobacterium tuberculosis from the complete genome f. A;Reference number: A70500; MUID:98295997; PMID:9634230
A;Accession: A70646
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-380 <COL>
A;Cross-references: GB:Z83867; GB:AL123456; NID:93261695; PIDN:CAB06278:1; PID:e291015; R
A;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                          292 IPK------SSLGAGLGLRSGLSAGLAHAASAGLGQANLVGDLSVPPSWASATPAV 341
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SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 TAQAAAVSQATDPLSL--LIETVTQALQALTIPSFIPEDFTFLDAIFAGYATVGVTQDVE
                                                SSAGMAAAAPYVTWMSGTSAQAKAAADQARAAVVAYETAFAAVVPPPQIAANRSQLISL
                                                                                                   IATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGGI
                                                                                                                           180 AGÓAAATGOATALASGTNAVTTALSSAAAQFPFDIIPTLLÓGLA--TLSTQYTQLMGQLI
                                                                                                                                                                                                                                                                                                    -----WKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQ
                                                                                                                                                                                                                                                                                                                                                    238 NAIFGPTGATTYQNVFVTAANVTKFSTWÄNDAMSAPNLGMTEFKVF-----WQPPPAPE
                                                                                                                                                                                                                                                                                                                                                                                                       277 AVQTAAQNGVRAMSSLGSSLG----SSGLGGGVAANLGRAASVGSLSVPQAWAAANQAV
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                                                                                                                                                                                                      ----DIAAANQLMMVPQALQQLAQPTQGTTPSSKLGGL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.6%; Score 675; DB 2; Length 38 43.1%; Pred. No. 6.2e-33; ative 56; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 RLVANTLPATSLAAAPATQIPANLLGGMALGSM---TGGAL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 TPAARALPLISLISA-AERGPGOMLGGLPVGOMGARAGGGL 371
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Best Local Simil
Matches 172;
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                                                                                                     A;Residues: 1-463 <COL>
A;Residues: 1-463 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:G3250699; PIDN:CAA17723.1; PID:e125461
A;Experimental source: strain H37Rv
C;Gene:ins:
A;Gene: PPE
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A;Experimental source: strain H37Rv
C;Genetics:
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Riference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 -SALGAGLGLRSAISSGLGSTAPAISAGASQAGSVGGMSVPPSWAAATPAIRTVAAVFSS 342
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                                                     A;Status: preliminary, nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul.1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70932
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                                                                                                                                                                                                                                                                                                                                                                                                       1 MDFGVLPPEINSGRMYAGPGSGPMLAAAAAWDGLATELQSTAADYGSVISVLT-GVWSGQ
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                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                              Length 463;
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                                                                                                                                                                                                                                                                                                            Indels
     A; Reference number: A70500; MUID: 98295987; PMID: 9634230
                                                                                                                                                                                                                                                      35.3%; Score 688.5; DB 2;
42.8%; Pred. No. 1.3e-33;
tive 48; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.0%; Score 682.5; DB 2;
40.9%; Pred. No. 2.9e-33;
live 59; Mismatches 125;
                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity 40.9%
Matches 164; Conservative
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Best Local Similarity
Matches 174; Conserv
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61 9 120

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RESULT 15
G7081
probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
S.Conor, R.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Conor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajadresan, M.; Ragers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A,Reference number: A70500; MUID:98295987; PMID:9634230
A,Rocession: G70881
A,Molecule type: DNA
A,Residues: 1-394 cCOL>
A,Gross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15564.1; PID:e117389
A,Genetics:
A,Genetics:
A,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 ITFVQNAINGAVN----TTAWFVMATIPNAVFLGHAFAALNPATVTAAADAVPAAAAAG 295
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290 GAASVGNTVLASVGRANSIGQLSVPPSWAAPSTRPVSALSPAGLTTLPGTDVAEHGMPG- 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 34.3%; Score 668.5; DB 2; Length 394; Best Local Similarity 40.8%; Pred. No. 1.6e-32; Matches 161; Conservative 61; Mismatches 156; Indels 17,
                                                                                             349 -VPGVPV-----AAGRASGVLPRYGVRLTVMAHPPAAG 380
                                                     354 MLGGLPVGQMGARAGGGLSGVL-RVPPRPYVMPHSPAAG 391
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Search completed: June 22, 2004, 17:24:52 Job time : 11.9397 secs . 1

OM protein - protein search, using sw model

June 22, 2004, 16:46:13 ; Search time 6.50724 Seconds (without alignments) 3128.737 Million cell updates/sec Run on:

US-09-886-349A-14 1949 1 MVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG 391 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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YM96_YEAST HYF1_ALCEU	SLAP_CAUCR Z236_HUMAN	P121_RAT HMLA_DROME	A180 RAT	EXPR_XANCP	FSH DROME	BCSC XANAC	Y808_CHLPN	PICA_HUMAN
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                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                       85.0%; Score 1656.5; DB 1; Length 396; 85.1%; Pred. No. 1.3e-89;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                34; Indels
Pfam; PF00823; PPE; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
158 159 TA -> AT (IN REF. 2).
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15-DEC-1998 (Rel. 37, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein RV2892c/MT2959/Mb2916c.
RV2892C OR MT2959 OR MTCY274.23C OR MB2916C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||:||:
|GLPLGQLTNSGGGFGGVSNALRMPRAYVMPRVPAAG 396
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                                                                                                                                                                                                                                                                                                    Pred. No. 1.3e-89,
18; Mismatches 34
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                                                                                                                                                                                                                                                                                                    Best Local Similarity 85.13
Matches 338; Conservative
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Nature 393:537-544 (1998).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                   SPECIES=M.Dovis; STRAIN=AF2122/97; MEDLINE=22709107; PubMed=12788972; Garnier T., Eiglaneier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.Y., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-788212003).
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Pfam; PF00823; PPE; 1.
Hypochetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 AA; 41469 MW; 3E3D1F20D7827199 CRC64;
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36.2%; Score 705; DB 1; L.
Best Local Similarity 41.8%; Pred. No. 2.7e-34;
Matches 182; Conservative 47; Mismatches 134;
                                                                                                                                                     laboratory strains.";
J. Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, Z74024; CAA98377.1; -.
EMBL, AE07713; AAK47285.1; -.
EMBL, BX248344; CA996603.1; -.
PIK, G70925; G70925.
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TIGR; MT2959; -.
TubercuList; Rv2892c;
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EE64828BF09FA551 CRC64;

46021 MW;

463 AA;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=M. tuberculosis; STRAIN-H37Rv;
SPECIES=M. tuberculosis; STRAIN-H37Rv;
SPECIES=M. tuberculosis; STRAIN-H37Rv;
A CDLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. II, Tekkia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S., A Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L., A Oliver S., Seeger K., Skelton S., Squares S., Squares R., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
The Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
Ill Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES—M. tuberculosis; STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kollonay JF., Nalson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill JJ., Mikula A., Bishai W., Jacobs W.R. Jr., Veneer J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100.7877-7882(2003).
-! SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-0cr-2003 (Rel. 42, Last annotation update)
Hypothetical PPF-family protein Rv1802/WT1851/Mb1830.
Mycobacterium tuberculosis, and
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EMBL; AE007044; ARX46123.1; -.
EMBL; BX248340; CAD94533.1; -.
PIR; C70931; C70931.
TIGR; MT1881; -.
Tuberculat; PR000030; Microbac_PPE.
InterPro; IPR000030; Microbac_PPE.
PHypochetical Proper; 1.
Hypochetical Proper; 1.
CONFLICT 401 401 8 -> L (IN REF. 2).
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                                                                                                         463
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                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                   Mycobacterium bovis.
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ID _Y102_MYCTU
AC 053951;
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                                                                                               182 LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI-
                                                                                                                                                                                                                                                                                                                                                                                                              236 NSMLGLGFAESKAVLPANDTVISTIFGAVQFQKFFNPVTPFNPDLIPK------
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                                                                          VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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D Y442_MCTU

STANDARD; PRT; 487 AA.

AC P42611, 033727,

DT 01-NOV-1955 (Rel. 32, Created)

DT 16-OCT-2003 (Rel. 40, Last sequence update)

DT 16-OCT-2003 (Rel. 42, Last annotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE NYO442C OR MT0458 OR MTV037.06C.

GN RV0442C OR MT0458 OR MTV037.06C.

OS MYCODACTETIUM tubberculosis.

OC Corynebacterineae, Mycobacteriaceae, Mycobacterium.

OX NOSI TaxID=1773;

RN [1]
                                     49;
Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 TSLTS--AAERGPGOML-----GGLPVGOMGARAGGGLSGVLRV 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 TGLQAVPAAAISEGSLLSQMALASVAGGALGGAAARATGGFLGGGRV 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Erdmann;
MEDLINE=8737260; PubMed=3029018;
MEDLINE=87137260; PubMed=3029018;
MEDLINE=87160; T.M.;
MIND 65-Kilodalton antigen of Mycobacterium tuberculosis.";
J. Bacteriol. 169:1080-1088(1987).
                                     Indels
35.3%; Score 688.5; DB 1;
42.8%; Pred. No. 2.8e-33;
ive 48; Mismatches 136;
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
                    al Similarity 42.8
174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 KNGQINLGFGNTGSGNIGNNNIGNNNIGSGNTGTGNIGSGNTGSGNLGLGLGNLGDGNIGFG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 KTVS-----PHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 GSGNIGIGNSGSLNSGIGTSGT---INAGLG---SAGSLNT-SFWNAGMONAALGSAAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 LISLISAAERGPGQM-----LGGLPVGQMGARAG--GGLSGVLR--VPPRPYVMPHSPAA
MEDLINE=22206494; PubMed=12218036; Fleisban U.A., Carpenter L., White O., Fleisban R.D., Fland D., Eisen U.A., Carpenter L., White O., Kelerson U., DeBoy R., Godson R., Gwinn M., Haft D., Hickey E., Kolonay U.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman U.A., Khouri H., Gill U., Mikula A., Bishai W., Jacobs W.R. T., Venter U.C., Fraser C.M., "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 1; Length 487; 4.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GILEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTOGTTPSSKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                     22.8%; Score 444; DB 1; Length 48 32.1%; Pred. No. 4.8e-19; .ive 48; Wismatches 180; Indels
                                                                                                           -!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                            244 NTGSGNIGFGITGDHQMGFGGFNSGSGN-IGFGNSGTGNVGLFNS
                                                                                                                                                                                                                                                                                                             InterPro, IPR000030; Microbac_PPE.
InterPro, IPR002899; Mycobac_Dentapep.
Pfam; PF01469; Pentapeptide_2; 5.
Pfam; PF00823; PPE, 1.
                                                                                                                                                                                                                                   EMBL; MIS467; AAA88235.1; ALT_INIT.

EMBL; AL001932; CAA17399.1; --

EMBL; AE006948; AAK44681.1; --

PIR; C70830; C70830.

TIGR; MT0458; --
                                                                                    laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                                                                            47247 MW;
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                                                                                                                                                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                                                                                                                                                    211
                                                                                                                                                                                                                                                                                                  Tuberculist; Rv0442c;
                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                              487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
MBDLINE=22206494; PubMed=12218036;
MFDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 184:5479-5490(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Repeat; Complete proteome
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv0878c/MT0901.
RV0878C OR MT0901 OR MTCY31.06C.
Mycobacterium tuberculosia, Actinobacteridae, Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.9%; Score 426.5; DB 1; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 X 10 AA APPROXIMATE REPEATS
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                                                                                                                                                                                                                                               Corynebacterineae, Mycobacteriaceae, Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 31.2%; Pred. No. 4.5e-18;
Matches 125; Conservative 56; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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ALA-RICH.
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InterPro; IPR000030; Microbac PPB.
InterPro; IPR002899; Mycobac Dentapep.
Pfam; PP01469; Pentapeptide_2; 4.
Pfam; PF00823; PPB; 1.
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PIR; C70780; C70780.
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98295987; PubMed=9634230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete genome sequence.";
Nature 393:537-544(1998),
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14;

Gaps

87;

Indels

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RESULT 7
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                                                   IGSSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAEL 118
                                                                                                        119 MILIATNILIGONTPAIAVNEABYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSA 178
                                                                                                                         174 --LLSVLPPVVTAAPAGAV----GVPAA---LAIPALGV---ENIG------V 208
                                                                                                                                                                                                                                    209 GNFLGIGNINNVGSGNTGDYNFGIGNIGNANLGNGNIGNANLGSGNAGFFNFGNGNDG 268
                                                                                                                                                                                                                                                                       279 QTAAQNGVRAMSSLGS-SLGSSGLGGGVAA--NLGRAASVGSLSVPQAWAAANQAVTPAA 335
                                                                                                                                                                                                                                                                                      269 NINFGSGNAGFLNIGSGNEGSGNLGFGNAGDDNTG------309
                                                                                                                                                                                                                  SNMV---SMANNHMSMTNSG-----VSMTN-----TLSSMLKGFAPAAAQAV 278
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"Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."
              1 MNFMVLPPEVNSARIYAGAGPAPMLAAAVAWDGLAABLGMAAASFSLLISGLTAGPGSAW
                                                                    o)
                                                                                                                                                              GGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M., "Whole-genome comparison of Mycobacterium tuberculosis clinical and
 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;

    Bacteriol. 184:5479-5490(2002).
    SIMILARITY: Belongs to the mycobacterial PPE family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1548c/MT1599.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                       678 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAGLMVAAASPYVAWMSVIAGQAELIAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AVIIAGFPFLDLGNVTIGGFNLASGNLGLGNGS----FNPGSANTGSVNLGN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 21.4%; Score 418; DB 1; Length 67
Best Local Similarity 31.9%; Pred. No. 2.2e-17;
Matches 106; Conservative 48; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                     Tuberculist; Rv1948c; -.
Tuberculist; Rv1948c; -.
Tuberculist; Rv1948c; -.
InterPro; IPR002030; Mycobac PPE.
InterPro; IPR002039; Mycobac Dentapep.
Pfam; PF00323; PPE; 1.
Pychetical protein; Transmembrane; Complete proteome.
TRANSMEM 14 200 POTENTIAL.
TRANSMEM 180 200 POTENTIAL.
CONFLICT 258 258 D -> G (IN REF. 2).
SEQUENCE 678 AA; 66736 MW; 209F1593D52533A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 SLGSSLGSSGLGGGVA--ANLGRAASVGSLSV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 LGGGNLGSYNLGSGNTGDTNFG-GGNTGNLNV 307
                                                                                                                                                              EMBL; AE007026; AAK45866.1; ALT_INIT.
PIR: A70762; A70762.
TIGR; MITS99;
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SEQUENCE FROM N.A.
MEDI-INE-931238; PubDMed=8478104;
MEDI-INE-9312338; PubDMed=8478104;
MEGA-LODEZ F. Brooks L.A., Dockrell H.M., de Smet K.A.L.,
Thompson J.K., Hussain R., Stoker N.G.;
"Sequence and immunological characterization of a serine-rich antigen
from Mycobacterium leprae."
Infect. Immun. 61:2145-2153(1993). SRA MYCLE STANDARD; PRT; 408 AA.

007297;
001-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine-rich antigen (25L) (45 kDa protein).
SRA OR MLC1383.14.
Mycobacterium leprae.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium.

Infect. Immun. 61: [2] SEQUENCE FROM N.A.

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316 341

381

----VSGPLEGV

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317 SLSVPQAWAAANQAVTPAARALP--LTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGV 374
                                                                         287 ASSIM----PIVASOVTETLGRSOV-AVERMIOSISSTAVSVDVAASKVVAGVGOAVSVG
                                                  LSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAAN----LGRAASVG
 ---GITPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNT
                                                                                                                  240 PFGTPSÖSSOSNDLSATSLTQQLGGL
                                                                                                                                                    375 LRVPPRPYVMPHSPAAG 391
                                                                                                                                                                            382 TQ--PAEEVLTASVAGG 396
                                                                                                                                                                                                                                                                 (Rel. 34, Created)
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PIR; H70750; H70750.
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                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                          MEDLINE=1128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Qaull M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
MEDLINE=95020554; PubMed=7934845;
Kinke de Wit T.F., Clark-Curtiss J.E., Abebe F., Kolkon A.H.J.,
Jonson A.A.M., Thole J.E.R.;
"A Mycobacterium leprae-specific gene encoding an immunologically
recognized 45 kDa protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-SER.
2 X 6 AA REPEATS OF S-V-A-Q-S-E.
                                                                                                                                                                                                                                     "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
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S -> L (IN REF. 2).
H -> D (IN REF. 2).
P -> L (IN REF. 2).
SCOCZBEODGEGA9D8 CRC64;
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26.3%; Pred. No. 1.7e-14;
Live 72; Mismatches 163;
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Interpro; IPR0000010; Microbac_PPE.
Pfam; PF00623; PPE; 1.
Antigen; Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                      . Microbiol. 10:829-838(1993)
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Best Local Similarity 26.33
Matches 115; Conservative
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4 08 AA;
                                                                                     SEQUENCE FROM N.A.
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Leproma; ML0411;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-19825987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Erown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Rutter S., Seeger K., Skelton S., Squares S., Squares J.,

Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 184:5479-5490(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                            01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypochetical PPB-family protein Rv0096/MT0105
RV0096 OR MT0105 OR MTCY251.15.
463 AA
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TubercuList; Rv0096; -.
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Nature 393:537-544(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 QLYDFLWYPYYASYGLLLPFFTP-----TLSALTALSALTHLLNLPPAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GGLW-----KTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLK---
                                                                                                                                                                                                                                                                                                                                      93;
                                                                                                                                                                                                                                                                                       16.6%; Score 324.5; DB 1; Length 463; larity 27.8%; Pred. No. 4e-12; Conservative 54; Mismatches 144; Indels 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p3150; 053265;
01-JUJ-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
Hypothetical PPE-family protein RV3018C/MT3098/MT3101.
RV3018C OR MT3098/MT3101 OR MTV012.32C.
Mycobacterium tuberculosis. Actinobacterias Actinobacterias Actinobacterium Actinobacterias Actinobacterias Actinobacterias Actinobacterias Actinobacterias Actinobacterias.
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                                                                                                                                                                                                                                                42D9D66A033D0DDB CRC64;
                                                     Complete
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InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hypochetical protein; Transmembrane;
TRANSMEM 112 132 POTENTI.
TRANSMEM 112 132 POTENTI.
TRANSMEM 216 296 POTENTI.
TRANSMEM 276 296 POTENTI.
TRANSMEM 323 343 POTENTI.
TRANSMEM 323 343 POTENTI.
TRANSMEM 419 439 POTENTI.
TRANSMEM 419 439 POTENTI.
SEQUENCE 463 AA; 46894 MW; 42D9D
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                                                                                                                                                                                                                                                                                                               Local Similarity
les 112; Conserv
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                                                                                                                                                                                                                                                                                          Query Match
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YUL WICTU
DY P31500
DT 16-0CT-
DT 10-0CT-
DE HYPOCH
ON RV3018
OC BACTET
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL custation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reductase.
-!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
in positions 294; 337 and 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PAAAAQAVQTAAQNGVRAMSSLGSSGLGGGGVAANLGRAASV-GSLSVPQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 MVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 FVAAYVPYVAWLVQASADSAAAAGEHEAAAAGYVCALAEMPTLPELAANHLTHAVLVATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAVEEASDTAAAN-----QLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --ANEASNAVAAATITPPPWHEIVQFLEETFAAYDQYLSALLSELPA--VAWVWFQLFVD
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Meterson J., DeBoy R., Jana D., Eisen J.A., Haft D., Hickey E., Kolnay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Isolate 50410;
Patki A.H., Dale J.W.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
-!- CAUTION: In strain Oshkosh the gene for this protein is interrupted in position 307 by an IS6110 element.
-!- CAUTION: Was originally (Ref.3) thought to be a dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; MT3101; -.
TUBCTULLIST; RV3018c; -.
InterPro; IPR000030; Microbac_PPE.
Fiam; PF00823; PPE; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 434 AA; 43029 MW; 41D673C4BD389DD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL021287; CAA16103.1; -.
EMBL; AE07129; AAK47427.1; ALT SEQ.
EMBL; AE077129; AAK47430.1; ALT SEQ.
EMBL; X59271; CAA41961.1; ALT FRAME.
PIR; E70857; E70857.
                                                                                                                                                                                                                                                                                                                laboratory strains.";
J. Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 160-374 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 115; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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006246;
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GGPLLGALAAAVVPGVAGLAGVAGLAAL-PAVGAA--AGAPAALVGSVAPVSGGVVSPQA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CDC 1551 / Oshkosh,

MEDLINE=220644; Pubmed=1218036;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Eate D., Hickey E.,
Kolonay J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                Gold S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Biglmeier K., Gas S., Barry C.E. III. Tekaia B. P., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentlee S., Hamlin N., Holrcyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rutter S., Geeger K., Skelton S., Squares S., Murphy L., Sulton J.S., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                       355 RLVS--AVEPAPASTSVSVL--ASDRGAGAL--GF-VGTAGKESVGQPAGL 398
                                    324 WAAANQAVTPAARALPLISLISAAERGPGQMLGGLPVGQMGARAGGGLSGV 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the mycobacterial PPB family.
-!- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 82.
                                                                                                                                                                                                                                                                                                            Bacteria; Actinobactería; Actinobacteridae; Actinomycetales;
                                                                                                                                                                          053268; 053269;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypochetical PPE family protein Rv3021c/Rv3022c/MT3106.
Rv3021C/Rv3022C OR MT3106 OR MTV012.35C/MTV012.36C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein, Complete proteome.
299 299 G -> A (IN REF. 2).
317 320 LAGV -> VTGL (IN REF. 2).
326 326 L -> V (IN REF. 2).
435 AA, 42876 MW, 3B157643EAA8484A CRC64,
                                                                                                                                                                                                                                                                                                                           Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                              435 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL021287; CAA16106.1; ALT_FRAME.
FMBL: AL021287; CAA16107.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculist, Rv3022c, -.
InterPro, IPR000030, Microbac_PPE.
Pfam, PF00823; PPE, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AE007129, AAK47435.1;
TIGR, MT3106; -.
Tuberculist, Rv3021c; -.
                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 393:537-544 (1998).
                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aboratory strains.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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   298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 GGGVAANLGRAASV-GSLSVPQAWAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 FFGINTIPIALNEADYVRMWVQAATVMSAYEAVVGAALVATPHTGPAPVIVKPGANEASN 187
                                                                                                                                                                                                                                                                                                                                                             68 FVAAYVPYVAWLVQASADSAAAGEHEAAAAGYVCALAEMPTLPELAANHLTHAVLVATN
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                                                                                                                                                                                                                    8 ASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSVVVAAVGAGVWQGPSAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                126 LLGONTPAIAVNEAEYGEMWAQDAAMFGYAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 ATATATATLLPFEE-----APEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 AVAAATITPFFFGELAKFLEMAAQAFTEVGELIMKSAEAWAVGFVELITGLVNFEP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----WLV-----LTGMIDMFFATVGFALGVFVLVPLLEFAVVLE
                                                                                                                                             6 ALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGL
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                                                                          Gaps
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   Length 435;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 QLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSM-----
16.5%; Score 321.5; DB 1; 26.5%; Pred. No. 5.6e-12; live 53; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Eamily protein RV3429/MT3533
RV3429 OR MT3533 OR MICY77.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 GTAGKESVĞQPAĞL 399
       Query Match
Best Local Similarity 26.5
Matches 115; Conservative
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 SIMILARITY: Belongs to the mycobacterial PPE family
                                                                                                                                              EMBL, 277165, CABO1031.1; -. PIR, F70738, F70738.
Tuberculist, RV3425; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
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ELS_MOUSE
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                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 RLIASNVAGVNTPAIAGLDAQYQQYRAQNIAVMDYQSTARFILAYLPRWQEPPQIYGG 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LPPEINSARMYAGPGSASLVAAAQ----MWDS---VASDLFSAASAFQSVVWGLTVGSWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 IPAEYISNIIYEGPGADSISAAEQLRIMYNSANMTAKSLTDRLGELQE-----NWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 ILIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAG
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                 12.0%; Score 233.5; DB 1; Length 178; 35.9%; Pred. No. 2.8e-07; ive 25; Mismatches 76; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                              family.
                                                                                                                                                                                                                                                                                                                                      .l protein; Complete proteome.
178 AA; 19811 MW; 8BEIFC025ABFBEA6 CRC64;
                                               J. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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01-NOV-1997 (Rel. 35, Last sequence upd
16-OCT-2001 (Rel. 40, Last annotation u
Hypothetical PPE-family protein Rv3425.
RV3425 OR MTCY78.04C.
                                                                                                                                                                                                                                        EMBL, AE007158; AAK47873.1; -. PIR, C70975, C70975. TIGR, MT3533 -. TUBerculist; RV3429; -. Tuberculist; RV3429; -. Tuberculist; RV3429; -. Fam: PF00823; PPE, 1. Hypothetical protein; Complete protein.
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                                                                                                                                                                                                                                                                                                                                                                                               67 VAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 ADAVERYLOWLSKHSSOLKHAAWVINGLANAYNDTRRKVVPPEEIAANREERRRLIASNV 123
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STRAIN=BALB/c; TISSUE=Lung;
MEDIJINE=95130069; PubMed=7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
Wydner K.S., an intron polymorphism to localize the tropoelastin gene to mouse chromosome 5 in a region of linkage conservation with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 LGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLIPFEEAPEMTSAG 179
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Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 176;
                                                                                                                                           Match 11.2%; Score 217.5; DB 1; Length : Local Similarity 33.5%; Pred. No. 2.3e-06; es 58; Conservative 31; Mismatches 83; Indels
InterPro; IPR000030; Microbac_PPE.
Pfam, PP00823; PBE; I.
Hypothetical protein; Complete proteome,
SEQUENCE 176 AA; 19855 MW; B8CEF2E9463B87B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
11-OCT-2003 (Rel. 42, Last annotation update)
Blastin precursor (Tropoelastin).
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127 LG 128
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Genomics 12
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                   Length
                                                                                                                                                           BY SIMILARITY.

OCOBESAAELEDD7F1 CRC64;
                                                                                   Structural protein; Repeat; Signal; Connective tissue.
                                                                                                                                                                                                                                                                          34; Mismatches 192;
                                                                                                                                                                                                                                   DB 1;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RV3426 OR MICY78.03C
                                                                                                                                                                                                                                7.9%; Score 153.5; DB 24.4%; Pred. No. 0.068;
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                                                                                                            POTENTIAL.
PIR; A55721; EAMS.
AGD; MGI-95317; Eln.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
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860 AA; 71955 MW;
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860
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                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 115; Conserv
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Q50702;
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YY26_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ADAALRYLDWLSKHSROILRTARVIESLVMAYEETLLRVVPPATIANNREEVRRLIASNV 123
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PUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely. SUBDATT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=91104868; PubMed=1702999;
Bierce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
Biochemistry 29:9677-9683(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=92241859; PubMed=1572637;
Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
"Elements of the rat tropoelastin gene associated with alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÷,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
"Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.";
"Bat Chem. 263:13504-13507(1988).
                 Nature 393:537-544(1998).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein; Complete proteome.
232 AA; 25872 MW; D76512D49EB272C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%; Score 151.5; DB
35.2%; Pred. No. 0.021;
ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                864 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR000030; Microbac_PPE.
Pfam, PF00823; PPE; I.
Hypothetical protein; Complete prot
SEQUENCE 232 AA; 25872 MW: N767
                                                                                                                                                                                                                                                                                                                  EMBL; Z77165; CAB01030.1; -.
PIR; G70738; G70738.
Tuberculist; Rv3426; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
ELASTIN.
BY SIMILARITY.
Missing (in isoform 2, isoform 5, isoform 7 and isoform 8).
/FTIG=VSP 004244.
Missing (In isoform 3, isoform 5, isoform 6 and isoform 8).
/FTIG=VSP 004245.
Missing (In isoform 4, isoform 6, isoform 7 and isoform 8).
/FTIG=VSP_004246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q99372-8; Sequence=VSP 004244, VSP_004245, VSP_004246; PTM: The crosslinks are made of deaminated Lys.
  Extracellular matrix of elastic fibers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 150; DB 1; Length 864;
25.9%; Pred. No. 0.11;
tive 31; Mismatches 153; Indels 108;
-!- SUBCELLULAR LOCATION: Extracellular matrix of elastic i
-!- ALTENATIVE PRODUCTS:
Event-alternative splicing; Named isoforms=8;
Comment=Experimental confirmation may be lacking for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M60647; AAA42269.1; --
R EMBL; M66572; AAA42269.1; --
R EMBL; M66572; AAA42261.1; --
R EMBL; M66535; AAA42271.1; JOINED.
R EMBL; M66535; AAA42271.1; JOINED.
R EMBL; M66536; AAA42271.1; JOINED.
R EMBL; M66316; AAA42271.1; JOINED.
R EMBL; M66316; AAA42271.1; JOINED.
R EMBL; M66317; AAA42271.1; JOINED.
R EMBL; M66373; AAA42272.1; JOINED.
R EMBL; M66373; AAA42272.1; JOINED.
R EMBL; M66373; AAA42272.1; JOINED.
R EMBL; M66373; AAA42272.1; JOINED.
R EMBL; M66373; AAA42272.1; JOINED.
R EMBL; M66373; AAA42272.1; JOINED.
R EMBL; M66375; RAA42272.1; JOINED.
R EMBL; M66375; RAA42272.1; JOINED.
R AAA42270; PRODELAGIN.
R AAA42270; DRODELAGIN.
R AAA42270; R CONNECTIVE tissue; Repeat; Signal;
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IsoId=299372-5; Sequence=VSP_004244, VSP_004245;
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Isold=Q99372-6; Sequence=VSP_004245, VSP_004246;
Name=7;
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Name=8;
                                                                                                                                                                        Name=2;
Isold=Q99372-2; Sequence=VSP_004244;
Name=3;
                                                                                                                                                                                                                                               IsoId=Q99372-3; Sequence=VSP_004245;
Name=4;
IsoId=Q99372-4; Sequence=VSP_004246;
                                                                                                 isoforms;
Name=1;
IsoId=299372-1; Sequence=Displayed;
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399 daipavaapaiaapaivaapaaakahaakaaka--yaakadvaiptydvaadappa 456

--IGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIABNRA

5 GALP----PEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSW-- 58

Best Local Similarity 25.9 Matches 102; Conservative

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233 PHRSPISNWVSMANNHMSMTNSGVSM-TNTLSSMLKGF-APAAAAQAVQTAAQNGVRAMS 290 580 PG-------GVTGIGTGPGTGLVPGDLGGAGTPAAKSAAKAAKAAKAAA 624 625 GLGAGVPGLGVGAGVPGFGAGAGGFGAGAVPGFGAGAVPGSLAASKAAKYGAAGGL--- 681 117 ELMILIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMT 176 -----GAGTLGGLVPG------AVPGALPGAVPGALPGAVPGALPGAVPGALP-GAVPGVP 527 291 SLGSSLGSSGLGGGV----AANLGRAASV---GSLSVPQAWAAANQAVTPAARALPLT 341 SAGGLL----EQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSS-KLGGLWKTVS ------gebegnedpegneserespectedy 708 342 SLTSAAERGPGOMLGGLPVGOMGARAG-GGLSGV 177 ò g \$ g à qq ð

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SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      005298;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (PPE family protein).
RV1196 OR MTCI364.08 OR MI1234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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P95190
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     PRELIMINARY;
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STRAINS-REJ22/97;
MEDLINE-22102/97;
MEDLINE-22109107;
PUDME T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Paror M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Parkhill J., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.3%; Score 1779.5; DB 16; Length 396; 91.7%; Pred. No. 7.7e-93; cive 9; Mismatches 17; Indels 7;
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SEQUENCE 396 AA; 39651 MW; 698A92A50E3CBA3F CRC64;
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Matches 364; Conservative
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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391 AA; 39158 MW; E409396B3ABDCOF8 CRC64;
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Last annotation update)
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ilarity 100.0%; Pred. No. 2.1e-102;
Conservative 0; Mismatchee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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EMBL, 293777; CAB07839.1; --
EMBL, AE007000, AAK45491.1; --
EMBL, BT0668; B70608.
TICR; MT1234; --
TUBErCUList; Rv1196; --
InterPro; IPR000030; Microbac_PPE.
Pfam, PF00823; PPE.
Hypothetical protein; Complete prote
SEQUENCE 391 AA; 39158 MW; E4093
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                              Similarity
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STRAIN=AF2122/97;
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             IVSMINNHVSMTNSGVSMASTIHSMIKGFAP-AAAQAVETAAZNGVQAMSSIGSQLGSSI 299
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MEDIINE=8829587; PubMed=9634230;

A Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F.,
A Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F.,
A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S.,
A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares G.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
I meciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
I Nature 393:537-544(1998).
R PERE, 295390, CAB08702.1;
Puberculist; Novel
                                                                                              MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL
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                                                                 GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG
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81.5%; Pred. No. 9.3e-82;
ive 20; Mismatches 47; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
47pothetical protein Rv3478.
87y478 OR MCV13121.31.
Mycobacterium tuberculosis.
Bacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae; Mycobacterium.
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Pfam, PF00823; PPE; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 393 AA; 39413 MW; AF4C20C95DAE7DD4 CRC64;
                                                                                                                                                                                               357 GLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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Best Local Similarity 81.5%
Matches 322; Conservative
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240
                                            LLEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHLSPISN 240
                                                                                                                                                                                            GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGOMLG 356
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                              MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL
                                                                                                                                          IVSMLNNHVSMTNSGVSMTNTLHSMLKGFAP-AAAQAVETAAQNGVQAMSSLGSQLGSSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007161; AAK47941.1; -.
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Last annotation update)
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                                                                                                                                                                                                                                                                                             391
                                                                                                                                                                                                                                                                                                                                            GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008508; P:protecolysis and peptidolysis;
InterPro; IPR000030; Microbac_PPE.
InterPro; IPR000508; Peptidase_S26.
Pfam; PF00823; PPE; I.
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Pred. No. 26
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SEQUENCE 393 AA; 39688 MW;
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01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family protein.
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Matches 335; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishai W.;
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                                                                                                   NCBI_TaxID=1765;
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                                             PPE26 OR MB1817
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Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Kearing L.,
Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. US. A. 100:7877-7882(2003).";
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                                                                                                                                                                                                                                                  Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                             357 GLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                              360 GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
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|GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG
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MEDLINE=22709107; PubMed=12788972;
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01-OCT-2003 (TrEMBLrel.
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                                                                                                                                               PRELIMINARY;
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Q7TWF5;
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393 AA.

QTZJ3 ID QTZJ3 PRELIMINARY; PRT; AC QTZJ3; DT 01-OCT-2003 (TrEMBLrel: 25, Created)

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293 GDAAKGLPGLGGMLG----GGPVAAGLGNAASVGKLSVPPVWSGPLPGSVTPGAAPLPVS 348
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MEDIANE-22709107; PubMed=12788972;
MEDIANE-22709107; PubMed=12788972;
MEDIANE-22709107; PubMed=12788972;
MEDIANE-2709107; PubMed=12.0 Camus N., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Colle S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium Dovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.0%; Score 779.5; DB 16; Length 393; 43.7%; Pred. No. 2e-36; ive 65; Mismatches 129; Indels 37;
                                                                                                  Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Last sequence update)
Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Matches 179; Conservative
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SEQUENCE FROM N.A.
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Length 410;

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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1806;
                                                                            SEQUENCE FROM N.A.
STRAIN=myc 94-2272, and OV254;
Sivabon V. Heym B., Mazancourt P., Gaillard J.-L.L.;
Sivabon V. Heym B., Mazancourt P., Gaillard J.-L.L.;
"PPB Rv1808 orthologue of Mycobacterium microti.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF335180; AMX20894.1;
EMBL, AF335189; AAX20893.1;
                                                                                                                                                                                        InterPr7; IPR000030, Microbac_PPE.
Pfam; P700823; PPE; 1.
SEQUENCE 410 AA; 40044 MW; 389DA3174655A5EA CRC64;
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Davies R., Batham D., Brown D., Chillingworth T., Connor R., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Hamlin N., Holroyd S., Csborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Complete genome sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.0%; Score 779.5; DB 16; Length 411; 43.7%; Pred. No. 2.1e-36; ive 65; Mismatches 129; Indels 37;
                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17711.1; ALT_INIT.
EMBL; AE007043; AAK46108.1; -.
PIR; G70929; G70929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 AA; 40557 MW; 03C90B5E0590B7DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculist; Rv1789; -.
InterPro; IPR000030; Microbac_PPE
Pfam; PF00823; PPE; 1.
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Matches 179; Conserv
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 411 AA;
                                                                                                                                                                                                                                                                             Bishai W.;
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61 PSSITWAAAVAPYVAWISVTAGQAEQAGAQAKIAAGVYETAFAATVPPPVIEANRALLMS 120
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                                                                                     1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Bronaby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Owall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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| ALAAEAPGALFGEMALSSLAGRALAGTAVRSGAGAARV 389
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Last annotation update)
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38.7%; Score 754; DB 2;
44.5%; Pred. No. 5.7e-35;
                                            51; Mismatches
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RV1808 OR MT1856.1 OR MTV049.30.
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                                              177; Conservative
                        Similarity
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Created) Last sequence update) Last annotation update)

17, 17, 22,

Q99Q11; 01-JUN-2001 (TrEMBLrel. 1 01-JUN-2001 (TrEMBLrel. 1 01-OCT-2002 (TREMBLrel. 2 RV1608-like protein. MYC1808 OR OV1808.

410

PRELIMINARY;

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38.0%; Score 740.5;
 STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
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                                                                                                                                                                                                             Matches 176; Conservative
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Fleischmann R.D., Alland D., Eisen J.A.; Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1988).
                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                                                                                             38.5%; Score 751; DB 16; Length 409;
.larity 44.7%; Pred. No. 8.4e-35;
Conservative 53; Mismatches 138; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17729.1; -...
EMBL; AE007044; AAK46129.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                39917 MW; 1E15202BACF36379 CRC64;
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Last annotation update)
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InterPro, IPR000030; Microbac_PPE.
Pfam, PF00823; PPE, 1.
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
PPE family protein.
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TIGR; MT1856.1; -.
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SEQUENCE 409 AA;
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                                                                          FROM N.A
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SEQUENCE B
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Best Local
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Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L.,
Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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SEQUENCE FROM N.A.

MEDIJUE=2709107; PubMed=12788972;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Garnier T., Duthoy, S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

Proc. Natl. Acad Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                Length 409;
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                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                     409 AA; 39931 MW; D57892628B131A9E CRC64;
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                                                                                                                                                                                                                                                                                                                                                        Mismatches 140;
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Last annotation updat
                                                                                                                                                                                                                                                                                             38.4%; Score 749; DB 16; 44.3%; Pred. No. 1.1e-34;
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Length 399;

DB 16;

13; 121 120 181 182 LEQAAAVEEASDTAAA-----NQLMNNVPQALQQLAQPTQGTT---PSSKLG----- 225 239 278 289 333 334 AARAL---PLISLISAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPP----RPYVMPH 386 61 9 240 WLDKLWALLDDN.-----SNFWNTIASSGLFLPSNTIAPFLGLLGGVAAADAAGDV QTAAQNGVRAMSSLGSSL----GSSGLGGGVAANLGRAASVGSLSVPQAWAANQAVTP 62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL ---GLWKTVSPHRSPISNMVSMANNHMSMTNSGVSM-TNTLS---SMLKGFAPAAAAQAV 2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS 122 IATNLLGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL Gaps 61; Pred. No. 3.2e-34;); Mismatches 122; Indels 903 42.8%; 182; Conservative SPAAG 391 PPAAG 399 Local Similarity 345 279 387 226 엄 g q qq g $\frac{5}{2}$ g ò 상 음 ò ò $\dot{\delta}$ ò δ

laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AL02021; CAA17728.1; -.
EMBL, AE007044; AAK46128.1; -.
PIR; H70931; H70931.
TIGR, MT1856; -.
Tuberculist; RV1807; -.
Interbro; IRF000030; Microbac_PPE.
PFem; PF000823; PPE; 1.

Complete proteome.

CONFLICT

STRAIN=H3TRY;

MEDLINE=98295987; PubMed=9634230;

MEDLINE=98295987; PubMed=9634230;

A Cole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekaia F.,

Cole S.T., Brosch R., Barkhill J., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Badcock K., Basham D., Roullingworth T., Connor R.,

A Hornsby T., Jagels K., Krogh A., Mclean J., Murphy L.,

A Hornsby T., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Sulscon J.E., Taylor K., Whitehead S., Barrell B.G.;

The Complete genome sequence...;

In Nature 393:537-544(1998). Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. NCBI_TaxID=1773; Created) Last sequence update) Last annotation update) 403 01-JUN-1998 (TrEMBLrel. 06, Crea 01-JUN-1998 (TrEMBLrel. 06, Last 01-JUN-2003 (TrEMBLrel. 24, Last PPE-family protein. RV1807 OR MT1856 OR MTV049.29. Mycobacterium tuberculosis. SEQUENCE FROM N.A. 053956 RESULT 13
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AC 053956
AC 05395
BDT 01-JU
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DDT 01-JU
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SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Petesson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

Bishai W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and

12; 243 349 LGSALGGTEMVAPPEAVAGG -----RAVPOYGFRPNEVAR 398 222 62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121 65 ASASMTAAAAPYVAWMSVTAVRAEQAGAQAEAAAAYEAAFAATVPPPVIEANRAQLMAL 124 181 61 64 279 QTAAQNGVRAMSSLGSSL-----GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTP 334 AARAL---PLISLISAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPP----RPYVMPH IATNILIGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGGL 182 LEQAAAVEEASDTAAA-----NOLMMNVPOALQQLAQPTQGT------TPSS 244 WLDKLWALLDPN-----SNFWNTIASSGEFLPSNTIAPFLGELGGVAAADAAGDV 294 LGEATSG-----GLGGALVAPLGSAGGLGGTVAAGLGNAATVGTLSVPPSWTAAAPLASP 2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS s: Gaps STRAIN=H37Rv;
MEDLINE=98955987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
Cole S.T. Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Lighmeier K., Gas S., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., 61; 403; PPE-family protein.
RV1801 OR MTV049.23 OR MT1850.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium. Length 123; Indels 227 227 F -> S (IN REF. 2). 238 238 V -> L (IN REF. 2). 403 AA, 39243 MW, DCB18880FD15CBFE CRC64; 01-UN-1998 (TrEMBLrel. 06, Created) 01-UN-1998 (TrEMBLrel. 06, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 16; 37.8%; Score 737.5; DB 16 42.6%; Pred. No. 4.8e-34; tive 60; Mismatches 123; Æ 423 PRT; Best Local Similarity 42.6 Matches 181; Conservative PRELIMINARY; 399 PPAAG 403 SEQUENCE FROM N.A. 387 SPAAG 391 NCBI_TaxID=1773; CONFLICT 122 Query Match 053950 RESULT 14 셤 셤 ò DP à a ò g $\stackrel{>}{\circ}$ g δ g ŏ q 8

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Mycobacterium bovis
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                                                                                                             SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Empler B., Hickey E.,
Foterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                           2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J. Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from th Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                           37.8%; Score 736; DB 16; Length 4 41.8%; Pred. No. 6.2e-34; Live 50; Mismatches 123; Indels
                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17722.1; -.
EMBL; AE007044; AAK46122.1; -.
PIR; B70931; B70931.
                                                                                                                                                                                                                                                                                                                                      423 AA; 41477 MW; 26E52CC271FBBF57 CRC64;
                                                                                                                                                                                                                                                                          TIGR; MT1850; -.
Tuberculist; Rv1801; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Complete proteome.
SEQUENCE 423 AA; 41477 MW; 26E
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Last sequence update) Last annotation update)

01-OCT-2003 (TEMBLES 25, 01-OCT-2003 (TEMBLES 25, 01-OCT-2003 (TEMBLES 25, PPE family protein.

CELTICATION

Created)

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PRT;

PRELIMINARY;

Q7TZI4 RESULT 15 Q7TZI4

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60 SSTSMASAAAPYVAWMSATAVHAELAGAQARLAIAAYEAAFAATVPPPVIAANRAQLMVL 119
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                                                                                                                                                                                                Garnier T., Eiglmeier K., Camus J.-C., Medina N., Manscor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.",
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TAXID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 423;
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41.8%; Pred. No. 6.2e-34;
live 50; Mismatches 123;
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                                                                                                                                                                       MEDLINE=22709107; PubMed=12788972;
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Matches 182; Conservative
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                                                                                                                   SEQUENCE
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12;

61 59

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model	June 22, 2004, 17:07:54 ; Search time 26.0232 Seconds (without alignments) 1446.225 Million cell updates/sec
និខ្មែ	22,
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OM protein	Run on:

US-09-886-349A-16 3686 1 MHHHHHTAASDNFQLSQGG......SGGFVVNGLGQVVGMNTAAS 729 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Searched:

389414 seqs, 51625971 residues

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Issued_Patents AA:*
1: /cgT2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgT2_6/ptodata/2/iaa/5B_COMB.pep:*
4: /cgT2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgT2_6/ptodata/2/iaa/B_COMB.pep:*
5: /cgT2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgT2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	edneuce	equence 2,	equence 26	22	equence 10	equence 10	10	equence 10	equence 10	equence 11	equence 106	equence 111	equence 106	equence 111	equence 109	104	equence 109	equence 104	109	equence 8,	equence 91,	equence 92,	91,	equence 92,	e 91,	equence 79,	es es
ID	-09-223-040-	-09-287-84	-09-287-849-2	-09-287-8	-08-818-112-10	-08-818-111-10	-09-056-556-10	-09-072-596-10	-09-072-967-10	-08-818-112-11	-08-818-111-10	9-026-	-09-072-596-10	-09-072-967-11	-08-818-112-10	18-111-10	-09-056-556-10	-09-072-596-10	US-09-072-967-109	-09-287-849-	-08-818-112-9	-08-818-111-9	09-056-5	-09-072-596-9	2-967-9	-818-112-7	US-08-818-111-80
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-09-056-556-7 -09-072-596-8	-09-072-967-79 -09-073-009-12	-09-073-010-12 -09-287-849-28	US-09-620-412C-341 US-09-598-419-341	-09-620-412C-3	-09-528-412C-3	-09-598-419-321	-09-620-412C-3	-09-598-41	US-09-620-412C-325	US-09-598-419-325	US-09-556-877-196	US-09-620-412C-196
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ALIGNMENTS

RESULT 1 US-09-223-040-2 US-09-223-040-2 US-09-223-040-2 Patent No. 654452 Sequence 2, Application US/09223040 Patent No. 654452 GENERAL INFORMATION: APPLICANT: Alderson, Mark APPLICANT: Corrixa Corporation TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens TITLE OF INVENTION: and Their Uses FILE REFERENCE: 014058-009010US CURRENT APPLICATION NUMBER: US/09/223,040 CURRENT FILING DATE: 1998-12-30 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 2 LENGTH: 729 TYPE: PRT PRATURE: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-223-040-2	Query Match 100.0%; Score 3686; DB 4; Length 729; Best Local Similarity 100.0%; Pred. No. 3.6e-261; Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 MEHHHHHTAASDNFQLSQGGGFAIPIGQAWAIAGQIRSGGGSPTVHIGPTAFLGLGVVD 60	61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120 	121 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL 180 	181 FSAASAFOSVVMGLTVGSWIGSSAGIMVAAASPYVAWMSVTAGGAELTAAQVRVAAAAYE 240 	241 TAYGLTUPPPVIAENRAELMILIATNLLGQNTPAIAVNBAEYGEWWAQDAAAMFGYAAAT 300 241 TAYGLTUPPPVIAENRAELMILIATNLLGQNTPAIAVNBAEYGEWWAQDAAAMFGYAAAT 300	301 ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTGGTT 360
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1 MHHHHHHAASDNFQLSQGGGFALPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Adderson, Mark
APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Neto, Antonio
APPLICANT: Carixa Corporation to TITLE OF INVENTION: Fusion Prociens of Myco, TITLE OF INVENTION: and Their Uses
FILE REPERBNCE: 014058-009020US
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/9128, 19810R FILING DATE: 1997-03-13
PRIOR PLLING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR PELICATION NUMBER: US 08/942,578
PRIOR PELING DATE: 1997-10-01
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GENERAL INFORMATION:
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Sequence 2. Application US/09287849

Patent No. 6627188

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skelky, Yasir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

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APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Dillon Presion Proteins of Mycobacterium tuberculosis Antigens

FILE REFERENCE: 014058-009020US

CURRENT FILING DATE: 1999-04-07

PRIOR APPLICATION NUMBER: US 08/912,578

PRIOR APPLICATION NUMBER: US 09/025,197

PRIOR PILING DATE: 1998-04-07

PRIOR APPLICATION NUMBER: US 09/025,197

PRIOR APPLICATION NUMBER: US 09/025,197

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    ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT 360
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                                                   PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQ
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100.0%; Score 3686; DB 4; Length 729;
Best Local Similarity 100.0%; Pred. No. 3.6e-261;
Matches 729; Conservative 0; Mismatches 0; Indels 0
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ORGANISM: Artificial Sequence
FEATURE:
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, OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-22
                 CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-05-14
PRIOR FILING DATE: 1997-06-01
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NOS: 46
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Matches 431; Conservative
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                                                                                                                                                                                                                                                                                                        142 MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                      9 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 GYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQT
                                                                                                                                                                                                                                                                                                                                                                       SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
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                                                                                                                                                                                                                                     Ouery Match
79.8%; Score 2941; DB 4; Length 5
Best Local Similarity 99.8%; Pred. No. 7.6e-207;
Matches 587; Conservative 0; Mismatches 1; Indels
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SGQ ID NO 26
LENGTH: 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-287-849-22
; Sequence 22, Application US/09287849
: Patent No. 627198
; GENERAL INFORMATION:
                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                       US-09-287-849-26
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LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381

LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 321

69 SSAGLMVAAAASPYVAWMSVTAGQAELTAAQVRVAAAAAYETAYGLTVPPPVIAENRAELMI

202 SSAGIMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI

249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 308

MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQTAAQNGVRAMSSLGSSG

GOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAP-----

502

LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV

442

128

68

9 MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG

142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG

67; 600;

Length

53.4%; Score 1967.5; DB 4; Length 72.0%; Pred. No. 1e-135; tive 19; Mismatches 82; Indels

Similarity

TYPE: PRT ORGANISM: Artificial Sequence FEATURE:

CURRENT APPLICATION NUMBER: US/09/287,849

368 543

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501

441

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428
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544 FADFPALPLDPS------AMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPN
                                                                            429 AAQFNASPVAQSYLRNFLAAPPPQRAAMAAQL-QAVPGAAQYIGLVESVAGSCN----N
                                                                                                                                                483 YELMİINYOFG---DVDA----HGAMIRAQAASLEAEHQAİVRDVLAAĞDFWGGA--GSV
                                                                                                               590 GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGV
                                                                                                                                                                                ...----NSGGOGGTPRAVPGRVVALGQTVQASDSLTGAE-ETLNG
                                                                                                                                                                                                                                                                                                           Sequence 107, Application US/08818112
Patent No. 6280969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis i

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TUBERCULOSIS
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APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardich, Thomas S.
APPLICANT: Twardick, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.7%; Score 1944; DB 4;
99.7%; Pred. No. 3e-134;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: "USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                 Sequence 102, Application US/08918111 Patent No. 6338852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAXi, David J.
REGIETRATION NUMBER: 31,392
REFERENCE/DOCKET: 2101
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (206) 622-4900
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 amino acids
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Best Local Similarity 99.77
Matches 390; Conservative
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anino acid
sanaras: single
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STATE: Washington
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                                                                                                                                                                               JS-08-818-111-102
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US-08-818-111-102
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APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Netc, Antonio

APPLICANT: Houghton, Raymond

APPLICANT: Houghton, Paymond

APPLICANT: Twardzik, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and The Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound of the Compound o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGBNT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 21,32
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99,77
Matches 390, Conservative
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STREET: 6300 C.
CITY: Seattle
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STRANDEDNESS: siz
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ZIP: 98104-7092
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US-08-818-112-107
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502 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532

121 LIATNILGGNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG 180 181 LLEQAAAVEBASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240 262 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 321 322 LLEQAAAVEBASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381 1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60 61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPVIAEUMI 202 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG Sequence 102, Application US/09072596
Fatent No. 6458366
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Fatent Fat Query Match 52.7%; Score 1944; DB 4; Length 391; Best Local Similarity 99.7%; Pred. No. 3e-134; Matches 390; Conservative 0; Mismatches 1; Indels 0 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTONNEY/AGENT INPORMATION:
NAME: MAKE, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900 E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue 502 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532 ZIP: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single CITY: Seattle STATE: Washington linear ADDRESSEE: STREET: 63 COUNTRY: g ð g ð g 8 TREATM 261 121 LIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLFFEEAPEMTSAGG 180 181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQTAAQNGVRAMSSLGSSLGSSG 441 241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300 61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120 LIEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381 1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60 262 LIATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 202 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI Sequence 107, Application US/09056556
| Patent No. 6350456
| GENERAL INFORMATION:
| APPLICANT: Reed, Steven G. | APPLICANT: Skeiky, Yasir A.W. |
| APPLICANT: Skeiky, Yasir A.W. |
| APPLICANT: Dillon, Davin C. |
| TILLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241 |
| CORRESPONDENCE ADDRESS: | ADDRESSE: SEED and BERRY LLP |
| STREET: 6300 Columbia Center, 701 Fifth Avenue ô Query Match 52.7%; Score 1944; DB 4; Length 391; Best Local Similarity 99.7%; Pred. No. 3e-134; Matches 390; Conservative 0; Mismatches 1; Indels COUNTRY: USA
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OFFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION: 502 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532 361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391 ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 210121.457
TELEBORMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900 LENGTH: 391 amino acids TYPE: amino acid STRANDEDNESS: single TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS; CITY: Seattle STATE: Washington ; US-09-056-556-107 322 382 301 442

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Wed Jun 23 16:34:29 2004

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121 LIATNILGONIPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLIPEEAPEMTSAGG 180
                                                                                                                           181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                          381
                                                                                                                                                                                                                             241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
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                                                                                                                                                                                                                                                                                     442 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 501
                                                                                                                                                                                                                                                                                                                                301 IGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
262 LIAINLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 321
                                                                                          LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos.Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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MEDIUM TYPE: FICHOPY disk
COMPUTER: IBM PC compatible
COMPARE: TOWN FORM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

44.8%; Score 1652.5; DB 3;
Best Local Similarity 84.9%; Pred. No. 6.2e-113;
Matches 337; Conservative 19; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                  502 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
                                                                                                                                                                                                                                                                                                                                                                                                                           361 GOMGARAGGGLSGVLRVPPRPPVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210121.411C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 111, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: 6300 CCTY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-08-818-112-111
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                                          241 MYSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                                                                                                     301 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLISLISAAERGPGQMLGGLPV 360
     382 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTAAQNGVRAMSSLGSSLGSSG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 201
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APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Necto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: COMPOUNDS AND METHODS FOR INMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1944; DB 4; I Pred. No. 3e-134; 0; Mismatches 1;
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                                                                                                                                                                                          502 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
                                                                                                                                                                                                                                     GOMGARAGGGLSGVLRVPPRPYVMPHSPAG 391
                                                                                                                                                                                                                                                                                                                                                            Sequence 107, Application US/09072967
Patent No. 6592877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed, Steven G.
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amino acid
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Best Local Similarity 99.73
Matches 390; Conservative
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CORRESPONDENCE ADDRESS:
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US-09-072-967-107
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                                                                                                         LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGG 321
                                                                                                                                 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381
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1 VVDFGALPPEINSARMYAGPGSASLVAAAKMWDSVASDLFSSAASAFQSVVWGLTTGSWIG 60
                                    SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 106, Application US/08818111

Sequence 106, Application US/08818111

Patent No. 6338852

Patent No. 6338852

APPLICANT: Reed, Steven G.

APPLICANT: Skalky, Yasir A.W.

APPLICANT: Davin C.

APPLICANT: Campos-Neto, Antonia

APPLICANT: Houghton, Raymond

APPLICANT: Twardzik, Thomas S.

APPLICANT: Twardzik, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF THUMER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

STREET: 6300 Columbi-
                                                                                                                                                                                                                                                                                                                                                                                                      498 GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 532
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NAME: Maki, David J.
RECISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAC: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MRR-1997

CLASSIFICATION: 424
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STATE: Washing
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US-08-818-111-106
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JS-08-818-111-106
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Score 1652.5;

44.8%;

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                          Gaps
84.9%; Pred. No. 6.2e-113;
live 19; Mismatches 34; Indels
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INDIIION, DOWNOUNDS AND METHODS FOR THE PRE NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STEET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 GLPLGOLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 84.9
Matches 337, Conservative
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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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Reed, Steven G.
            LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 84.99
Matches 337; Conservative
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STREET: 6300
CITY: Seattle
...me: Washington
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US-09-072-596-106
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                                                                142 MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 201
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                                                                                    SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                 Gaps
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Slillon, Davin C.
APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                               7;
 DB 4; Length 396;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 GLPVGQMGARAG - GGLSGVLRVPPRPYVMPHSPAAG 532
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
Query Match
44.8%; Score 1652.5; DB 4;
Best Local Similarity 84.9%; Pred. No. 6.2e-113;
Matches 337; Conservative 19; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Maki, David J.
REGISTRATION UNDRER: 31,392
REFERENCE/DOCKET UNDRER: 21011
TELECOMMUNICATION INFORMATION:
TELEFAN: (206) 622-4900
TELEFAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 106:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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STATE: Washington
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GENERAL INFORMATION:
APPLICANT: Reed, S
APPLICANT: Skeiky,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 GSSGLGAGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
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                                                                                                         142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                         MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTAAQNGVRAMSS----LGSSL
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neco, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wardzik, Daniel R.
APPLICANT: Lodes, Michael S.
APPLICANT: Compounds C.
APPLICANT: Compounds C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
                                                    7;
  DB 4; Length 396;
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COMPUTER READABLE FORM:

MEDIUM TYER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/09/072,967
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                                                          34;
                             Pred. No. 6.2e-113;
19; Mismatches 34;
44.8%; Score 1652.5;
84.9%; Pred. No. 6.2e
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Patent No. 6592877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 IVSMLNNHVSMTNSGVSMASTLHSMLKGFAPAAA-QAVETAAQNGVQAMSSLGSQLGSSL 299
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US-08-818-112-109
| US-08-818-112-109
| Sequence 109, Application US/08818112
| Patent No. 629069
| GENERAL INCORNATION:
| APPLICANT: Read, Steven G. APPLICANT: Skeiky, Yasir A.W. |
| APPLICANT: Campos-Netc, Antonio APPLICANT: Houghton, Raymond |
| APPLICANT: Houghton, Raymond |
| APPLICANT: Wardzik, Thomas S. APPLICANT: Wardzik, Daniel R. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNCTHERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS |
| NUMBER OF SEQUENCES: |
| CORRESPONDENCE ADDRESS: |
                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                          Length 396;
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                                                                                                                                                                                                                                                                                                                        Query Match

44.8%; Score 1652.5; DB 4. Best Local Similarity 84.9%; Pred. No. 6.2e-113; Matches 337; Conservative 19; Mismatches 34;
ATTORNEY/AGENT INFORMATION:
NAME: MAK: David J.
REGISTRATICH NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 682-6931
INFORMATION FOR SEQ ID NO: 111:
SEGUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                             LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS:
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CITY: Seattle
STATE: Washington
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US-09-072-967-111
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61 SSAGLMAAAASFYVAMMSVTAGQAQLTAAQVRVAAAAYETAYRLTVPPPVIAENRTELMT 120
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: J3-MAR-1997
FLING DATE: J3-MAR-1997
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: MAKI, DATIG J. 392
REGISTRATION NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAK: (206) 622-4900
TELETAK: (206) 622-691
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
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TYPE: Amino acids
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84.2%; Pred. No. 7.3e-101;
tive 16; Mismatches 36;
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Job time : 28.0232 secs
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Best Local Similarity 84.2'
Matches 303; Conservative
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US-08-818-112-109
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June 22, 2004, 17:23:10; Search time 67.5195 Seconds (without alignments) 3048.105 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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3686
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	:	ilqc	Appl	2, Appli	Appl	Appli	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
		Ą.	16,	2,	16,	7	21,	15,	14,	13,	65,	12,	18,	17,	16,	18,
	Description	Sequence 2, Appli	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
	ΩI	US-09-287-849-2	US-09-886-349A-16	US-10-359-460-2	US-10-098-732A-16	US-10-359-459-2	US-10-369-983-21	US-10-369-983-15	US-10-369-983-14	US-10-369-983-13	US-10-098-732A-65	US-10-369-983-12	US-10-369-983-18	US-10-369-983-17	US-10-369-983-16	US-09-886-349A-18
	DB	. 6	12	14	14	15	15	15	15	15	14	12	15	15	15	12
	Query Match Length	729	729	729	729	729	729	813	825	875	930	930	1016	1022	1154	729
æ	Query Match	100.0	100.0	100.0	100.0	100.0	99.8	8.66	9.66	99.8	8.66	8.66	99.8	99.8	8.66	8
	Score	3686	3686	3686	3686	3686	3680	3680	3680	3680	3680	3680	3680	3680	3680	3677
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Sequence 18, Appl	Sequence 22,	quence 26,	ednence	equence 26,	20	4	Sequence 2,	7	22	14	equence 103	equence 10	equence 14	equence 8,	equence 10	equence 11	equence 62	equence 64	equence 1(i, e	quence 8,	ednence 8	equence 13	Sequence 92, Appl	ednence 3:	⊕	16	equence 4	
98-73	10-369-98	87-849-2	886-349A-	359-4	098-732A-	369-9	-69E	87-849-22	359-460	886-349A-1	.193-002-10;	.084-843-10	.098-732A	872-186-	.193-002-10	.084-843-111	-282-122A-624	-282-122A-6489	-193-002-	-084-843-1	-287-849-8	-359-460-	-886-349A-	US-10-193-002-92	-10-084-843-91	0-098-732A-	12-363-	-09-886-349	US-10-098-732A-4
14	in		\sim	4	4	LΩ	M		₹#	N	4	4	4	N	4	4	N	N	4	4,	σı	14	12	14	14	14	φ	12	14
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99.8			79.8					53.4	53.4	52.7	52.7	52.7	52.7	52.3	44.8	44.8	42.9	42.9	40.3	40.3	32.1	32.1	32.1	32.1	32.1	32.1	26.8	26.8	26.8
3677	3677	2941	2941	2941	2941	2637		196		13	σ	1944	σ	6	652	\sim	ഗ	ഗ	486	ശ	Ξ	-	Н	1182	\vdash	-	686	987	987
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ALIGNMENTS

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RESULT 1
US-09-287-849-2
US-09-287-849-2
Sequence 2, Application US/09287849
Sequence 2, Application US/09287849
Sequence 2, Application US/09287849
GENERAL INPORMATION:
APPLICANT: SKeiky, Yasir A.W.
APPLICANT: SKeiky, Yasir A.W.
APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Neto, Antonio
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APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Neto, Antonio
APPLICANT: US 08/942,578
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 46
SOGTHARE: PRECHEIN Ver. 2.1
SEQ ID NO 2
IENGTH: 729
ITYPE: PRT
COTHER INPORMATION: Description of Artificial Sequence: TENTURE INPORMATION: Description of Artificial Sequence
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Score 3686; DB 9; Length 729; Pred. No. 7.4e-244;

100.0%;

Query Match Best Local Similarity ~

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Sequence 2, Application US/10359460 Publication No. US20030147911A1 GENERAL INFORMATION:
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Sequence 16, Application US/0986349A

Publication No. US20040086523A1

GENERAL INPORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Pain Proteins of Mycobacterium Tuberculosis
TITLE OF INVANION: Pusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/09/886,349A

CURRENT FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: US 09/597,796

PRIOR APPLICATION NUMBER: US 00/265,737

PRIOR PLILNG DATE: 2001-02-01

NUMBER OF SEQ ID NOS: 50
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                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:tri-fusion; OTHER INFORMATION: protein MTB72F (Ral2-TbH9-Ra35 or MTB32-MTB39; OTHER INFORMATION: fusion)
05-09-886-349A-16
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                                                                                                        ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 16
LENGTH: 729
TYPE: PRT
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Best Local Similarity 100.
Matches 729; Conservative
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                       QDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
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COTHER INFORMATION: Description of Artificial Sequence:tri-fusion
COTHER INFORMATION: protein MTB72F (Ral2-TbH9-Ra35 or MTB32-MTB39
COTHER INFORMATION: fusion)
US-10-098-732A-16
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Best Local Similarity 100.0%; Pred. No. 7.4e-244;
Matches 729; Conservative 0; Mismatches 0; 1
                                                           APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Prociens of Mycobs
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US 09/287,849
PRIOR FILING DATE: 1997-00-13
PRIOR FILING DATE: 1997-01-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
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               Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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LENGTH: 729
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Publication No US20030235593A1

GENERAL INPORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Greven
TILL OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
FILE REFREENCE: 014058-009081US
CURRENT PLILOGATION NUMBER: US/10/369,983
CURRENT PLILOGATE: 2002-03
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR PLILOG DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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US-10-369-983-21
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US-10-369-983-21
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LENGTH: 729
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Fublication No. US20040013677A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Vasir
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neco, Antonio
APPLICANT: Corrixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009010US
CURRENT APPLICATION NUMBER: US/0359,459
CURRENT FILING DATE: 2003-02-05
FRIOR APPLICATION NUMBER: US/09/223,040
FRIOR PILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 10
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                                                                                 TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP
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ORCANISM: Artificial Sequence
FEATURE:
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SEQ ID NO 2
LENGTH: 729
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                                                       ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT
                                        TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
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PUBLICANT: Skeiky, Yasir

GENERAL INFORMATION:

APPLICANT: Guderian, Jeff

APPLICANT: Red, Steven

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

FILE REFERENCE: 014058-009081US

CURRENT APPLICATION NUMBER: US,10/369,983

CURRENT FILING DATE: 2003-02-18

PRIOR APPLICATION NUMBER: US,60/357,351

PRIOR FILING DATE: 2002-02-15

SOFTWARE: PARILING DATE: 2002-02-15

SOFTWARE: PARILING PATE: 2002-02-15

SOFTWARE: PARILING VET. 21

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SOFTWARE: PARILING VET. 21
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OTHER INFORMATION: Description of Artificial Sequence:fusion protein
CTHER INFORMATION: MTB81F (MTB72F-DPV)
US-10-369-983-15
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                                     Gaps
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APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Red, Steven
APPLICANT: Red, Steven
APPLICANT: Corist Corporation
TILLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
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   Length 813;
                                     Indels
Score 3680; DB 15;
Pred. No. 2.2e-243;
0; Mismatches 1;
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     al Similarity 99.9
728; Conservative
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     Query Match
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Matches 728
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                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence:fusion protein; OTHER INFORMATION: MTB83F (MTB72F-MTI)
US-10-369-983-14
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                                                                                                                                               Length
                                                                                                                                                                       Indels
                                                                                                                                            Score 3680; DB 15;
Pred. No. 2.3e-243;
0; Mismatches 1;
                                                                                                                                          Query Match
Best Local Similarity 99.9%;
Matches 728; Conservative 0
                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 825
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RESULT 9
US-10-369-983-13
Sequence 13, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:

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APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFRENCE: 014058-00909103
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·,
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99.9%; Pred. No. 2.4e-243;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 99.9
Matches 728; Conservative
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US-10-369-983-13
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241 541 301 361 661 601 661 721 721 541 g $\stackrel{>}{\circ}$ g $\dot{\delta}$ 엄 à g à g ð 임 8 8 $\stackrel{>}{\circ}$ 9 6 9 ò 540 120 61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120 180 FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE 240 TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT 300 241 TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEWWAQDAAAMFGYAAAT 300 ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT 360 ATATATLI PFEEAPEMTSAGGLI EQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT 360 PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQ 420 PSSKIGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQ 420 TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP 480 TAAQNGVRAMSSIGSSIGSSGIGGGVAANLGRAASVGSLSVPQAWAAANQAVTFAARAFP 480 LISLISAAERGPGOMLGGLPVGOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS 540 9 9 1 MHHHHHHAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD 1 MHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ TKSGGTRTGNVTLAEGPPAEFWVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL OTHER INFORMATION: Description of Artificial Sequence:MTB72F-MAPS
OTHER INFORMATION: (195f) fusion construct, TB MTB72F (Ral2-TbH9-Ral3S)
OTHER INFORMATION: linked to Leishmania thiol-specific antioxidant
CTHER INFORMATION: (TSA or MAPS)
US-10-098-732A-65 Gaps .; 0 Ouery Match

99.8%; Score 3680; DB 14; Length 930;
Best Local Similarity 99.9%; Pred. No. 2.6e-243;
Matches 728; Conservative 0; Mismatches 1; Indels 0 Constructs RESULT 10
US-10-098-732A-65
Sequence 65, Application US/10098732A
Sequence 65, Application US/10098732A
Seduence 65, Application US/10098732A
Sublication No. US20030175294A1
GENERAL INPORMATION:
APPLICANT: Brannon, Mark
APPLICANT: Gooixa Corporation
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 0140658-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR FILING DATE: 2003-04-313
NUMBER OF SEQ ID NOS: 80
SOCTWARE: Patentin Ver: 2.1
SEQ ID NO 65 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: VVGMNTAAS VVGMNTAAS 301 301 361 19 121 181 181 241 421 481 481 361 421 721 Sp 8 6 ò d 임 dd ò g ò 음 $\dot{\delta}$ ò ð 8 G ਨੇ qq

ö 300 120 180 240 241 TAYGLTVPPPVIAENRAELMILIATNILGQNTPAIAVNEABYGEWWAQDAAMFGYAAAT 300 ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT 360 720 PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQ 420 9 61 NNGNGARVORVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 181 FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQABLTAAQVRVAAAAYB TAYGLTVPPPVIAENRAELMILIATNLLGONTPAIAVNBAEYGEMWAQDAAAMFGYAAAT 301 ATATATLIPEERAPEMTSAGGILEQAAVEEASDTAAANQLMNNVPQALQQLAQPTGGTT SGGQGGTPRAVPGRVVALGQTVQASDSLTGABETINGLIQFDAAIQPGDSGGPVVNGLGQ 1 MHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD 121 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL QDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN Gaps RESULT 11
US-10-169-983-12
; Sequence 12, Application US/10369983
; Publication No. US2030235593A1
; Publication No. US2030235593A1
; APPLICANT: Skeiky, Yasir
; APPLICANT: Skeiky, Yasir
; APPLICANT: Gaderian, Jeff
; APPLICANT: Gorixa Corporation
; TITLE OF INVENTON: Fusion Proteins of Mycobacterium Tuberculosis
; TITLE OF INVENTON: Eusion Proteins of Mycobacterium Tuberculosis
; TITLE OF INVENTON: Eusion Proteins of Mycobacterium Tuberculosis
; TITLE OF INVENTON: Eusion Proteins of Mycobacterium Tuberculosis
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 930
***CONTINUENTON NUMBER: US CTHER INFORMATION: Description of Artificial Sequence:fusion protein; CTHER INFORMATION: R95F (MTB72F-MAPS)
US-10-369-983-12 ö Length 930; 1; Indels Query Match
99.8%; Score 3680; DB 15;
Best Local Similarity 99.9%; Pred. No. 2.6e-243;
Matches 728; Conservative 0; Mismatches 1; TYPE: PRT ORGANISM: Artificial Sequence FEATURE: VVGMNTAAS 729 VVGMINTAAS

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                                      TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT
                                                                                   241 TAYGLTVPPPVIAENRAELMILIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT
                                                                                                                                                                                                                  301 ATATALLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT
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OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB102tm2F (MTB102FTM2, MTB72F-hTCC#1)
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APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERBNCE: 014056-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
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Publication No. US20030235593A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver, 2.1
EQ ID NO 17
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US-10-369-983-17
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TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALP
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                                                                                         TAAQNGVRAMSSLGSSLGSSCLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP
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| Publication No. US2003023593A1
| GENERAL INFORMATION:
| APPLICANT: Skeiky, Yasir
| APPLICANT: Guderian, Jeff
| APPLICANT: Reed, Steven
| APPLICANT: Reed, Steven
| TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
| TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
| TITLE REFERENCE: 014058-009081US
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TYPE: PRT
PREATURE:
PRATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB103F (MTB72F-85b)
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llarity 99.9%; Pred. No. 2.9e-243;
Conservative 0; Mismatches 1;
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                                                  TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
                                                                                                                    FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE
                                                                                                                                                                                      TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT
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                                                                                TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
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APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Redd, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: 2003-02-18
PRICR APPLICATION NUMBER: US 60/357,351
PRICR TILING DATE: 2003-02-18
PRICR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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임 ò TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP LISLISAAERGPGOMLGGLPVGOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS

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61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL 180

MHHHHHHAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD 61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ

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MHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD

Score 3680; DB 15; Pred. No. 3.5e-243; 0; Mismatches 1;

99.8%; ilarity 99.9%; Conservative

Similarity

Query Match Best Local Simi Matches 728;

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121 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE

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GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN
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                                             QDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
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APPLICANT: Red, Steven
APPLICANT: Red, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/09886349A Publication No. US20040086523A1 GENERAL INFORMATION:
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protein

CTHER INFORMATION: Description of Artificial Sequence:fusion OTHER INFORMATION: MTB114F (MTB72F-mTCC#2)
US-10-369-983-16

TYPE: PRT ORGANISM: Artificial Sequence

FEATURE:

SEQ ID NO 16

720

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                                                                                                                                                     CTHER INFORMATION: Description of Artificial Sequence:MTB72FMutSA; CTHER INFORMATION: (Ral2-TbHp-Ra35MutSA)
US-09-886-349A-18
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                                                                                                                                                                                                                        Length 729;
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PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 729
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Search completed: June 22, 2004, 18:07:58 Job time : 70.5195 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

June 22, 2004, 17:23:10 ; Search time 67.5195 Seconds (without alignments) 3048.105 Million cell updates/sec Run on:

US-09-886-349A-18 Title: Perfect score:

3685 1 MHHHHHHTAASDNFQLSQGG......AGGPVVNGLGQVVGMVTAAS 729 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1163542 seqs, 282313646 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/Pcr_PubCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/Pcr_Pub Pubp.*

3: /cgn2_6/ptodata/2/pubpaa/Pcr_Pub Pubp.pep:*

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19: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	App	App	App.	App	App	App	App	App	App	App.	App	Appl	ppli	Appl	Appli
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence 2, Appl	Sequence 16,	Sequence 2
ΙD	US-09-886-349A-18	US-10-098-732A-18	US-10-369-983-22	US-10-369-983-21	US-10-369-983-15	US-10-369-983-14	US-10-369-983-13	US-10-098-732A-65	US-10-369-983-12	US-10-369-983-18	US-10-369-983-17	US-10-369-983-16	JS-09-287-849-2	US-09-886-349A-16	US-10-359-460-2
	12	14	15	15	15	15	15	14	15	15	15	15	9	12	14
* Query Match Length DB	729	729	729	729	813	825	875	930	930	1016	1022	1154	729	729	729
% Query Match	100.0	100.0	100.0	99.9	6.66	99.	6.66	99.9	6.66	99.0	99.0	99.9	8.66	8.66	99.8
Score	3685	3685	3685	3682	3682	3682	3682	3682	3682	3682	3682	3682	3677	3677	3677
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11.0 10.0	S-100-193-9-
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US-09-866-349A-18
; Sequence 18, Application US/0988349A
; Sequence 18, Application US/0988349A
; Publication No. US20040086523A1
; Publication No. US20040086523A1
; Publication No. US20040086523A1
; APPLICANT: Skeiky, Yasir
; APPLICANT: Reed, Steven
; APPLICANT: Corixa Corporation
; APPLICANT: Corixa Corporation
; APPLICANT: Corixa Corporation
; APPLICANT: Corixa US-09-0970US
; TITLE REFERENCE: 010458-00970US
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/597,796
; PRIOR APPLICATION NUMBER: US 09/597,796
; PRIOR PILING DATE: 2001-06-20
; PRIOR FILING DATE: 2001-06-20
; WUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
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OTHER INFORMATION: Description of Artificial Sequence:MTB72FMutSA
OTHER INFORMATION: (Ra12-TbHp-Ra35MutSA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 18
LENGHH: 729
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 729, Conservative
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Gaps

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Length 729; Indels 9

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300 300 360 360 420 480

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121 TKSGGTRTGNVTLAEGPPAEFWVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL 180
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                     DB 14;
                   100.0%; Score 3685; DB 14,
Similarity 100.0%; Pred. No. 3.4e-239,
29; Conservative 0; Mismatches 0;
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NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120
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Publication No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising of TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-01201040
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:WTB72FMutSA
OTHER INFORMATION: (Ral2-TDH9-Ra35MutSA)
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PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 729
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LISLISAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS
                                                                              481 LISLISAAERGPGOMLGGLPVGOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS
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Sequence 22, Application US/10369983

Sequence 22, Application US/10369983

Publication No. US20030235593A1

GENERAL INFORMATION.

APPLICANT: Skeiky, Yasir

APPLICANT: Red, Steven

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

FILE REFERENCE: 014058-009081US

CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT FLING DATE: 2003-02-18

PRICE APPLICATION NUMBER: US 60/357.351
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720 180 120 120 180 240 FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE 240 300 300 ATATATLIPFEEAPEMTSAGGILEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT 360 PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQ 420 PSSKLGGLWKTVSPHRSPISNWVSMANNHMSMTNSGVSWTNTLSSMLKGFAPAAAQAVQ 420 TAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP 480 540 QDRFADFPALFLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA 600 GATDINAFSVGSGOTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN 660 9 9 LISLISAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS SGGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPVVNGLGQ 121 TKSGGTRIGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDL 241 TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAMFGYAAAT 1 MIHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYE TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT Gaps ., Sequence:mutated Length Indels 100.0%; Score 3685; DB 15; 100.0%; Pred. No. 3.4e-239; iive 0; Mismatches 0; ; OTHER INFORMATION: Description of Artificial ; OTHER INFORMATION: MTB72FMutSA (Mtb72f-mutSA) US-10-369-983-22 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: Conservative 729 NUMBER OF SEQ ID NOS: 22 SOFTWARE: Patentin Ver. SEQ ID NO 22 LENGTH: 729 VVGMNTAAS VVGMNTAAS Query Match Best Local Similarity Matches 729; Conserv 181 361 481 481 541 541 601 661 661 721 61 181 241 301 301 361 421 421 601 721 පු g S g 임 δ οp δ Dp $\dot{\delta}$ $\dot{\circ}$ d $\dot{\delta}$ δ g $\dot{\delta}$ ద g ò g δ qq à ò

Sequence 21, Application US/10369983; Publication No. US20030235593A1; GENERAL INFORMATION: RESULT 4 US-10-369-983-21

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540 540 600 600 120 61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120 180 180 240 240 300 300 360 360 420 420 480 480 09 9 QDRFADFPALFLDFSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDFNGVVLTNNHVIA 1 MHHHHHHAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ TAYGLTVPPPVIAENRAELMILIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT QDR.FADF.PAL.PLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA 1 MHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGGAELTAAQVRVAAAAYE ATATATLI PFEEAPEMTSAGGLI EQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQ TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP LISLISAAERGPGOMLGGLPVGOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Grad, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
FILE REFRENCE: 014658-00908108
FILE REFRENCE: 014658-00908108
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGRAME: 729 ö Length 729, , OTHER INFORMATION: Description of Artificial Sequence: WTB72F US-10-369-983-21 Indels Query Match 99.9%; Score 3682; DB 15; Best Local Similarity 99.9%; Pred. No. 5.4e-239; Matches 728; Conservative 1; Mismatches 0; TYPE: PRT ORGANISM: Artificial Sequence 541 61 181 241 301 301 361 481 541 121 241 361 421 421 481 181 FEATURE: 셤 Бþ à g 8 d ò В δ g 8 a δ a S G ò g ð ò

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661 SGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQ 720
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                                                                GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Steiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR PILING DATE: 2003-02-18
PRIOR PLING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22-15
SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
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LENGTH: 825
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OTHER INFORMATION: Description of Artificial Sequence:fusion protein

OTHER INFORMATION: MTB81F (MTB72F-DPV)
US-10-369-983-15
                                                                                                                                                                                                APPLICANT: Skelky, Yasir
APPLICANT: Skelky, Yasir
APPLICANT: Skelky, Yasir
APPLICANT: Guderian Jeff
APPLICANT: Reed, Steven
TILLS OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SSQ ID NO 15
LENGTH: 813
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Best Local Similarity 99.9%; Pred. No. 6.2e-239;
Matches 728; Conservative 1; Mismatches 0;
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US-10-369-983-15
Sequence 15, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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QDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
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US-10-369-983-13

US-10-369-983-13

Sequence 13, Application US/10369983

Publication No. US20030235593A1

GENERAL INFORMATION:

APPLICANT: Greix, Tasir

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

FILE REFERENCE: 014058-009081US

CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT FILING DATE: 2002-02-18

PRIOR APPLICATION NUMBER: US 60/357,351

PRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22

SEQ ID NOS: 22

LENGTH, 875

LENGTH, 875
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ORGANISM: Artificial Sequence
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US-10-008-53.2A-65

Sequence 65, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:

APPLICANT: Skelky, Yasir

APPLICANT: Skelky, Yasir

APPLICANT: Guderian, Jeffrey

APPLICANT: Corixa Corporation

ITILE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

FILE REFERENCE: 014058-012010US

CURRENT APPLICATION NUMBER: US/10/099,732A

CURRENT FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 65

LENGTH: 930

TYPE: PRT

ORGANISM: Artificial Sequence

FRATURE:

ORGANISM: Artificial Sequence
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CTHER INFORMATION: (r95f) fusion construct, TB MTB72F (Ral2-TDH9-Ra35)
CTHER INFORMATION: linked to Leishmania thiol-specific antioxidant
CTHER INFORMATION: (TSA or MAPS)
US-10-098-732A-65
ATATATILIPFEBAPEMTSAGGILEQAAAVEBASDTAAANQLMNNVPQALQQLAQPTQGTT
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Best Local Similarity 99.9%; Score 3682; DB 14; Length 930;
Best Local Similarity 99.9%; Pred. No. 7.3e-239;
Matches 728; Conservative 1; Mismatches 0; Indels 0;
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                                                                                                                            Gaps
                                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB103F (MTB72F-85b)
US-10-369-983-18
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                                                                                                        1016
                                                                                                       Length
                                                                                                                            Indels
                                                                                                      Score 3682; DB 15;
Pred. No. 8.2e-239;
1; Mismatches 0;
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Best Local Similarity 99.9%;
Matches 728; Conservative
                             TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 1016
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Sequence 17, Application US/10369983; Publication No. US20030235593A1 GENERAL INFORMATION: APPLICANT: Skelky, Yasir

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APPLICANT: Guderian, uet.
APPLICANT: Reed, Steven
APPLICANT: COIXA CORPORATION
TITLE ONLYA CORPORATION
FILE REPERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US,10/369,983
CURRENT PAPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 1022
                                                                                                                                                                                                                          FEATURE:
CHER INFORMATION: Description of Artificial Sequence:fusion protein
CHER INFORMATION: MTB102tm2F (MTB102FTM2, MTB72F-hTCC#1)
US-10-369-963-17
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Best Local Similarity 99.9
Matches 728; Conservative
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GENERAL INCOMPAIRMENT Seed, Steven G.
APPLICANT Skeiky, Yasir A.W.
APPLICANT Skeiky, Wasir A.W.
APPLICANT Skeiky, Warin C.
APPLICANT Dillon, Davin C.
APPLICANT Campos-Neto, Antonio
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APPLICANTON: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
CURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-00-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICANTON NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-04-07
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                                   GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN
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; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-2
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99.7%; Pred. No. 1.2e-238;
live 1; Mismatches 1;
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SOFTWARE: Patentin Ve
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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-00908110
FILE REFERENCE: 014058-00908116
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR PILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:fusion protein OTHER INFORMATION: MTB114F (MTB72F-mTCC#2)
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99.9%; Score 3682; DB 15; Length 1154;
Best Local Similarity 99.9%; Pred. No. 9.7e-239;
Matches 728; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                Sequence 16, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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                                                            PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQ
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               ATATATLI PFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT
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US-09-866-349A-16

US-09-866-349A-16

SQUEENCE 16, Application US/0986349A

PUBLICATION NO. US20040086523A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven

APPLICANT: Aderson, Mark

APPLICANT: Alderson, Mark

APPLICANT: Alderson, Mark

COTIAN COLIAN COLONOTION

TITLE OF INVENTION Fusion Froteins of Mycobacterium Tuberculosis

FILE REFERENCE: 014058-009070US

CUTRAIN APPLICATION NUMBER: US/09/886,349A

CUTRAIN APPLICATION NUMBER: US 60/597,796

PRIOR FILING DATE: 2001-06-20

PRIOR FILING DATE: 2001-06-20

PRIOR FILING DATE: 2001-06-20

PRIOR FILING DATE: 2010-06-30

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 729
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US-09-886-349A-16
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99.8%; Score 3677; DB 12; Length 729;
Best Local Similarity 99.7%; Pred. No. 1.2e-238;
Matches 727; Conservative 1; Mismatches 1; Indels 0
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ORGANISM: Artificial Seguence
FEATURE:
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US-1U-35Y-400-4
; Sequence 2. Application US/10359460
; Publication No. US20030147911A1
; GENERAL IMPORMATION:
   APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa Corporation
TITLE OF INVENTION: Englos Protiens of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and Their Uses
; TITLE OF INVENTION: 1945-00902008
; CURRENT APPLICATION NUMBER: US/10/359,460
; CURRENT FILING DATE: 1999-04-07
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: US 08/942,578
; PRIOR APPLICATION NUMBER: US 08/942,578
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
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                                                                                           TYPE: PRT SOGANISM: Artificial Sequence PEATURE: PRETURE: OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-10-359-460-2
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                                                                                                                                                                                      Length 729;
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                                                                                                                                                                                    Score 3677; DB 14;
Pred. No. 1.2e-238;
1; Mismatches 1;
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 729
                                                                                                                                                                                   Query Match
Best Local Similarity 99.7%;
Matches 727; Conservative
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Search completed: June 22, 2004, 18:08:00 Job time : 69.5195 secs

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June 22, 2004, 17:07:54; Search time 21.2754 Seconds (without alignments) 1446.225 Million cell updates/sec
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3007
1 HWHHHHHHWUDFGALPPEIN.....SGGPVVNGLGQVVGMNTAAS 596
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Sequence 26, Appl	ď	'n	22	10	100	10	100	10	Sequence 111, App	100	Ξ	10	e 11:	20	, 10	Sequence 109, App	10	equence 10:	equence 8,	equence 91	Sequence 92, Appl	91	Sequence 92, Appl	Sequence 91, Appl	7	80
SOUTHERE	ID	-09-287-849-	-09	-849-	-09-287-849-	08-818-11	111-1	-60-	-09-072-	9-072-9	3-818-112-	US-08-818-111-106	ç	19-072-596	09-072-967	US-08-818-112-109	US-08-818-111-104	-60	US-09-072-596-104	072-967	US-09-287-849-8	-08-818-11	38-81	09-056-556-9	US-09-072-596-92	09-07	US-08-818-112-79	US-08-818-111-80
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æ	Query Match	100.0	97.8	97.8	67.6	64.8	64.8	64.8	64.8	64.8	55.0	55.0	55.0	55.0	55.0	49.4	49.4	49.4	49.4	49.4	39.5	39.5	39.5	39.5	39.5	39.5	32.7	32.7
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Sequence 80, Appl Sequence 80, Appl Sequence 126, Appl Sequence 126, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 15, Appl Sequence 208, Appl Sequence 208, Appl Sequence 208, Appl Sequence 14, Appl Sequence 14, Appl Sequence 114, Appl Sequence 114, Appl Sequence 114, Appl Sequence 119, Appl Sequence 119, Appl	cterium tuberculosis Antigens Sequence:bi-fusion	Length 596; ; Indels 0; Gaps 0;	MDSVASDLFSAASAFOSVVWG 60	RVAAAAYETAYGLTVPPPVIA 120
4 US-09-056-556-79 55 4 US-09-072-596-80 64 US-09-073-009-126 60 4 US-09-073-009-126 60 4 US-09-073-009-126 60 4 US-09-287-849-12 61 4 US-09-073-009-142 62 4 US-09-073-009-142 63 4 US-09-073-009-15 64 US-09-073-009-15 65 4 US-08-311-731A-57 66 4 US-08-311-731A-57 67 4 US-08-311-731A-57 68 4 US-08-311-731A-58 69 4 US-08-311-731A-58 60 4 US-08-311-731A-58 60 4 US-08-311-731A-58 60 4 US-08-311-731A-58 60 4 US-08-311-731A-58 60 4 US-08-311-731A-58 60 4 US-08-311-731A-58 60 4 US-08-311-731A-58 60 4 US-08-311-731A-58 60 4 US-08-311-731A-58 60 4 US-08-311-731A-58 60 4 US-08-318-731A-58 60 4 US-08-31A-78 60 4 US-08-31A-78 60 5 5 5 5 5 5 5 5 5 5 5 5 5	IGNMENTS 15 of Mycoba 16,12 12,578 15,197 16,556 16,556 16,556 17,197 18,112	100.0%; Score 3007; DB 4; 100.0%; Pred. No. 1.3e-219; ative 0; Mismatches 0;	HMEHHEHEMVDFGALPPEINSARMYAGPGSASLVAAAQMADSVASDLF: 	LIVGSWIGSSAGLMVAAASPYVAMMSVTAQQAELTAAQVRVAAAYETAYGLTVPPPVI.
983 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 3553 32.7 32.7 32.7 32.7 32.7 32.7 32.7 32.	RESULT 1 US-09-287-849-26 Sequence 26, Application US/09287845; Sequence 26, Application US/09287845; Patent No. 6627198 GENERAL INFORMATION: APPLICANT: Reed, Stewn G. APPLICANT: Alderson, Marin C. APPLICANT: Dillon, Davin C. APPLICANT: Ocrixa Corporation TITLE OF INVENTION: Fusion Protier TITLE OF INVENTION: Tusion Protier TITLE OF INVENTION: and Their Use FILE REFERENCE: 014058-009020US CURRENT FILING DATE: 1999-04-07 PRIOR PRILING DATE: 1999-04-07 PRIOR PRILING DATE: 1999-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR FILING DATE: 1998-04-07 PRIOR FILING DATE: 1998-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR PLILING DATE: 1998-04-07 PRIOR PRILING DATE: 1998-04-07 PRIOR PRILING DATE: 1998-04-07 PRIOR PLING DATE: 1998-04-07 PRIOR PLING DATE: 1998-04-07 PRIOR PLING DATE: 1998-04-07 PRIOR PLING DATE: 1998-04-07 PRIOR PLING DATE: 1998-04-07 PRIOR PRING DATE: 1998-04-07 PRIOR PLING DATE: 1998-	Query Match Best Local Similarity Matches 596; Conservat:	Qy 1 HMHHHHHWUDF 	61 LTVGSWIGSSAG 61 LTVGSWIGSSAG

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       LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVV 488
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                                                                                                                                                  MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562 GPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVV
                                                                                                                                                                                                                                                                                                                                                                                                                             502 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622 GYDRTÓDVAVLÓLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGÓGGTPRAVPGRVVALGGT
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US-09-287-849-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       682 VQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGNNTAAS 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 VQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS 596
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Best Local Similarity 99.8%; Pred. No. 1.7e-214;
Matches 587; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09287849;
Sequence 2, Application US/09287849;
PREDENT NO. 6627198
GENERAL INFORMATION;
APPLICANT: Skeed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Caps Corporation
ITILE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-0090200S
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR PRIUGE DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US/09/056,556
PRIOR APPLICATION NUMBER: US/09/056,556
PRIOR APPLICATION NUMBER: US/09/056,556
PRIOR APPLICATION NUMBER: US/09/056,556
PRIOR APPLICATION NUMBER: US/09/056,556
PRIOR APPLICATION NUMBER: US/09/056,556
PRIOR PRIUGE DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIN Ver: 2.1
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US-09-287-849-2
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APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Netos Net
ENPABLMILIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEA 180
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                                                                                                                                                                                                                    PHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSL
                                                                     PEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09223040; Patent No. 6544522; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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6300 Columbia Center, 701 Fifth Avenue
  81;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 107, Application US/08818112
Patent No. 629059
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND MET
TITLE OF INVENTION: AND DIAGNOSIS OF
NUMBER OF SEQUENCES:
ADDRESSER: SEED and BERRY LLP
STEET: 6300 Columbia Center, 701 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  19;
  440; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washington
COUNTRY: USA
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patent No. 6627198

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Allon, Davin C.

APPLICANT: Campos Neto, Antonio

APPLICANT: Clampos Neto, Antonio

APPLICANT: Corixa Corporation

TITLE OF INVENTION: and Their Uses

FILE REFERENCE: 014058-009020US

FILE REFERENCE: 014058-009020US

FILE REFERENCE: 014058-009020US

FILE REFERENCE: 014058-009020US

FILE REPRENCE: 014058-009020US

FILE REPRENCE: 014058-009020US

FILE REPRENCE: 014058-009020US

FURRENT FILING DATE: 1999-04-07

PRIOR APPLICATION NUMBER: US 08/912,578

PRIOR PELING DATE: 1998-04-07

PRIOR PELING DATE: 1998-04-07

PRIOR PELING DATE: 1998-04-07

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                                                                                               321
                                                                                                                                              LLEQAAAVEEASDTAAANQLANNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
                                                                                                                                                                                     LIEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381
                                                                                                                                                                                                                                      MYSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 308
                                                                                                                                                                                                                                                                                                                                 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 368
       SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOMGARAGGGISGVIRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV
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                                                     LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                             LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
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J. OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
02-09-287-849-22
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Pred. No. 6.7e-146;
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ORGANISM: Artificial Sequence
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Best Local Similarity
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404 -PALSQDRFADFPALPLDPS-------AWVAQVGPQVVNINTKLGYNNAVGAG 448
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                                                                                                                                                        LTVGSWIGSSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIA 120
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                                                                                                                                                                                             61 LTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIA
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                                                                                              1 HMHHHHHHMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWG
                                                                                                                                                                                                                                                                  ENRAELMILIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEA
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                                                   1 HMHHHHHHHWYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWG
Gaps
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CITY: Seattle
STATE: Washingt
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US-08-818-111-102
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neco, Antonia
APPLICANT: Waymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/818,112
FILING DATE: US/08/818,112
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: MAIL, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPAS: (206) 622-4900
TELEPAS: (206) 622-4900
TELEPAS: (206) 622-601
INFORMATION FOR EQ ID No: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TENGTH: 391 amino acids
STRANDBURSS: single
STRANDBURSS: single
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6300 Columbia Center, 701 Fifth Avenue
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Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100. Matches 391, Conservative
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Washington
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US-08-818-111-102
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 391; Conservative 0; Mismatches 0;
                                                                                                                                                                       Version #1.30
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASASIFICATION: WA24
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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US-09-072-596-102
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                                                                                                                                                                                                                                                                                                                                                                                                                    64.8%; Score 1949; DB 4; L
100.0%; Pred. No. 9.4e-140;
iive 0; Mismatches 0;
                                    COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
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Patent No. 6458366
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Dillon, Davin C.
Campos-Neto, Antonia
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                                                                                                                                                                                                                                                                                                                            391 amino acids
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                                                                                                                                                                                                                                                                                                                                                          single
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APPLICANT: Reed, St.
APPLICANT: Skeiky,
APPLICANT: Dillon,
APPLICANT: HOUGHLON,
APPLICANT: HOUGHLON,
APPLICANT: HOUGHLON,
APPLICANT: TWARCAZIK,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                         linear
                        98104-7092
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US-09-072-596-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
ALL RESIDES OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 64.8%; Score 1949; DB 4; :
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 391; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210121.41709
                                                                                                                                                                            COUNTRY: USA

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
NAME: Maki, David d', 1,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417
TELECHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 107, Application US/09072967; Patent No. 6592877; GENERAL INFORMATION: APPLICANT: Skeiky, Yasir A.W.
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Campos-Neco, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romaid C.
VERVICK COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
VERVICOR: AND DIAGNOSIS OF TUBERCULOSIS
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64.8%; Score 1949; DB 4; Length 391;

Best Local Similarity 100.0%; Pred. No. 9.4e-140;

Matches 391; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                    3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILLING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
                                                                                                                                                                                                                                                                                                                      ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
                                                                                                                                                                             355
                                                             APPLICANT: TWATGZIK, DAN
APPLICANT: Lodes, Michae
APPLICANT: Hendrickson
TITLE OF INVENTION: COMP
TITLE OF INVENTION: AND
TITLE OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BEB
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                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 396;
                                                                                                                                                             APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 55.0%; Score 1652.5; DB 3; Length Best Local Similarity 84.9%; Pred. No. 2.7e-117; Matches 337; Conservative 19; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                   E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible,
OPERATING SYSTEM: PC-DOS/MS-DOS
                    Sequence 111, Application US/08818112
Patent No. 6290969
                                                                                                          Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
TELEPRAX: (206) 682-6031
INPERMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 396 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Colun
CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-818-112-111
US-08-818-112-111
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121 LIATNILGGNIPAIAVNBARYGEMWAQDAAAMFGYAATAATATRALLPFEDAPLITNPGG 180
                                                        305 GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 364
                                                                                    241 IVSMLNNHVSMTNSGVSMASTLHSMLKGFAP-AAAQAVETAAQNGVQAMSSLGSQLGSSL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                       Sequence 111, Application US/09056556

Batent No. 6350456

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Indels
                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/056,556 FILING DATE: 07-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.0%; Score 1652.5; DB 4;
84.9%; Pred. No. 2.7e-117;
tive 19; Mismatches 34;
                                                                                                                                             365 GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 2101.
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 anino acids
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amino acid
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Matches 337; Conservative
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STATE: Washington
COUNTRY: USA
ZIP: 98104-77092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WYSMANNHMSMINSGVSMINTLSSMLKGFAPAAAQAVQTAAQNGVRAMSS----LGSSL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VVDFGALPPEINSARMYAGPGSASLVAAARNWDSVASDLFSAASAFQSVVWGLTTGSWIG 60
            300 GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 168
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: BACHOLIN RELEASE #1.0, Version #1.30
SOFTWARE: Patentln Release #1.0, Version #1.30
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/818,111
FLING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J
REGISTRATION NUMBER: 21,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
                                                    365 GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                          360 GLPLGOLINSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.0%; Score 1652.5; D Best Local Similarity 84.9%; Pred. No. 2.7e-1 Matches 337; Conservative 19; Mismatches
                                                                                                                                                     RESULT 11
US-08-018-111-106
; Sequence 106, Application US/08818111
; Patent No. 6338852
; Patent Turner Part No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
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98104-7092
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US-08-818-111-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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LIEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
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                                                                                                                                                           304
                                                                                                                                                                                                                                                                               300 GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPITSLTSAAQTAPGHMLG 359
                                                                                                                                                                                                                                               GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 364
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                                                                                                                                                         249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Twardik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
WENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
WENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                              360 GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
                                                                                                                                                                                                                                                                                                                                  365 GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZUMATTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/072,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.0%; Score 1652.5; DB 4; Best Local Similarity 84.9%; Pred. No. 2.7e-117; Matches 337; Conservative 19; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210121.41109
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05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 111, Application US/09072967
Patent No. 6592877
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-WAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEFONE: (206) 622-4900
TELEFONE: (206) 622-4900
TELEFONE: (206) 632-6011
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and 1
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CITY: Seattle
STATE: Washingt
COUNTRY: USA
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APPLICANT:
APPLICANT:
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                         300 GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
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                                                                                   305 GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 364
249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.0%; Score 1652.5; DB 4; Length 84.9%; Pred. No. 2.7e-117; ive 19; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLESSIFICATION NUMBER: 31,392
ATTORNEY/AGANT INFORMATION:
NAME: MAXI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMULICATION INFORMATION:
TELEFONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
TEMMATION FOR SEQ ID NO: 106:
                                                                                                                                                                         GLPVGQMGARAG - GGLSGVLRVPPRPYVMPHSPAAG 399
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|GLPLGOLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                           Sequence 106, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
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Reed, Steven G.
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Best Local Similarity 84.9
Matches 337; Conservative
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US-09-072-596-106
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                                                                                                                                           GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 364
                                                                                                                                                                                           LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
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SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                        LIAINLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCOMANTION:

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: David: Campos-Neco, Antonio

APPLICANT: Houghton, Raymond

APPLICANT: Wedvick, Daniel S.

APPLICANT: Wedvick, Daniel S.

APPLICANT: Campos-Neco, Thomas S.

APPLICANT: Wedvick, Daniel S.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INVUNCHERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,112

FILING DATE: 13-MAR-1997

APPLICATION NUMBER: US/08/818,112

FILING DATE: LANDARTON.
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|GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
                                                                                                                                                                                                                                                                                                                                                                                                       GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 399
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ATTORNEY/AGENT INFORMATION:
NAME: MAAL, David J. 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-490
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: ATRADEDNESS:
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-818-112-109
US-08-818-112-109, Application US/08818112
; Patent No. 6290969.
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                                                                                               LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                                                                       9 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                    Gaps
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Length 359;
Query Match
49.4%; Score 1486.5; DB 3; Length
Best Local Similarity 84.2%; Pred. No. 8.8e-105;
Matches 303; Conservative 16; Mismatches 36; Indels
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Wed Jun 23 16:34:35 2004
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June 22, 2004, 17:23:10 ; Search time 55:2012 Seconds (without alignments) 3048:105 Million cell updates/sec
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3007
1 HMHHHHHHWUDFGALPPEIN......SGGPVVNGLGQVVGMVTAAS 596
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1: /cgn2_6/ptodata/2/pubpaa/PCT_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_RW PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
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	Description	Sequence 26,	Seguence	Seguence	Seguence	Sequence	Sequence	Seguence	Seguence	Sequence	Seguence	Seguence	Seguence	Sequence	Seguence	Seguence
	ID	US-09-287-849-26	US-09-886-349A-20	US-10-359-460-26	US-10-098-732A-20	US-10-369-983-21	US-10-369-983-15	US-10-369-983-14	US-10-369-983-13	US-10-098-732A-65	US-10-369-983-12	US-10-369-983-18	US-10-369-983-17	US-10-369-983-16	US-09-886-349A-18	US-10-098-732A-18
	DB	. 6	12	14	14	15	15	15	15	14	15		15	15	12	14
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Query Match Best Local Similarity

Sequence	N.	~	Sequence 2, Appli	-	N	α	O	ゼ	Н.	equence 1	М	equence 1	equence 2	œ	equence 1	equence 1	equence 6	equence 6	9 TO	ce 109	8	3e 8,	equence 12,	92	equence 91	e 12	quence 161	Sequence 4, Appli	Sequence 4, Appli
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ALIGNMENTS

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sequence 26, Application US/09287849
patent No. US20200009459A1
general INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: 0018-00902016
CURRENT APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR PRILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR PRILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR PRILING DATE: 1998-04-07
PRIOR SEQ ID NO: 8-05
PRIOR PRILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR PRILING DATE: 1998-04-07
PRIOR PRILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR PRILING DATE: 1998-04-07
PRIOR PRILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR APPLICATION NUMBER: US 09/056,566
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PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR APPLICATION NUMBER: US
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; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
US-09-287-849-26
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Pred. No. 5e-202;
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TYPE: PRT
ORGANISM: Artificial Sequence
RESULT 1
US-09-287-849-26
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Mismatches
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 Conservative
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VEDICATION US/0986349A

VERICATION OF USCO40086523A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
CURRENT APPLICATION NUMBER: US/09/886,349A

CURRENT APPLICATION NUMBER: US/09/886,349A

CURRENT FILING DATE: 2001-06-20

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 2001-06-20

PRIOR FILING DATE: 2001-06-20

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIN Ver. 2.1

LENGTH: 596
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description
OTHER INFORMATION: protein Tbi
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APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
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THOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-14-07
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30 120 180 ENRAELMILIATNILLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEA 180 61 LTVGSWIGSSAGIMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIA 120 240 240 300 360 PHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSL 300 OMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLD 420 420 480 480 09 QTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPG 540 481 ÓTYGVDVVGYDRTÓDVAVLÓLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPG 540 9 LTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIA HMHHHHHHWDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWG ENRAELMILIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILPFEEA PEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS PEMISAGGLIEQAAAVEEASDTAAANQIMNNVPQALQQIAQPTQGTTPSSKLGGLWKTVS PHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAAAQAVQTAAQNGVRAMSSL GSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPG QMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLD PSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSG PSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSG 596 RVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS 596

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| LENGTH: 596
| TYPE: PRT
| ORGANISM: Artificial Sequence
| FEATURE: | CARRATION: Description of Artificial Sequence:bi-fusion US-10-359-460-26
                                                                                                      Query Match 100.0%; Score 3007; DB 14; Length 596; Best Local Similarity 100.0%; Pred. No. 5e-202; Matches 596; Conservative 0; Mismatches 0; Indels 0;
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RESULT 4

US-10-08-732A-20

Sequence 20, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Brannon, Mark

APPLICANT: Guderian, Jeffrey

APPLICANT: Coriza Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION NUMBER: US 00/10/098,732A

CURRENT APPLICATION NUMBER: US 00/275,837

PRIOR FILING DATE: 2003-04-29

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SEQ ID NOS: 80

LENGTH: 596
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US-10-369-983-21
Sequence 21, Application US/10369983
Sequence 21, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Ged, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US 60/357,351
CURRENT PILING DATE: 2002-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 729
TYPE: PRI
CREANISM: Artificial Sequence
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TYPE: PRT
COGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
OTHER INFORMATION: protein TbH9-Ra35 (designated MTB59F)
US-10-098-732A-20
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Best Local Similarity 100.0%; Pred. No. 5e-202;
Matches 596; Conservative 0; Mismatches 0; Indels 0;
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Sequence 14, Application US/10369983

Publication No. US2003023559341

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Gederian, Jeff
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351

PRIOR FILING DATE: 2002-02-18

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1
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US-10-369-983-14
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                                                             Length 813;
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                                                          Score 2946; DB 15;
Pred. No. 1.4e-197;
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ORGANISM: Artificial Sequence
                                                                                  Best Local Similarity 100. Matches 588; Conservative
            US-10-369-983-15
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SEQ ID NO 14
LENGTH: 825
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                                                          Query Match
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; Bublication No. US20030235593A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Guderian, Joff
; APPLICANT: Gorixa Corporation
; TILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REPERENCE: 014058-009081US
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Parentin Ver: 2.1
; SEQ ID NO 15
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                                                                                                              Length 729;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MTB72F
US-10-369-983-21
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                                                                                                         Query Match 98.0%; Score 2946; DB 15; Best Local Similarity 100.0%; Pred. No. 1.2e-197; Matches 588; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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    Length
                              0; Indels
 98.0%; Score 2946; DB 15;
100.0%; Pred. No. 1.4e-197;
tive 0; Mismatches 0;
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Publication No. US20030235593A1
GENERAL INFORMATION:
Query Match
Best Local Similarity 100.0
Matches 588; Conservative
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LGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 501

LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAABRGPGQMLGGLPV

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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV

GPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVV

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RESULT 8

US-10-369-983-13

Sequence 13, Application US/10369983

Sequence 13, Application US/10369983

Publication No. US20030235593A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yesir
APPLICANT: Guderian, Jeff
APPLICANT: Gorixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 0140638-009081US
CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT FILING DATE: 2003-02-18

PRIOR PILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13

LENGTH: 875

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: MTB89F (WTB72F-Erd14)
US-10-369-983-13

US-10-369-983-13
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Length 875

Score 2946; DB 15; Pred. No. 1.5e-197;

98.0%; S

Query Match Best Local Similarity

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RESULT 9

US-10-098-732A-65

US-10-098-732A-65

US-10-098-732A-65

Sequence 65, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION.

APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeffrey

APPLICANT: Guderian, Jeffrey

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

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TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: Leishmania Antigen

TITLE OF INVENTION: US08-12010-03-13

NUVBER OF SEQ ID NOS: 80

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 65

LENGTH: 930

TYPE: PRT

OCHER INFORMATION: (158) Leishmania thiol-specific antioxidant

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                                     MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                          142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                              SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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Sequence 18, Application US/10369983

Sequence 18, Application US/10369983

GENERAL INFORMATION:
APPLICANT: General Jeff
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APPLICATION NUMBER: US 60/357,351

PRIOR APPLICATION NUMBER: US 60/357,351

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 18
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OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: WTB103F (MTB72F-85b)
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US-10-369-983-12

Sequence 12, Application US/10369983

Publication No. US20030235593A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir

APPLICANT: Reed, Steven

APPLICANT: Recomment of Mycobacterium Tuberculosis

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPRENCE: 0140-58-09881US

CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT FILING DATE: 2003-02-18

PRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 12

LENGTH: 930

TUBENT: PRIOR PRICHT: VERNICATION NUMBER: US/10/369,983

PRIOR FILING DATE: 2002-02-15

SEQ ID NO 12

LENGTH: 930
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US-10-369-983-12
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                                          588; Conservative
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9 MVDFGALPPEINSARMYAGPGSASIVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG

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428 488 622 GYDKTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQT 681 188 248 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 368 561 69 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 128 262 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG LEGGAAVEBASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 382 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 502 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDDSAMVAQV 562 GPQVVNINTKLGYNNAVGAGTGIVIDFNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVV 142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASARQSVVWGLTVGSWIG 249 MVSMANNHMSMTNSGVSMTNTLSSMLKGPAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG GOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV GPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVV 9 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG SSAGIMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPVIAENRAELMI LLEQAAAVEEASDTAAANQLMMWVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN GYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQT 0; Gaps Sequence 16, Application US/10369983

Sequence 16, Application US/10369983

Publication No. US20030235533A1

GENERAL INFORMATION:

APPLICANT: Seeiky, Taair

APPLICANT: Guderian, Jeff

APPLICANT: Corixa Corporation

TILLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

FILE REPERENCE: OCTOPATION Proteins of Mycobacterium Tuberculosis

CURRENT PLING DATE: 2002-02-18

PRIOR FILING DATE: 2002-02-15

NUMBER: OF SEQ ID NOS: 22

SOFTWARE: PATENTY FURNING PATE: 2003-02-15

NUMBER: OF SEQ ID NOS: 22

SOFTWARE: PATENTY FURNING PATE: 2005-02-15

SEQ ID NO 16

LENGTH: 1154 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: WIBIL4F (WIB72F-MICC#2)
US-10-369-983-16 Length 1154; 682 VQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS 729 549 VQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS 596 Query Match 98.0%; Score 2946; DB 15; Length Best Local Similarity 100.0%; Pred. No. 2.2e-197; Matches 588; Conservative 0; Mismatches 0; Indels RESULT 13 US-10-369-983-16 429 129 189 322 309 442 369 QQ g g 6 B 6 B 6 B 6 8 S Q \$ B à õ 8 8 δ

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                                                                                                                                                      LLEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                                                                  LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGG
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV
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APPLICANT: Guderian, Jeffrey
APPLICANT: Codecian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
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ORGANISM: Artificial Sequence
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APPLICANT: Skeiky, Yasir
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Best Local Similarity
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US-10-098-732A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 128
                                                                                                                                                           LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                  382 MVSMANNHIMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                           442 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                GPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562 GPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489 GYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                             SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                         LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG
                                                                                                                262 LIATNLLGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                    LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                       GOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV
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Publication No. US20040086523A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Aderson, Mark
APPLICANT: Adderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-0039070US
CURRENT APPLICATION NUMBER: US/09/886,349A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION: Description of Artificial Sequence:MTB72FMutSAINFORMATION: (Ra12-TbHp-Ra35MutSA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           682 VQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-886-349A-18
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LENGTH: 729
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Search completed: June 22, 2004, 18:08:01 Job time : 56.2012 secs

549 VQASDSLTGAEETINGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS 596

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Ouery Match 100.0%; Score 481; DB 3; Length 96; Best Local Similarity 100.0%; Pred. No. 2.2e-50; Matches 96; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKE, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C6
TELECOMMULICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-818-112-102
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Sequence 97, Appl
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Sequence 151, Appl
Sequence 4, Appli
Sequence 4, Appli
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Sequence 115, App
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Sequence 54, Appl
Sequence 54, Appl
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Sequence 16,
Sequence 5, A
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Sequence 12,
Sequence 19,
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481
1 VAMSLITVGAGVASADPVDAV......PGAAQYIGLVESVAGSCNNY
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-818-111-97
US-09-075-556-102
US-09-050-739-151
US-09-050-739-151
US-09-287-849-4
US-09-287-849-4
US-09-287-849-24
US-09-287-849-14
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US-09-287-849-13
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Listing first 45 summaries
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US-09-072	7.0-60-SD	US-09-32	US-08-29	US-08-29	US-08-04	US-09-33	US-10-14	US-09-33	US-10-14	US-09-68	US-09-25	3 US-08-928-3	US-09-58	US-08-92	US-08-70	US-08-92	US-09-58	ALIGNMENTS	0	2/ U8818112				ن ن	o, Antonio	mond	ກລຣ ຮ.	Α	COMPOUNDS AND MEIN	ó		BERRY LLP	ter, 701 F						isk	ble	MS-DOS	ease #1.0,		
6.9	9.3	5.4 14	5.2 6	5.2 6	5.0 3	5.0	5.0	5.0	3.0	4.7 4	4.7 5		4.7 10	4.7 10	4.7 17	4.7 17	4.7 17		27	Application US/ angés	MATION:	st	Skeiky, Yasir	Dillon, Davin	Campos-Neto,	Houghton, Raymond	Vedvick, Tho	×	OF INVENTION: COM		588:		300 Columbi	Seattle	Washington	USA	.04-7092	뇖	 Ei	IBM PC C	SYSTEM:	PatentIn Releas	CATION DA	
28 93	0		H		E	4	ı.			8 70	9 70	0 70	1 70	2 70	3 70	4 70	5 70		112-10	Sequence 102,	AL INFOR	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:		AT TO BIFTE	۰,	ROPERSPONDE	ADDRESSEE:	STREET:	CITY: Se	STATE: W	COUNTRY:	ZIP: 981	COMPUTER RE	MEDIUM TYPE:	COMPUTER:	OPERATING	SOFTWARE:	CURRENT APP	

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TYPE: amino acid
STRANDEDNESS: si
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                                                       1 VAMSLIVGAGVASADPVDAVINITCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 60
1 VAMSLIYGAGVASADPVDAVINITICNYGQVVAALNAIDPGAAAQFNASPVAQSYLRNFLA 60
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
WUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 481; DB 4; Length 96; 100.0%; Pred. No. 2.2e-50; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

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STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 97, Application US/08818111
Patent No. 6338852
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ATTORNEY/ACENT INFORMATION:
NAME: MAXI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-631
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 96; Conservative
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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US-08-818-111-97
                                                                                                                                                                                                                                                                                                                                                                                                       US-08-818-111-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
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US-09-056-556-102 Sequence 102, Application US/09056556 Patent No. 6350456 GENERAL INFORMATION: APPLICANT: Reed, Steven G.

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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
APFLICANT: Skeiky, Yasir A.W.
PSPLICANT: Dillon, Davin C.
TILLE OF INVENTION: COMPCUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Nero, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Compounds AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 481; DB 4; Length 96; Best Local Similarity 100.0%; Pred. No. 2.2e-50; Matches 96; Conservative 0; Mismatches 0; Indels
                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
SADRESSEE: SEED and BERRY LLP
STREET: SOJO COlumbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NOBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                          ZIF: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 97, Application US/09072596 Patent No. 6458366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David U.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21010
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 amino acids
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STATE: Washingt
COUNTRY: USA
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TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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INFORMATION FOR SEQ ID NO: 102: SEQUENCE CHREACTERISTICS: LENGTH: 96 amin TVEN
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SEQ ID NO 151
LENGTH: 110
                                                                                                                                                                                               LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: single
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US-09-072-967-102
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Danjon. Davin C.
APPLICANT: Campos-Netc, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Lodes, Michael G.
APPLICANT: Lodes, Michael G.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
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                                                                             OPERATION SYSTEM: PC_DOS/NS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAX., DAVId J.
REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 682-6900
TELEFAX: (206) 682-6910
TELEFAX: (206) 682-6011
INFORMATION FOR INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED INDICESSED IND
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COMPUTER READABLE FORM: A MEDIUM TYPE: FPOPDY disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OFFIANTING SYSTEM: PC-DOS/MS-DOS SOFFWARE: PATCHIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
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Patent No. 6592877
                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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STATE: Washington
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15 VAMSLEVGAGVASADPVDAVINITCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151, Application US/09050739

Sequence 151, Application US/09050739

Patent No. 6641814

GENERAL INFORMATION:

APPLICANT: ANDERSEN, Rikke

APPLICANT: NIELSEN, Rikke

APPLICANT: NCETTINGER, Thomas

APPLICANT: ROSENKRANDS, Ida

APPLICANT: RASWUSSEN, Peter Birk

APPLICANT: RASWUSSEN, Peter Birk

APPLICANT: RASWUSSEN, Peter Birk

APPLICANT: RASWUSSEN, Peter Birk

APPLICANT: RASWUSSEN, Peter Birk

APPLICANT: ROSENKRANDS, Ida

APPLICANT: ROSENKRANDS, Ida

APPLICANT: BADICATION: WILLER

TITLE OF INVENTION: DELIVED FROM M. TUBERCULOSIS

TITLE OF INVENTION: DELIVED FROM M. TUBERCULOSIS

TITLE OF INVENTION: DELIVED FROM M. TUBERCULOSIS

TITLE OF INVENTION: DELIVED FROM M. TUBERCULOSIS

CURRENT FILING DATE: 199-0-0-0-0

EARLIER FILING DATE: 1997-11-10

EARLIER PELING DATE: 1997-11-10

EARLIER FILING DATE: 1997-04-19

EARLIER FILING DATE: 1997-04-19

EARLIER FILING DATE: 1997-04-19

EARLIER FILING DATE: 1997-04-19

EARLIER FILING DATE: 1997-04-19

EARLIER FILING DATE: 1997-04-19

EARLIER FILING DATE: 1997-04-19
                                                                                                                                           1 VAMSLIVGAGVASADPVDAVINTICNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA
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                                                                           Gaps
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       Length 96;
                                                                       Indels
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Best Local Similarity 100.0%; Pred. No. 2.6e-50;
Matches 96; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                  61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e-50;
Matches 96; Conservative 0; Mismatches 0;
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## APPLICANT: Skeiky, Yasir
| APPLICANT: Skeiky, Wasir
| APPLICANT: Campos-Neto, Antonio |
| APPLICANT: Campos-Neto, Antonio |
| APPLICANT: Campos-Neto, Antonio |
| APPLICANT: Campos-Neto, Antonio |
| APPLICANT: Corixa Corporation |
| TITLE OF INVENTION: End Their Uses |
| TITLE OF INVENTION: And Their Uses |
| TITLE OF INVENTION: And Their Uses |
| TITLE OF INVENTION: UNDER: US/09/223,040 |
| CURRENT APPLICANTON NUMBER: US/09/223,040 |
| SEQ ID NOS: 10 |
| SEQ ID NOS: 10 |
| SEQ ID NO 4 |
| LENGTH: 331 |
| TYPE: principle |
| TYPE: principle |
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APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa Corporation
ITILE OF INVENTION: Erision Protiens of Mycobacterium tuberculosis Antigens
ITILE OF INVENTION: and Their Uses
FILE REPRENCE: 014058-00920303
GURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
FRIOR FILING DATE: 1999-04-07
FRIOR APPLICATION NUMBER: US 08/912,578
FRIOR APPLICATION NUMBER: US 09/025,197
FRIOR APPLICATION NUMBER: US 09/025,197
FRIOR PELING DATE: 1998-02-18
FRIOR APPLICATION NUMBER: US 09/025,197
FRIOR FILING DATE: 1998-02-18
FRIOR APPLICATION NUMBER: US 09/025,300
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 LTVGAGVASA------DPVDAVINTTCNYGQVVAALNATDPGAAAQFNASP 49
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Pred. No. 2.8e-42;
1; Mismatches 5; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-223-040-4
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, OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-4
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; Sequence 4, Application US/09287849
; Patent No. 6627198
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 80.4%;
Matches 86; Conservative
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ORGANISM: Artificial Sequence
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SEQ ID NO 4
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Gaps

15;

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SENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT APLING DATE: 1999-04-07
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FILE REFERENCE: 014058-00902002

CURRENT APPLICATION NUMBER: US/09/287,849
                                      130 LTVSVAVSEGKPTEKHIQIRSTNKLDPVDAVINTTCNYGQVVAALNATDPGAAAQFNASP 189
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---- DPVDAVINTICNYGQVVAALNATDPGAAAQFNASP 49
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                                                                                                                                                                        189 VAQSYLRNFLAAPPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 235
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                                                                                                                  96
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                                                                                                                     50 VAQSYLRNFLAAPPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY
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Best Local Similarity 80.4%; Pred. No. 3.2e-42;
Matches 86; Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR PELLON NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,566
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN VET: 2.1
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US-09-287-849-14
Sequence 14, Application US/09287849
Patent No. 6627198
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/09287849
Patent No. 6627198
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APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
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   5 LTVGAGVASA--
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SEQ ID NO 19
LENGTH: 299
TYPE: PRE
ORGANISM: Artificial Sequence
                                  LTVGAGVASA----
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US-09-287-849-22
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa Corporation
ITLLE OF INVENTION: and Their Uses
ITLLE OF INVENTION: and Their Uses
ITLLE OF INVENTION: and Their Uses
ITLLE OF INVENTION: and Their Uses
ITLLE OF INVENTION: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-04-07
PRIOR PLING DATE: 1999-04-07
PRIOR PLING DATE: 1999-04-07
PRIOR PLING DATE: 1999-04-07
PRIOR PLING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIN Ver: 2.1
SEQ ID NO 12
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; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion
US-09-287-849-14
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US-09-287-849-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 419.5; DB 4; Length 433;
Pred. No. 4e-42;
1; Mismatches 5; Indels 15;
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CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/918,112
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-0-01
PRIOR FILING DATE: 1997-0-01
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-04-07
PRIOR PELLOR DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 14
LENGTH: 433
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 80.4%;
Matches 86; Conservative
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ORGANISM: Artificial Sequence
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Gaps

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Indels

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APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
FILE REFERENCE: 014058-009020US
                                   of Mycobacterium tuberculosis Antigens
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---- DPVDAVINITCNYGQVVAALNATDPGAAAQFNASP 49
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                                                                                                                                                                                         190 VAÇSYLRNFLAAPPPQRAAMAAQLQAVFGAAQYIGLVESVAGSCNNY 236
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                                                                                                                                   50 VAQSYLRNFLAAPPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, rasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Cantonion Frait Uses
TITLE OF INVENTION: Tain on Their Uses
TITLE OF INVENTION: Tain on Their Uses
FILE REFERENCE: 014058-09920US
CURRENT APPLICATION NUMBER: US 08/227,849
CURRENT APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-0-0
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PELLING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIN Ver: 2.1
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Sequence 19, Application US/09287849
Patent No. 6627198
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Patent No. 6627198
GENERAL INFORMATION:
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US-10-005-920-5
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APPLICANT: Reed, Steven G.
APPLICANT: Seely, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Corica Corporation
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Pusion Protiens
TITLE OF INVENTION: Pusion Protiens
TITLE OF INVENTION: Pusion Protiens
TITLE OF INVENTION: UNMBER: US 08/912, 849
CURRENT FILING DATE: 1997-03-13
FRIOR PELING DATE: 1997-00-01
FRIOR APPLICATION NUMBER: US 08/925,197
FRIOR APPLICATION NUMBER: US 09/025,197
FRIOR APPLICATION NUMBER: US 09/025,556
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-02-30
NUMBER OF SEQ ID NOS: 46
FRIOR FILING DATE: 1998-12-30
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US-09-287-849-16
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US-09-287-849-22
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7.1e-42;
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9e-42;
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87.1%; Score 419; DB
Best Local Similarity 100.0%; Pred. No. 7.1
Matches 82; Conservative 0; Mismatches
                      CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 22
LENGTH: 600
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100.0%; Pred. No.
CURRENT APPLICATION NUMBER: US/09/287,849
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Patent No. 6627198
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ORGANISM: Artificial Sequence
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APPLICANT: Zhang, Ying
TITLE OF INVENTION: Methods for Improved Diagnosis and Treatment of Mycobacterial Infe
FILE REFERENCE: 0.3940034aa
CURRENT APPLICATION NUMBER: US/10/005,920
CURRENT FILING DATE: 2001-12-07
PRIOR PILING DATE: 2001-12-07
PRIOR PLING DATE: 2000-12-08
PRIOR PILING DATE: 2000-12-08
PRIOR FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SSQ ID NO 5
LENGTH: 30
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                                            15 DEVDAVINITICNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLAAPPPQRAAMAAQLQ
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Indels
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32.2%; Score 155;
Best Local Similarity 100.0%; Pred. No. Antches 30; Conservative 0; Mismatch
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                                                                                                                                                                             69 AVPGAAQYIGLVESVAGSCNNY 90
                                                                                                                                          75 AVPGAAQYIGLVESVAGSCNNY 96
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    82; Conservative
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us-09-886-349a-22.rapb

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June 22, 2004, 17:23:10 ; Search time 8.89146 Seconds (without alignments) 3048.105 Million cell updates/sec
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'(GRIZ 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
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'(GRIZ 6/ptodata/2/pubpaa/US60 NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Sequence 22, Appl Sequence 102, Appl Sequence 112, Appl Sequence 151, Appl Sequence 151, Appl Sequence 63, Appl Sequence 63, Appl Sequence 64, Appli Sequence 4, Appli Sequence 4, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Description US-09-886-349A-22 US-10-098-73A-22 US-10-098-73A-22 US-10-098-73A-22 US-09-791-11-151 US-09-791-11-151 US-09-980-151 US-10-098-73A-63 US-10-098-73A-63 US-10-098-73A-63 US-10-359-460-4 US-10-359-460-4 US-10-359-460-24 US-09-287-849-14 SUMMARIES Length DB Query 1000.00 00 Score Result

Sequence 12, Sequence 12, Sequence 12, Sequence 1, Sequence 6, Sequence 6, Sequence 5, Sequence 19, Sequence 19, Sequence 4, Sequence 4, Sequence 4, Sequence 6, S	Sequence 22, Appl Sequence 22, Appl Sequence 16, Appl Sequence 49, Appl Sequence 16, Appl Sequence 16, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 15, Appli Sequence 115, Appl Sequence 115, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 64, Appl Sequence 64, Appl Sequence 68, Appl Sequence 8095, Appl S
5.10-359-466-5.50-287-849-1.50-287-849-1.50-5.50-87-32A-5.50-6.50-88-732A-5.50-6.50-6.50-6.50-6.50-6.50-6.50-6.50	- 0 - 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1
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ALIGNMENTS

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                                                                                    APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
IIILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR PILING DATE: 2001-02-01
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 22
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 96;
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100.0%; Pred. No. 3.8e-45;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                 Sequence 22, Application US/09886349A Publication No. US20040086523A1 GENERAL INFORMATION:
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Matches 96; Conserv
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                                                                               Skeiky, Yasir A.W.

Dillon, Davin C.

Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.

Twardzik, Daniel R.

Lodes, Michael T.

Hendrickson, Romald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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100.0%; Score 481; DB 14;
Best Local Similarity 100.0%; Pred. No. 3.8e-45;
Matches 96; Conservative 0; Mismatches 0;
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FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMUNICATION INFORMATION:
TELEFAX: (206) 682-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 97:
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Publication No. USZ0030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Sequence 97, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 96 amino acids
TYPE: amino acid
                                                                     APPLICANT: Reed, Steven G.
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                               SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
                                                                                                                                                                                                                                                                                                                               NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-10-084-843-102
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Sequence 22, Application US/10098732A

Publication No. US20030175294A1

GENERAL INFORMATION:
APPLICANT: Brannon, Mark
APPLICANT: Graderian, Jeffrey
APPLICANT: Graderian, Jeffrey
APPLICANT: Graderian, Jeffrey
APPLICANT: Ociva Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Corixa Cor
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Skeiky, Yasir A.M.
Dillon, Davin C.
Campos-Neto. Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Columbia Center, 701 Fifth Avenue
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100.0%; Score 481; DB 14;
Best Local Similarity 100.0%; Pred. No. 3.8e-45;
Matches 96; Conservative 0; Mismatches 0;
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-631
INFORMATION FOR SEQ. ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
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SEQUENCE DESCRIPTION: SEQ ID NO: 102:
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ADDRESSEE: SEED and BERRY LLP
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MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
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COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCES:
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Sequence 151, Application US/09791171

Sequence 151, Application US/09791171

GENERAL INFORMATION: Peter APPLICANT: ANDERSEN, Rikke APPLICANT: ASMUSSEN, Peter Birk APPLICANT: RASMUSSEN, Peter Birk APPLICANT: RASMUSSEN, Peter Birk APPLICANT: ROSENKRANDS, Ida APPLICANT: ROSENKRANDS, Ida APPLICANT: PLORIO, Walter ITILE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS; TILLE OF INVENTION: DISTURD FROM M. TUBERCULOSIS; TILLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS; TILLE OF INVENTION UNDERS: US/09/791,171

CURRENT APPLICATION NUMBER: 09/09-03-30

FRIOR FILING DATE: 1998-03-30

FRIOR FILING DATE: 1997-04-02

FRIOR FILING DATE: 1997-04-02

FRIOR FILING DATE: 1997-04-18

FRIOR FILING DATE: 1997-04-18

FRIOR FILING DATE: 1997-04-18

FRIOR FILING DATE: 1997-04-18

FRIOR FILING DATE: 1997-04-18

FRIOR FILING DATE: 1997-04-18

FRIOR FILING DATE: 1998-01-05

NUMBER: 05 SEQ ID NOWS: 1730-04-05

NUMBER: 05 SEQ ID NOS: 1730-04-05

NUMBER: 100 NOS: 1730-04-05

NUMBER: 100 NOS: 1730-04-05

NUMBER: 100 NOS: 1730-04-05

NUMBER: 100 NOS: 1730-04-05

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NUMBER: 100 NOS: 1730-04
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100.0%; Score 481; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.8e-45;
Matches 96; Conservative 0; Mismatches 0; Indels 0
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PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 96
                                                                                                                                                                                                                                                                                         ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-151
                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: MTB8.4 (DPV)
US-10-098-732A-22
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Best Local Similarity
Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 VAMSLTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 74
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APPLICANT: ANUBESEN, FELCE
APPLICANT: NIELSEN, Rike
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSEN, Peter Birk
APPLICANT: RASMUSENS, Deter Birk
APPLICANT: RESENCEANDS Ida
APPLICANT: RECENCEANDS Ida
APPLICANT: PLONEO, Walter
ITILE OF INVENTION: UNCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
ITILE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
ITILE OF INVENTION: 0.001-2002.1
CURRENT APPLICATION NUMBER: LSO01-08-30
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/050,739
FRIOR FILING DATE: BARLIER FILING DATE: 1997-11-10
FRIOR PELLOR AND NUMBER: EARLIER REPLICATION NUMBER: 60/070,488
FRIOR PRILING DATE: EARLIER FILING DATE: 1997-04-18
FRIOR PELLING DATE: EARLIER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PAGENTIN VET. Z.0
LENGTH: 110
LENGTH: 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 4.5e-45;
Matches 96; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 APPPORAMMAQLOAVPGAAQYIGLVESVAGSCNNY 110
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NEGOLIS ON CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF 
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; ORGANISM: Mycobacterium tuberculosis
US-09-943-443-151
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Sequence 15: Application US/09943443

Publication No. US20030017172A1

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
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Query Match
Best Local Similarity
Matches 85; Conserv
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US-09-287-849-4
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                                                                                                                                                                                                                                        APPLICANT: Skeiky, Yaair
APPLICANT: Skeiky, Yaair
APPLICANT: Brannon, Mark
APPLICANT: Brannon, Mark
APPLICANT: Brannon, Mark
APPLICANT: Cuderian, Jeffrey
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-01201005
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2001-03-13
PRIOR PILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 63
LENTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLAAPPP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:MAPS(N10)-DPV-ACOTHER INFORMATION: fusion construct, first 10 amino acids of Leishmania CTHER INFORMATION: thiol-specific antioxidant (TSA or MAPS) linked with COTHER INFORMATION: TB DPV (MTBB.4) codon optimized for eukaryotic US-10-098-732A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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US-10-369-983-15

Sequence 15, Application US/10369983

Publication No. US20030235593A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Reed, Steven

TITLE REPERENCE: Orioration

TITLE REPERENCE: Orioration

TITLE REPERENCE: Orioration

FILE REPERENCE: 014058-00981US

CURRENT FILING DATE: 2003-02-18

PRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 15

LENGTH: 813

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SEQ ID NO 15

LENGTH: 813
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US-10-369-983-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                     75 APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 110
61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 QRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
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                                                                                                                                                                         ; Sequence 63, Application US/10098732A; Publication No. US20030175294A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                         RESULT 8
US-10-098-732A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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GAPPLICANT: Read, Steven G.
APPLICANT: Read, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bilon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANTON: and Their Uses
TITLE OF INVENTION: Busion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Busion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
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PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
                                                                                                                                                                                                                                               129 LTVSVAVSEGKPTEKHIQIRSTNKLDPVDAVINTTCNYGQVVAALNATDPGAAAQFNASP 188
                                                                                                                                                                             7 VGAGVASA--DPVDAVINTICNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLAAPPP 64
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                                                                                         Gaps
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80.4%; Pred. No. 9.5e-38;
ive 1; Mismatches 5; Indels 15.
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Length 813;
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                                                                                    Indels
Score 423; DB 15;
Pred. No. 1.2e-37;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                   782 QRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 813
                                                                                                                                                                                                                                                                                                                                                               65 QRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
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Publication No. US20030147911A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09287849
Patent No. US20020009459A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
87.9%;
ilarity 92.4%;
Conservative
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Best Local Similarity
Matches 86; Conserv
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129 LIVSVAVSEGKPTEKHIQIRSTNKLDPVDAVINTTCNYGQVVAALNATDPGAAAQFNASP 188
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
          APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LIVGAGVASA-------DPVDAVINTICNYGQVVAALNATDPGAAAQFNASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
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80.4%; Pred. No. 9.5e-38;
Live 1; Mismatches 5; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 419.5; DB 14; Length 331;
Pred. No. 9.5e-38;
1; Mismatches 5; Indels 15;
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                                                                  TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-00902005
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/918,112
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR PAPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
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ORGANISM: Artificial Sequence
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Best Local Similarity
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APPLICANT: Skeiky, iss...
APPLICANT: APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Anderson, Mark
APPLICANT: Campos-Netc, Antonio
APPLICANT: Campos-Netc, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: To 1800 Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
FRIOR APPLICATION NUMBER: US 08/918,112
PRIOR APPLICATION NUMBER: US 08/925,58
FRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR PILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR PILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR PILING DATE: 1998-04-07
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PRIOR PILING DATE: 1998-04-07
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PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR PILING DATE: 1908-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR PILING DATE: 1908-04-07
PRIOR PILING DATE: 1908-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
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PRIOR APPLICATION NUMBER: US 09/056,556
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PRIOR APPLICATION NUMBER: US 09/056,556
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Blilon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: AND Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/0359,460
CURRENT APPLICATION DATE: 2003-02-02
PRIOR APPLICATION NUMBER: US/09/287,849
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80.4%; Pred. No. 1.1e-37;
iive 1; Mismatches 5; Indels 15;
                                                                                 189 VAQSYLKNFLAAPPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 235
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50 VAQSYLRNFLAAPPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY
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                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/09287849
Patent No. US20020009459Al
GENERAL INFORMATION:
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APPLICANT: Ullicul, Death. C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Coriax Corporation
TITLE OF INVENTION: Eusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REPERBENCE: 014058-0090008
FURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR PLICATION NUMBER: US 08/942,578
PRIOR PLICATION NUMBER: US 09/025,197
PRIOR PLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver: 2.1
SGOTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 LTVSVAVSEGKPTEKHIQIRSTNKLDPVDAVINTTCNYGQVVAALNATDPGAAAQFNASP 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence

PEATURE:

OTHER INFORMATION: Description of Artificial Sequence:tri-fusion

US-10-359-460-24
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87.2%; Score 419.5; DB 14; Length 368;
Best Local Similarity 80.4%; Pred. No. 1.1e-37;
Matches 86; Conservative 1; Mismatches 5; Indels 15;
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               PRIOR FILING DATE: 1397-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 24
LENGTH: 368
TYPE: PRI
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Patent No. US20020009459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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PRIOR FILING DATE: 1999-04-07
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Gaps

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130 LTVSVAVSEGKPTEKHIQIRSTNKLDPVDAVINTTCNYGQVVAALNATDPGAAAQFNASP 189
                                                                                                                                    190 VAQSYLRNFLAAPPPQRAAMAQLQAVPGAAQYIGLVESVAGSCNNY 236
                                                                                           50 VAQSYLRNFLAAPPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
5 LTVGAGVASA--
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Search completed: June 22, 2004, 18:08:02 Job time: 9.89146 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 22, 2004, 16:44:25; Search time 11.7858 Seconds (without alignments) 2301.458 Million cell updates/sec Run on:

US-09-886-349A-22 481 1 VAMSLIVGAGVASADPVDAV......PGAAQYIGLVESVAGSCNNY 96 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_29Jan04;*

1: geneseqp1980s;*

3: geneseqp200s;*

4: geneseqp2001s;*

5: geneseqp2003s;*

6: geneseqp2003s;*

7: geneseqp2003bs;*

8: geneseqp2003bs;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ion	Mycobacte	Mycobacte	Mycobacte	M. tuberc	M. tuberc	M. tuberc	M. tuberc	Mycobacte	Mycobacte	Mycobacte	Amino aci	Leishmani	Mycobacte	Antigenic	Mycobacte	Mycobacte	Antigenic	Mycobacte	Antigenic	Mycobacte	Antigenic	M. tuberc	Leishmani	Mycobacte	Leishmani
Description	Aaw32349	Aaw32417	Aaw64333	0	Aay38987	Aay39130	Aau01894	Aae29711	Aae17575	Aaw72936	Aay21956	Aae29730	Ada26367	Aau74589	Aay32060	Aay32069	Aau74598	Aay32065	Aau74594	Aay32064	Aau74593	Aay96924	Aae29729	Aae29736	Aae29727
ΩI	AAW32349	AAW32417	AAW64333	AAW81700	AAY38987	AAY39130	AAU01894	AAE29711	AAE17575	AAW72936	AAY21956	AAE29730	ADA26367	AAU74589	AAY32060	AAY32069	AAU74598	AAY32065	AAU74594	AAY32064	AAU74593	AAY96924	AAE29729	AAE29736	AAE29727
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ALIGNMENTS

YX XX New immunogenic polypeptide (s) from soluble M. tuberculosis antigens - PT useful for diagnosis of M. tuberculosis infection. XX XX XX XX XX XX XX XX A new immunogenic polypeptide has been developed comprising an CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or CC oxidifications). The present sequence represents a M. tuberculosis antigen, CC DPV. The immunogenic polypeptide can be used to diagnose M. tuberculosis CC infection by forming complexes with specific antibodies in the sample.	WPI; 1997-192904/17. N-PSDB; AAT91424.		22-MAR-1996;	AA PN W09709429-A2.	XX OS Mycobacterium tuberculosis.	AA Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; KW skin testing; M.tuberculosis.	AAA AAW32349; XX	AAW32349 standard; protein; 96 AA. XX
Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton Vedvick TH, Twardzik DR; WPI; 1997-192904/17. N-PSDB; AAT91424.	Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton Vedvick TH, Twardzik DR;		12-JUL-1996;	XX XX XX XX XX XX XX PF 30-AUG-1996; 96W0-US014675. XX PR 22-SEP-1995; 95US-00523435. PR 22-MAR-1996; 95US-00520280. PR 22-WAR-1996; 96US-006520280. PR 12-UIN-1996; 96US-00680573.	WO9709429-A2. 13-MAR-1997. 30-AUG-1996; 01-SEP-1995; 22-SEP-1995; 22-MAR-1996; 05-UUN-1996; 12-UUL-1996;	Mycobacterium W09709429-A2. 13-WAR-1997. 30-AUG-1996; 01-SEP-1995; 22-SEP-1995; 22-MAR-1996; 05-UUN-1996; 12-UUL-1996;	13-JAN-1998 (first entry) Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. MO9709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-00523435. 22-SEP-1995; 95US-0052300. 05-UUN-1996; 96US-0065800. 12-UUN-1996; 96US-0065800. 12-UUL-1996; 96US-0065800.	AAW32349; 13-JAN-1998 (first entry) Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. WO9709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-00523435. 22-SEP-1995; 95US-0052300. 05-UUN-1996; 96US-0065800. 12-UUN-1996; 96US-0065800. 12-UUL-1996; 96US-0065800.
<pre>(CORI-) CORIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton Vedvick TH, Twardzik DR; WPI; 1997-192904/17. N-PSDB; AAT91424.</pre>	(CORI-) CORIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton Vedvick TH, Twardzik DR;	(CORI-) CORIXA	. 400	13-MAR-1997. 30-AUG-1996; 01-SEP-1995; 22-SEP-1996; 22-MAR-1996;	MO9709429-A2. 13-WAR-1997. 30-AUG-1996; 01-SEP-1995; 22-SEP-1995; 22-YAR-1996;	Mycobacterium W09709429-A2. 13-MAR-1997. 30-AUG-1996; 22-SEP-1995; 22-YAR-1996;	13-JAN-1998 (first entry) Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. WO9709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-00523435. 22-SEP-1995; 95US-00522480.	AAW32349; 13-JAN-1998 (first entry) Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. WO9709429-A2. 13-WAR-1997. 30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-00523435. 22-SEP-1995; 95US-00523280.
22-YAR-1996; 96US-0055280. 05-UNN-1996; 96US-00558800. 12-UUL-1996; 96US-00658800. (CORI-) CORIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton Vedvick TH, Twardzik DR; WPI; 1997-192904/17. N-PSDB; AAT91424.	22-YAR-1996; 96US-0055280. 05-UNN-1996; 96US-00658800. 12-UUL-1996; 96US-00680573. (CORI-) CORIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton Vedvick IH, Twardzik DR;	22-MAR-1996; 05-UUN-1996; 12-UUL-1996; (CORI-) CORIXA	֡	13-MAR-1997. 30-AUG-1996;	WO9709429-A2. 13-MAR-1997. 30-AUG-1996;	Mycobacterium t W09709429-A2. 13-MAR-1997. 30-AUG-1996;	13-JAN-1998 (first entry) Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. W09709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675.	AAW32349; 13-JAN-1998 (first entry) Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. W09709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675.
01-SEP-1995; 95US-00523435. 22-SEP-1995; 95US-0052136. 22-MAR-1996; 96US-00520280. 22-UAR-1996; 96US-0058800. 12-UUL-1996; 96US-00680573. (CORI-) CORIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton Vedvick IH, Twardzik DR; WPI; 1997-192904/17. N-PSDB; AAT91424.	01-SEP-1995; 95US-00523435. 22-SEP-1995; 95US-00522136. 22-MAR-1996; 96US-00520280. 22-UAN-1996; 96US-0058800. 12-UUL-1996; 96US-00680573. (CORI-) CORIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton Vedvick IH, Twardzik DR;	01-SEP-1995; 22-SEP-1995; 22-WAR-1996; 05-UUN-1996; 12-UUL-1996; (CORI-) CORIXA	01-SEP-1995;		•	Mycob W0970	13-JAN-1998 (first entry) Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. WO9709429-A2. 13-WAR-1997.	AAW32349; 13-JAN-1998 (first entry) Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. WO9709429-A2. 13-MAR-1997.
30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-00532435. 22-SEP-1995; 95US-00532136. 22-MAR-1996; 96US-0052800. 05-UUN-1996; 96US-0058800. 12-UUL-1996; 96US-00680573. (CORI-) CCRIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton Vedvick TH, Twardzik DR; WPI; 1997-192904/17. N-PSDB; AAT91424.	30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-00532435. 22-SEP-1995; 95US-00522136. 22-WAR-1996; 96US-0062080. 05-UUN-1996; 96US-00688800. 12-UUL-1996; 96US-00680573. (CORI-) CCRIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton Vedvick IH, Twardzik DR;	30-AUG-1996; 01-SEP-1995; 22-SEP-1995; 22-MAR-1996; 05-UUN-1996; 12-UUL-1996;	30-AUG-1996; 01-SEP-1995; 22-SEP-1995;		-	Mycok W0970	13-JAN-1998 (first entry) Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. W09709429-A2.	AAW32349; 13-JAN-1998 (first entry) Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. W09709429-A2.
Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. W09709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-00523435. 22-SEP-1995; 95US-00620280. 22-MAR-1996; 96US-00620280. 12-UUN-1996; 96US-0068800. 12-UUL-1996; 96US-00680573. (CORI-) CORIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Hough Vedvick TH, Twardzik DR; WPI; 1997-192904/17. N-FSDB; AAT91424.	Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. W09709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-00523435. 22-SEP-1995; 95US-00620280. 05-UNN-1996; 96US-00680800. 12-UL-1996; 96US-00680573. (CORI-) CORIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Hough Vedvick TH, Twardzik DR;	Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. WO9709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-00523435. 22-SEP-1995; 96US-00620280. 05-UWN-1996; 96US-00688800. 12-UUL-1996; 96US-00688800. 12-UUL-1996; 96US-00680573. (CORI-) CORIXA CORP.	Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. WO9709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675.	Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis.	Antigen, immunogen, vaccine, tuberculosis, non specific skin testing, M.tuberculosis.		13-JAN-1998 (first	AAW32349; 13-JAN-1998 (first
Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. Mycobacterium tuberculosis. W09709429-A2. 13-WAR-1997. 30-AUG-1996; 96WO-US014675. 22-SEP-1995; 95US-00523435. 22-SEP-1995; 96US-00620280. 52-VAR-1996; 96US-00620800. 12-UUL-1996; 96US-00680873. (CORI-) CORIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Hough Vedvick TH, Twardzik DR; WPI; 1997-192904/17. N-FSDB; AAT91424.	Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. W09709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-005213186. 22-MAR-1996; 96US-00621386. 22-MAR-1996; 96US-00688000. 12-UUN-1996; 96US-00688000. 12-UUL-1996; 96US-00680573. (CORI-) CORIXA CORP. Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Hough Vedvick TH, Twardzik DR;	Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. W09709429-A2. 13-MAR-1997. 30-AUG-1996; 96WO-US014675. 01-SEP-1995; 95US-00523435. 22-SEP-1995; 96US-00628800. 12-WAR-1996; 96US-00658800. 12-UUL-1996; 96US-00688800. 12-UUL-1996; 96US-00688573.	Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis. W09709429-A2. 13-WAR-1997. 30-AUG-1996; 96WO-US014675.	Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis. Mycobacterium tuberculosis.	Mycobacterium tuberculosis antigen DPV. Antigen; immunogen; vaccine; tuberculosis; non specific skin testing; M.tuberculosis.	Mycobacterium tuberculosis		
tuberculosis antigens		<pre>w, Dillon DC, Campos-Neto A, Houghton ik DR;</pre>	00000 00001110. 90105-00610110. 80110-00610110.		uberculosis.	tuberculosis; non specific		96

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especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis
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                                                                                                                         1 VAMSLTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 60
                                                                                                                                          1 VAMSLTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
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tuberculosis, also
                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 96;
                                                                                                0; Indels
                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunogenic polypeptide(s) from Mycobacterium useful in vaccines for prevention or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campos-Neto A,
                                                                      100.0%; Score 481; DB 2; 100.0%; Pred. No. 8.6e-47;
                                                                                                                                                                                                  APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 481; DB 2;
Pred. No. 8.6e-47;
                                                                                                                                                                               61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis antigen DPV.
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DR;
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100.0%;
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95US-00533634.
96US-00620874.
96US-00659683.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
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                                                                                                  Conservative
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I, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
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N-PSDB; AAT91488.
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Best Local Similarity
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nes 96; Conserv
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                                              Sequence 96 AA;
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Vedvick TH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 96
                                                                                                                                                                                                                                                                                                                                    08-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-1997
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prevention)
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                                                                        Query Match
                                                                                       Best Loca
Matches
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AAW32417
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                                                       1. VAMSLIVGAGVASADPVDAVINITCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA
                           1 VAMSLTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
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Indels
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illarity 100.0%; Pred. No. 8.6e-47;
Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                           Tuberculosis; infection; diagnosis; antigen; DPV.
                                                                                                                     61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                           96
                                                                                             61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis; strain H37Rv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 129-130; 250pp; English
                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis antigen DPV.
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DR, Lodes MJ;
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                                                                                                                                                                                                       AAW64333 standard; protein; 96
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97US-00818111.
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(first entry)
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   96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV44392
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13-MAR-1997;
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09-NOV-1998
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                                                                                                                                                                                                                                      AAW64333
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      Matches
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This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against W. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VAMSLIVGAGVASADPVDAVINTICNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VAMSLIVGAGVASADPVDAVINITCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA
                                    Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunocherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                          Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
Vedvick IS, Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 481; DB 2;
100.0%; Pred. No. 8.6e-47;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. tuberculosis antigen DPV amino acid sequence.
M. tuberculosis recombinant antigen protein DPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 164-165; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY39130 standard; protein; 96
                                                                                                                                                                                                                                       98US-00024753.
                                                                                                                                                                                                       99WO-US003265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
                                                                                              Mycobacterium tuberculosis.
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Best Local Similarity 100.
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-527416/44.
N-PSDB; AAZ19090.
                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 96 AA;
                                                                                                                                                                                                       17-FEB-1999;
                                                                                                                                                                                                                                         18-FEB-1998;
05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1999
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                                                                                                                                WO9942118-A2
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                                                                                                                                                                   26-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VAMSLITVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VAMSLIVGAGVASADPVDAVINITCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                             Tuberculosis, immunogenic, soluble, antigen, protective immunity, TB; vaccine, pharmaceutical, infection, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A, Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 100.0%; Score 481; DB 2; Local Similarity 100.0%; Pred. No. 8.6e-47; nes 96; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPPORAMMAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                  61 APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
         61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                                                                                                                                            M. tuberculosis immunogenic polypeptide DPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW, Dillon DC, Ca
S, Twardzik DR, Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 125; 230pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 96
                                                                                                                                      AAW81700 standard; protein; 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-00730510.
97US-00818112.
                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US018293
                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
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                                                                                                                                                                                                          27-JAN-1999 (first entry)
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N-PSDB; AAV64500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY38987 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-1996;
13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                            07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                        WO9816646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed SG, Sk
Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                        AAW81700
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Length 96; Indels 9

18-FEB-1998; 05-MAY-1998;

N-PSDB; AAZ19302

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The sequence represents Mycobacterium tuberculosis Mtb8.4 (also known as byb), an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymuclectide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, MIS, and 6H polymucleotides. Sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VAMSLTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; immunity; diagnostic agent; gene therapy; DPV antigen; MTB8.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VAMSLIVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASFVAQSYLRNFLA
                                                                                                                                                                                                                                                                              frequently affecting patients with acquired immunodeficiency disease, AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                        Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 481; DB 4;
100.0%; Pred. No. 8.6e-47;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis DPV antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPPÓRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY
                                                                                           Page 155; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 100; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE29711 standard; protein; 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2002; 2002WO-US008223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2001; 2001US-0275837P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Watches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-759844/82.
N-PSDB; AAD47087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                      Sequence 96 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                     The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. M. tuberculosis Ag's. M. other polypeptides fragments, can be used in pharmaceutical compositions or polypeptides to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AZ19249 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VAMSLTVGAGVASADPVDAVINTICNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VAMSLTVGAGVASADPVDAVINTICNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 60
                                                                                                                                                                                                                                                 New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lodes ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·,
                                                                                                               Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                            Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Hor
Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mtb8.4; DPV; antigen; vaccine; tuberculosis; AIDS; acquired immunodeficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 481; DB 2;
100.0%; Pred. No. 8.6e-47;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. tuberculosis partial antigen Mtb8.4 (DPV)
                                                                                                                                                                                                                                                                                                                   Example 1; Page 119; 299pp; English
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98US-00025197
98US-00072967
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99US-0158425P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU01894 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 96; Conservative
                                                                                                                                                                              WPI; 1999-527409/44.
                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
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Sequence 96 AA;

N-PSDB; AAS03785

WO200124820-A1

29-AUG-2001

07-OCT-1999; 07-OCT-1999;

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are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-imman animal. The invention is used in gene therapy. The present sequence is M. tuberculosis DPV antigenic protein. DPV is also referred to as MTBR.4
                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                    1 VAMSLIVGAGVASADPVDAVINTICNYGQVVAALNATDPGAAAQFINASPVAQSYLRNFLA 60
                                                                                                                                                                                                                                                                                                            1 VAMSLIVGAGVASADPVDAVINTICNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA
                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                       Length 96
                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                       100.0%; Score 481; DB 5;
100.0%; Pred. No. 8.6e-47;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              96
                                                                                                                                                                                                                                                                                                                                                                                                    61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY
                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 96; Conservative
                                                                                                                                                                               Sequence 96 AA;
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Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB8.4; DPV protein. Mycobacterium species MTB8.4 (DPV) protein

Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject. Claim 9; Page 116; 136pp; English The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprobations comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase include two or more individual M. tuberculosis antigens which increase include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium in vitro and in vivo assays for detecting humoral of nutioodies or cell-mediated immunity against M. tuberculosis, for the

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

for

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

WPI; 1998-542705/46. N-PSDB; AAV63946 Claim 1; Page 225; 163pp; English

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diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodise in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species
                                                                                                                                                     VAMSLIVGAGVASADPVDAVINTICNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 60
                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen;
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rasmussen PB;
                                                                                                                                  ..
                                                                                                             96;
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosenkrands I, Weldingh K,
                                                                                                           100.0%; Score 481; DB 5;
100.0%; Pred. No. 8.6e-47;
iive 0; Mismatches 0;
                                                                                                                                                                                                                61 APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY
                                                                                                                                                                                                   61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY
                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis antigen CFP8B.
                                                                                                                                                                                                                                                                                AAW72936 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97DK-00000376.
97US-0044624P.
97DK-0001277.
98US-0070488P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nielsen R,
Florio W;
                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 96; Conservative
                                                           for intradermal skin
MTB8.4 (DPV) protein
                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andersen P,
Oettinger T,
                                                                                                                                                                                                                                                                                                                                                                                                                            409844119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .8-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-NOV-1997;
05-JAN-1998;
                                                                                                                                                                                                                                                                                                                          21-JAN-1999
                                                                                         Sequence 96
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The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a profective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion perturns; (2) a fusion polypeptide fragment (I) and at least cone fusion partners; (2) a fusion polypeptide fragment comprising a T-cell conficient amino acid sequence from M. tuberculosis, and/or including a different amino acid sequence from M. tuberculosis, and/or including a cequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid care useful as pharmaceuticals, for diagnosis of and as antigane for are useful as pharmaceuticals, for diagnosis of an antigane for the bovis. The polypeptides are also useful for diagnosing ongoing or bovis. The polypeptides are also useful for diagnosing ongoing or the tuberculosis complex. The invention also describes the use of CFP7A or CFP30A or a T-cell epitope of for the induction of a strong immune the response in a mammal; use of GFP7B, CFP93 or MPTS9-ESAT6 or a T-cell epitope of for TB in a mammal by performing a DTH type skin cet; use of GFP27, CFP33, CFP25A, CFP30B, CFP7B or a T-cell epitope of EDP27, CFP33, CFP25A, CFP30B, CFP7B or a T-cell epitope of EDP27, CFP33, CFP25A, CFP30B, CFP7B or a T-cell epitope of EDP27, CFP33, CFP25A, CFP30B, CFP3B or a T-cell epitope of EDP27, CFP33, CFP33, CFP30B, CFP3B or a T-cell epitope of EDP27, CFP33, CFP33, CFP30B, CFP3B or a T-cell epitope of EDP27, CFP33, CFP33B, CFP3BB, CFP3B or a T-cell epitope of EDP27, CFP33, CFP33B, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CFP3BB, CF
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                                                                                                     1 VAMSLTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 60
                                                                                                                                                    15 VAMSLTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA 74
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic; Mycobacterium tuberculosis; immune response; infection;
tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
pharmaceutical; vacchiation; M. africanum; M. bovis; CFP7A; CFP30A;
CFP7B; CFP19; CFP27; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
CFP2SA; CFP30B; CFP7B.
                                                      .
0
Query Match
100.0%; Score 481; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 96; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunogenic fragment of Mycobacterium tuberculosis.
                                                                                                                                                                                                                                        APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 110
                                                                                                                                                                                                        61 APPPORAAMAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of antigen CFP8B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 242; 265pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       AAY21956 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97DK-00001277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0070488P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-DK000438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-DK000132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-347282/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX81095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9924577-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1998;
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01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-1999
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                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium
                                                                                                                                                                                                 15 VAMSLTVGAGVASADPVDAVINTTCNYGOVVALNATDPGAAAOFNASPVAOSYLRNFLA 74
cell epitope of for the preparation of an immunological composition, and for the preparation of a subunit vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a recombinant nucleic acid molecule encoding a
                                                                                                                                                              1 VAMSLTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA
                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leishmania sp. MAPS (N10)-Mycobacterium sp. DPV-AC fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; immunity; diagnostic agent; gene therapy; MAPS; DPV;
                                                                                        Score 481; DB 2; Length 110;
Pred. No. 1e-46;
                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                  APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 110
                                                                                                                                                                                                                                     61 APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 127-128; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guderian J;
                                                                                                                                                                                                                                                                                                                                                                 AAE29730 standard; protein; 92 AA.
                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-2001; 2001US-0275837P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2002; 2002WO-US008223
                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-759844/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium sp.
                                                    Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD47109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200272792-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmania sp.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2003
27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                      AAE29730;
                                                                                                                                                                                                                                                                                                                                RESULT 12
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Wed Jun 23 Ib:34:36 2004
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701.77.0040-000-60-60

96

AAU74589 standard; protein; 330 AA

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AAU74589;

65 ORAMMAQLQAVPGAAQYIGLVESVAGSCNNY

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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have, a use in gene therapy, and as a polymucelotide of the invention may have, a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
the N-terminus linked with the TB antigen DPV (aka MTB8.4) which is codon optimised for expression in eukaryotic cells. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                LTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLAAPPP
                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB85A;
tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                Score 424; DB 5; Length 92;
Pred. No. 2.5e-40;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium MTB72F-DPV (fusion MTB81F) protein.
                                                                                                                                                                                                                              ORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                                                                                                                                                  QRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 92
                                                                                                                                                                                                                                                                                                                                            ADA26367 standard; protein; 813 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 85; Fig 15; 112pp; English.
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                                                                                                  88.1%;
90.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FEB-2002; 2002US-0357351P.
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                    Query Match
Best Local Similarity 90.2
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guderian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-697554/66.
N-PSDB; ADA26360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 813 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003070187-A2
                                                                     Sequence 92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky Y,
                                                                                                                                                                                                                                                                                                                                                                              ADA26367;
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                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DPVDAVINTTCNYGQVVAALNATDPGAAAQFNASP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                             Fusion protein; tuberculosis; Mycobacterium tuberculosis;
tuberculostatic; immunogen; vaccine; Erd14-DPV-MII; Erd14; DPV; MII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion proteins of Mycobacterium tuberculosis antigens, usefo diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.2%; Score 419.5; DB 5; Length 330; 80.4%; Pred. No. 3.8e-39; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC, Alderson M,
                                                                                                                 Antigenic fusion protein Erd14-DPV-MTI
                                                                                                                                                                                                                                                                                                                          97US-00818112.
97US-00942578.
98US-00025197.
98US-00056556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 2; 62pp; English.
                                                                                                                                                                                                                                                                                                 99US-00287849
                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 80.4
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LTVGAGVASA----
                                                                                                                                                                                                                                                                                                                                                                                                                (REED/) REED S G.
(SKEI/) SKEIKY Y A.
(DILL/) DILLON D C.
(LALDE/) ALDERSON M.
(CAMP/) CAMPOS-NETO A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reed SG, Skeiky YA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-171134/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK14129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 330 AA;
                                                                                                                                                                                                                                        US2002009459-A1.
                                                                                                                                                                                                                                                                                                                            13-MAR-1997;
01-OCT-1997;
18-FEB-1998;
07-APR-1998;
30-DEC-1998;
                                                                                                                                                                                                                                                                                                 07-APR-1999;
                                                                        29-AUG-2003
                                                                                                                                                                                                                                                                     24-JAN-2002
                                                                                      08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing,
                                                                                                                                                                                                            Chimeric
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7 VGAGVASA--DPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLAAPPP

Query Match 87.9%; Score 423; DB 7; Length 813; Best Local Similarity 92.4%; Pred. No. 4.5e-39; Matches 85; Conservative 2; Mismatches 3; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a recombinant Mycobacterium tuberculosis triantigen fusion protein, termed Mtb39, composed of the antigens ERD14, DPV and MTI. The fusion protein is expressed in host cells using a vector carrying a polynuclectide (see AAZ20195) comprising the 3 coding sequences for the antigens. The invention provides fusion proteins (see AAX3205-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polynuclectides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis or intradermal skin tests for detection of anti-M. tuberculosis antibocines). monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein components
129 LTVSVAVSEGKPTEKHIQIRSTNKLDPVDAVINTTCNYGQVVAALNATDPGAAAQFNASP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis.
                                                                                                                                                                                                                                                                Tuberculosis; antigen; fusion protein; Mtb39A; ERD14; DPV; MTI;
                                                          189 VAOSYLRNFLAAPPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 235
                               50 VAQSYLRNFLAAPPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen fusion protein Mtb39A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campos-Neto A;
                                                                                                                                                                                                                                                                               diagnosis; therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                  'note= "Met/His tag"
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                         AAY32060 standard; protein; 331 AA.
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/note= "ERD14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 2; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 154. .235
/note= "DPV"
238. .331
/note= "MTI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00056556.
98US-00223040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US007717
                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                  17-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky YAW, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-601610/51.
N-PSDB; AAZ20195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-OCT-1999
                                                                                                                                                                    AAY32060;
                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                           RESULT 15
                                                                                                                            AAY32060
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50 VAQSYLRNFLAAPPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                                                                         Search completed: June 22, 2004, 17:15:45
Job time : 12.7858 secs
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Query Match 87.2%; Score 419.5; DB 2; Best Local Similarity 80.4%; Pred. No. 3.8e-39; Matches 86; Conservative 1; Mismatches 5;

Sequence 331 AA;

1,

Indels 15; Gaps

DB 2; Length 331;

3

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

June 22, 2004, 16:59:04; Search time 2.68596 Seconds (without alignments) 3438.018 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-886-349A-22 481 1 VAMSLIVGAGVASADPVDAV......PGAAQYIGLVESVAGSCNNY 96

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ical prot	de synt	hypothetical prote	glucan 1,4-alpha-g	glucan 1,4-alpha-g	F26G16.12 protein	probable periplasm	probable hydrolase	major capsid prote	minor capsid prote	probable endoprote	mucin-like glycopr	conserved hypothet	protein F53A3.6 [i	thiamin monophosph	14	probable zinc fing	Ψ	ķe	кe	secr	spherulin 1b precu	anie	malate dehydrogena	q guipuiq-m	hypothetical prote	FREAC-4 - human	erved hypothe	u
SUMMARIES	ID	87	AG3009	G98274	536364	T49625	A86430	E81966	A70771	VABPA7	VBBPA7	B83123	T31113	D81022	D88395	G84351	G70555	D96707	D33858	AD1598	AF1235	G87470	B29624	T46192	AD3269	A47282	T31555	G02738	G87259	T02837
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	Result No.	 	N)	e	4	Ŋ	9	7	ထ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

potential transcri D-lactate dehydrog	probable membrane ornithine decarbox glycoprotein H pre	probable peptidase histidinol-phospha hypothetical prote	probable cation tr probable invasin Y UL36 protein - hum	hypothetical prote alpha-subuni L-ser probable porin PA4	hypothetical prote hypothetical prote
T03554 E84393	S53975 A40839 S18462	T36379 C83089 T24045	E87243 AB0480 WMBEH6	T03570 G86728 A83082	S55164 A75352
0.0	000			0 0 0	0 0
314 353	389 732 842	228 351 1226	1609 3013 3164	186 287 484	663 332
13.8 13.8	13.8 13.8	13.7	13.7 13.7 13.7	13.6 13.6 13.6	13.6
66.5 66.5	66.5 66.5 6.5 6.5 6.5	999	999	ດ ຕິດ ຕິດ ຕິດ	65.5 65
30	8 8 8 2 8 4	33 33 37		44 44 44 44 44 64 64	4 4 4 5

ALIGNMENTS

t matter

-	RESULT 1
	F70875
	hypothetical protein Rv1174c - Mycobacterium tuberculosis (strain H37RV)
_	C;Species: Mycobacterium tuberculosis
_	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
_	C,Accession: F70875
	R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
	; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.,
	Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
	Nature 393, 537-544, 1998
	A, Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
	A, Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome a
	A; Reference number: A70500; MUID: 98295987; PMID: 9634230
_	A, Accession: F70875
_	A;Status: preliminary; nucleic acid sequence not shown; translation not shown
_	A; Molecule type: DNA
_	A;Residues: 1-110 <col/>
_	A; Cross-references: GB: AL010186; GB: AL123456; NID: g3261493; PIDN: CAA15851.1; PID: g2695956
	A, Experimental source: strain H37Rv
_	C, Genetics:
_	A;Gene: Rv1174c
	C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1174c
	Ouerv Match 100.0%; Score 481; DB 2; Length 110;
	Similarity 100.0%;
	Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Qy 1 VAMSLTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA .60
	Db 15 VAMSLIVGAGVASADPVDAVINTICNYGQVVAALNATDFGAAAQFNASPVAQSYLRNFLA 74
	QY 61 APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
_	
	Db 75 APPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 110
-	

Agrobacterium tumefaciens (strain C58, Dupont)
polyketide synthetase Atu3681 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C)Species: Agrobacterium tumefaciens
C;Date: 11.Jan.2002 #sequence_revision 11.Jan.2002 #text_change 18-Nov-2002
C;Accession: AG3009
C;Accession: AG3009
R;Wood, D.W.; Setubal, C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
R;Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell&
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.

ster, E.W. Affile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AG3009 A;Status: preliminary

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A;Molecule type: protein A;Reaidues: 36-60,'X','62,'X','64-65 <KOH> A;Reaidues: 36-60,'X','62,'X','64-65 <KOH> B;Roh-Laur, S.I.; Parish, J.H.; Bleasby, A.J.; Pappin, D.J.C.; Ainley, K.; Johansen, F.E. submitted to the Protein Sequence Database, January 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha-C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-35/Domain: propeptide #status predicted <PRO>
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;Schulte, U.; Ajgn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 SVSTGTYSSSSSTYTAIINAVTTYADGFVDIVAQYTPSDGSLAEQFDKDSGAPLSATHLT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SLTVGAGVASADPVDAVINTTCNYG----QVVAALNATDPGAAAQF---NASPVAQSYL- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F26G16.12 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glucan 1,4-alpha-glucosidase [imported] - Neurospora crassa
NjAlternate names: protein B5022.70
C.Species: Neurospora crassa
C.Species: O2-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SLIVGAGVASADPVDAVINITICNYG----QVVAALNAIDPGAAAQF---NASPVAQSYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F,33-458/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
F,36-626/Product: glucan 1,4-alpha-glucosidase #status experimental <MAT>
                                                                                                                                                                                   A, Description: Exported proteins of Neurospora crassa 1: - glucoamylase. A, Reference number: $13711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 WSYASFLSAAARRAGIVPPSWGAASA---NSLPGSCS----ASTVAGS 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
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A;Cross-references: EMBL:AL355932; GSPDB:GN00116; NCSP:B5O22.70
A;Experimental source: BAC clone B5O22; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 26.9%; Pred. No. 13;
Matches 29; Conservative 19; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---RNFLAA-----PPPQRAAMAAQLQAVPGAAQYIGLVESVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.2%; Score 73; DB 2; Length 626 Best Local Similarity 26.9%; Pred. No. 13; Matches 29; Conservative 19; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---RNFLAA-----PPPQRAAMAAQLQAVPGAAQYIGLVESVAGS
                                                                                                                                                                                                                                                                       A,Accession: S13711
A,Molecule type: protein
A,Residues: 36-60,'X',62,'X',64-65 <KOW>
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A,Status: preliminary
A,Molecule type: DNA
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A; Accession: $13710
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                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: gla-1
A;Introns: 82/2
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C;Accession: G9827.
C;Accession: G9827.
Accession: G9827.
A; Liuu F:; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 249, 2323-2328, 2001
A;Tile: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G98274
A;Accession: G98274
A;Aclaule type: DNA
A;Residues: Dralininary
A;Acoss-references: GB:AE007870; PIDN:AAK89721.1; PID:g15159635; GSPDB:GN00170
C;Genetics: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: 
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N.Alternate names: glucoamylase; glycoamylase
C.Species: Neurospora crassa
C.Species: Neurospora crassa
C.Species: Neurospora crassa
C.Species: Neurospora crassa
C.Sacassion: S3634; S13710; S13711; S2539
R.Stone, P. U.; Makoff, A.U.; Parish, J.H.; Radford, A.
Curr. Genet. 24, 205-211, 1933
A.Title: Cloning and sequence analysis of the glucoamylase gene of Neurospora crassa.
A.Title: Cloning and sequence analysis of the glucoamylase gene of Neurospora crassa.
A.Reference number: S36364; MUID:94037144; PMID:821928
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-626 < STO>
A.Coss-references: EMBL:X67291
R.Koh-luar, S.I.; Parish, J.H.; Bleasby, A.J.; Pappin, D.J.C.; Ainley, K.; Johansen, F.E
Enzyme Microb: Technol. 11, 692-695, 1989
A.Reference number: S13710
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A;Residues: 1-1477 «KUR»
A;Cross-references: GB:AE008689; PIDN:AAL44493.1; PID:g17742100; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 LDTAAGIA-----GFIKTVLCLKHGRIPASLHFRQANÄKIDFPASPFAVNTVLRDWTAL 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LTVGAGVASADPVDAVINTT--CNYGQVVAALNATDPGAAAQFNASPVA-QSYLRNFLAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LTVGAGVASADPVDAVINTT -- CNYGQVVAALNATDPGAAAQFNASPVA-QSYLRNFLAA
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                     15.3%; Score 73.5; DB 2; Length 1477; 28.6%; Pred. No. 29; tive 18; Mismatches 36; Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 PPPORAAMAAQLQAVPGAAQYIGLVESVAGS 92
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A;Map position: linear chromosome
                                                                                                                                                                                                                                              A, Map position: linear chromosome
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Best Local Similarity 28.61
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 28.6
les 26; Conservative
                                                                                                                                                                                                            Gene: Atu3681
                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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genome

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A;Cross-references: GB:Z73902; GB:AL123456; NID:g3261576; PIDN:CAA98097.1; PID:e245027; F
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Note: host Escherichia coli

C.Specides: phage T7

A.Note: host Escherichia coli

C.Accession: A04344; 842325

R.Dun, J.J.; Thompson, K.

Submitted to the Nucleic Acid Sequence Database, September 1982

R.Reference number: A94615

A.Reference number: A94615

A.Residues: 1-345 < DUN>

R.Bunn, J.J.; Studier, P.W.

R.Dunn, J.J.; Studier, P.W.

R.Dunn, J.J.; Studier, P.W.

R.Dunn, J.J.; Studier, P.W.

A.Reference number: 842283; MUID:88241725; PMID:6864790
Rajandream, M.A.; Bavies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 339, 537-644, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230
A.Accession: A70771
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AAGNVVDPATGLPWMADLVGEFA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 GLGTAT-----VIETTQNKAALTDQVALGKEIIAAL--TKARAALTKNYVPAAD---RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GAGVASADPVDAVINTTCNYG------QVVAALNATDPGAAAQFNASPVAQSYLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AMSLIVGAGVASAD-----PVDAVINTICNYGQVVAALNATDPGAAAQFNASPVAQSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1.345 <DUW>
A;Cross-references: EMBL:V01146; NID:g431187; PIDN:CAA24427.1; PID:g15604
A;Note: the authors did not translate the codon for residue 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 72; DB 2; Length 344;
Pred. No. 8.7;
7; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLAAPPPORAAMAQLQAVPGAAQYIGLVESVAGSCNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72; DB 1;
Pred. No. 8.8;
8; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 57.51-60.49
C;Superfamily: phage T7 major capsid protein 10A
C;Keywords: capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 AGALKGGVGTASATLQSGVTVGVLAVVN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 LR----APPAEQIAALAQLSSPLGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 LRNFLAAPPPQRAAMAAQLQAVPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 34.1%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 15.0%;
1 Similarity 31.6%;
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        minor capsid protein 10B - phage C; Species: phage T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major capsid protein 10A - phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                    A; Residues: 1-344 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S42325
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VBBPA7
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   C;Accession: A86430

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.X.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A., Li, J.H., J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roorey, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roorey, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Teference and analysis of chromosome I of the plant Arabidopsis.
A;Reference and analysis of chromosome I of the plant Arabidopsis.
A;Reference and analysis of chromosome I of the plant Arabidopsis.
A;Reference unuber: A86141; MUID:21016719; PMID:11130712
A;Residues: 1-197 <STO>
A;Residues: 1-197 <STO>
A;Centeirences: GB:AE005172; NID:g6634774; PIDN:AAF19754.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
B81966
probles periplasmic transport protein NMA0488 [imported] - Neisseria meningitidis (stra c)robate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Species: Nature 2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: E81966
R;Parkhill, 1.7, Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Residues: Lelso ARR>
A;Residues: 1-196 APR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:97379120; PIDN:CAB83781.1; PID:9737923
A;Cross-references: GB:AL162753; GB:AL157959; NID:97379120; PIDN:CAB83781.1; PID:9737923
A;Genetics:
A;Genetics:
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C;Species: Mycobacterium tuberculosis
C;Date: Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70771
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 NYESIVTSLVYSDPGTTNSMAPGQY---PYPDPYYRS-IFAPPPQPYTGVHLQLMGVQQQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 GVASADFVDAVINTTCNYGQVVAALNATDFGAA---AQFNASFVAQSYLRNFLAAPPPQR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 NYGQVVAALNATDPG-----AAAQFNASPVAQSYLRNFLAAPPPQ-----RAAMAAQLQ 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72.5; DB
Pred. No. 4.3;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TASDAOKOALAKEFOTL-LIRTYSGT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 GVPLPSDAVEEPVFVNAKQYHGIL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.1%;
31.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 26; Conserv
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Matches 28; Consert
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Gaps

24;

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Conserved hypothetical protein NMB1963 [imported] - Neisseria meningitidis (strain MC58 in Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
R;Tettelin, H; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ti, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Reference number: A81000; MUID:2017575; PMID:10710337
                                                                                                                                                        C.Accession: T31113
R.Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Wu, J.; Gut, J.; Doyle, P.; Dubreme Mol. Biochem. Parasitol. 96, 93-110, 1998
A;Title: A novel multi-domain mucin-like glycoprotein of Cryptosporidium parvum mediates A;Reference number: Z20989; MUID:99066935; PMID:9851610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE002544; GB:AE002098; NID:g7227214; PIDN:AAF42292.1; PID:g722722:
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-1832 <BAR>
A;Cross-references: EMBL:AF068065; NID:g4063041; PID:g4063042; PIDN:AAC98153.1
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                                                                                                  C;Species: Cryptosporidium parvum
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein F53A3.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: D88395
R;anonymous, The C. elegans Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PPPQRAAMAAQLQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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Best Local Similarity 32.6%; Pred. No. 7.6;
Matches 28; Conservative 10; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 VAALNATDPGAAAQFNASPVAQSY----LRNFLAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                   mucin-like glycoprotein 900 - Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.7%; Score 70.5; I ilarity 28.4%; Pred. No. 74; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 AAMAAQLQAVPGAAQYIGLVESVAGS 92
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1750 AGGASAAVGLVAAV 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 VPGAAQYIGLVESV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                          A, Accession: T31113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: NMB1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 282,
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A;Note: host Escherichia coli
C;Date: 30-Sep-1990 #equence_revision 30-Sep-1990 #text_change 23-Jul-1999
C;Accession: B04344; 842326
R;Dunn, U.C.; Thompson, K.
B;Dunn, U.C.; Thompson, K.
A;Reference number: A4615
A;Reference number: A4615
A;Residues: 1-398 cDUN>
R;Dunn, U.C.; Studier, F.W.
A;Residues: 1-398 cDUN>
A;Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 ge
A;Reference number: 842283; MUID:83241725; PMID:6864790
A;Reference number: 842283; MUID:83241725; PMID:6864790
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Reference number: S42283; MUID:83241725; PMID:6864790
A;Reference number: S42283; MUID:83241725; PMID:6864790
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K., Lim,
                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Note: translation of the nucleotide sequence involves a -1 frameshift within codon 341 C,Superfamily: phage T7 major capsid protein 10A C;Keywords: capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-462 <STO>
A;Cross-references: GB:AE004834; GB:AE004091; NID:g9950382; PIDN:AAG07562.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable endoproteinase Arg-C precursor PA4175 [imported] - Pseudomonas aeruginosa (stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an opportunistic patho
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A.; Larbig,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- QVVAALNATDPGAAAQFNASPVAQSYLRN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 VINTTCNYGQVVAALNATD-PGAAAQFNASPVAQSYLR--------NFLAAPPPQR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 VLALAAGASQALAAPGASEMAGDVAVLQASPASTGHARFANPNAAISAAGIHFAAPPARR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83128
A;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportu
A;Reference number: A82950; MUID: 20437337; PMID: 10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72; DB 1; Length 398;
Pred. No. 10;
8; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 FLAAPPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 FYCDPDSYSAILAA---LMPNAANYAALIDPEKGSIRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.7%; Score 70.5; D
llarity 29.1%; Pred. No. 17;
Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 GAGVASADPVDAVINTTCNYG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 VARAAPLAPKPGTPLQVGV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 AAMAAQLQAVPGAAQYIGL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.6%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: 10B
A;Map position: 57.51-60.49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 23; Conserv
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RESULT

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ò 셤 à A.Title: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Reference number: A75000; MUID:99069613; PMID:9851916

Gene: PA4175

12

RESULT

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ò g us-09-886-349a-22.rpr

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A,Accesion: D88395
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-451 <STO
A,Cross-references: GB:chr_III; PIDN:AAB70991.1; PID:g2429454; GSPDB:GN00021; CESP:F53A3
C,Genetics: A,Agene: F53A3.6
A,Map position: 3
A,Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A,Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                        ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LIVGAGVASADPVDAVINITCNYGQVVAALNAIDPGAAAQFNASPVAQSYLRNFLAAPPP 64
                                                                                                                                                                                                                                                                                                                                          Score 70; DB 2; Length 451;
Pred. No. 19;
5; Mismatches 34; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 35.4%;
Matches 29; Conservative
```

65 ORAAMAAQLQAVPGAAQYIGLV 86

370 LTAGSGSAGIPYFSAL----SQQLNQLGAAAPGAPGTLNGLQFPAN----AALGP 416

d ò thiamin monophosphate kinase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: G84351
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: G84351
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-288 <5TO>
A;Cross-references: GB:AE004437; NID:g10581442; PIDN:AAG20179.1; GSPDB:GN00138
C;Genetics: A,Gene: thiL C,Superfamily: thiamine monophosphate kinase

Query Match
14.4%; Score 69.5; DB 2; Length 288;
Best Local Similarity 32.0%; Pred. No. 13;
Matches 33; Conservative 15; Mismatches 38; Indels 17; Gaps

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51 -AQSYLRNF--LAAPPPQRAAMAAQLQAVPGAAQYIGLVESVA 90

Search completed: June 22, 2004, 17:24:58 Job time : 5.68596 secs

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6 Wed Jun 23 16:34:38 2004
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June 22, 2004, 16:46:13; Search time 1.59768 Seconds (without alignments) 3128.737 Million cell updates/sec
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481
1 VAMSLIVGAGVASADPVDAV......PGAAQYIGLVESVAGSCNNY 96
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                   Title:
Perfect score:
Sequence:
                                                                                                                               Run on:
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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

n		P54817 bovine herp	gnw		Q10644	P19726 bacteriop	P19727	P08662	082868	P09350 physarum po	Q02910 drosophila	Q16676 homo sapien	Q04951 saccharomyc		escheri		pseudon	mycoba		saccha		Q07847 human papil	P37127 escherichia		Q90693 gallus gall	P13709 drosophila		pseudomor		ជាបាន ព	homod	pyrer	O95936 homo sapien	OLE
SUMMAKIES		VP40 HSVBC	TSSP_MOUSE	AMYG_NEUCR	YD33 MYCTU	VCAA_BPT7	VCAB_BPT7	MERA SERMA	REGA RHOSU	SRIA PHYPO	CPN DROME	FXD1 HUMAN	SCWA YEAST	TSSP_HUMAN	DCOS ECOLI	VGLH_HSVBC	HI81 PSEAE	CTPI MYCLE	TEGU_HSV11	YJO9 YEAST	MIAA RALSO	VE1 HPV63	AEGA ECOLI	SRA4 HUMAN	PIC1 CHICK	FSH_DROME	SR1B_PHYPO	LIP PSEGL		NOA1 MOUSE	1111	CUTI_PYRBR	1 1	TOTTOM LOTTO
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	ng.	621	509	626	344	345	398	460	183	246	865	465	389	514	732	842	351	1609	16	663	323	618	629	15	1442	03	248	358	474	493	510	203	686	1434
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	Ö	75.5	m	73	72	72	72	69	68	67.5	~	67	ø	66.5	ø	9	99	99	99	65.5	65	65	65	65	65		4	4	64.5	4	4	64	64	77
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09hb15 homo sapien 09ers1 rattus norv	Q00650 brassica na Q10900 mycobacteri P28955 equine herp	09a4c4 caulobacter 083525 t ispd/ispf	P17047 mus musculu P29836 bovine herp Ogn3v5 drosophila	P34288 caenorhabdi P09631 mus musculu
CIWC_HUMAN CIWC_RAT	13MS_BRANA CTPI_MYCTU TEGIT_HSVER	NADA_CAUCR ISDF_TREPA	LMP2_MOUSE ICPO_HSVBK TIDT_DBOME	GAP CABEL HXA9 MOUSE
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4 3 3 0	156	377	415 676 400	1317
13.2	13.1	12.9	0.21 0.00	22.2
63.5 63.5	63 63 57	62	622	62 62 63
3.4 3.5	33.0 3.7 8.0) W 4) W D	4 4 4 L 2 4	4 4 4 4

ALIGNMENTS

	SULT 1 40_HSVBC VP40_HSV	AC P54817; Q89855; DT 01-OCT-1996 (Rel. 34, Created) TT 01-OCT-1996 (Rel. 34, Last sequence update)	Capsid protein P40 [Contair Capsid assembly protein].		Viluses, usuna viluses, no ama scase, neipesvillado Alphahesphesvillade, Varicellovirus. NCBI Tavide 10323.			"The bovine herpesvirus 1 maturational proteinase proteins can substitute for the homologous herpes	proteins in the formation of hybrid type B capsids.";	KL J. VIFOL. 89: 3/3-/3/9(1395). CC -1- FUNCTION: THE CAPSID ASSEMBLY PROTEIN IS COMPONENT OF THE CAPSID	CC CORE INVOLVED IN PROCESSING AND PACKACING OF PROGENY DNA. CC -!- FUNCTION: ASSEMBLIN IS A PROTEASE WHICH CAN PROTECLYTICALLY CLEAVE	C ITSELF AND THE CAPSID ASSEMBLY PROTEIN AT THE C-TERMINUS.	the scaffold protein.	<pre>-:- ALTERNATIVE PRODUCTS: Event=Alternative initiation;</pre>			C -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP40.	This SWISS-PROT entry is	between the	the buropean Broinformatics institute. There are no restrictions on use by non-profit institutions as long as its content is in no	modified and this statement is not removed. Usage by and	encicles requires a incense or send an email to license@					MEKUPS; SZI.001; InterPro; IPR001847; Peptidase	Pfam; PF00716; Peptidase_S21; 1. PRINTS; PR00236; HSVCAPSIDP40.	KW Capsid assembly, Hydrolase, Serine protease, Coat protein, KW Alternative initiation.	CHAIN 314	
i		STTE	מממ	NS OS	οŌĊ) iz; iz	i EX EX	ńc ńc	DG F	צ ט	υΰ	υć	ט כ	UŪ	U	ט ט	υc	υ	O	O O	O	ט כ	טב	וֹם ב	മെ	Di	ם ב	מם	X X	[t ₁ [t	•

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                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                           313 AMSAAHQAGAASAHPLPAGDYVYVPTAQYNQLVVSQARGAAMTAAPPPAPYFLPAAAA- 371
                                                                                                                                                                                                                                            2 AMSLTVGAGVASADPV---DAVINTTCNYGQVV-----AALNATDPGAAAQFNASPVAQ 52
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: Protease that may play a role in T-cell development.
-!- SUBCELLULAR LOGATION: Vesicular, either lysosomal or endosomal.
-!- TISSUB SPECIFICITY: Expressed predominantly in cortical thymic epithelial cells, with highest expression around vessels and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: Expressed in developing thymus at 14 to 18
114 FOR ISOFORM UL26.5.
254 ASSEMBLIN (PROTEASE).
621 CAPSID ASSEMBLY PROTEIN.
622 CLEAVAGE (BY THE PROTEASE) (PROBABLE).
63 CHARGE RELAY SYSTEM (BY SIMILARITY).
136 CHARGE RELAY SYSTEM (BY SIMILARITY).
155 CHARGE RELAY SYSTEM (BY SIMILARITY).
63711 MW, AEF6D7C9BDE69003 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carrier A., Nguyen C., Victorero G., Granjeaud S., Rocha D., Bernard K., Miazek A., Ferrier P., Malissen M., Naquet P., Malissen B., Oordan B.R.; "Differential gene expression in CD3epsilon- and RAG1-deficient thymuses: definition of a set of genes potentially involved in thymocyte maturation.";
                                                                                                                                                                                                       30; Indels 35;
                                                                                                                                                                  Score 75.5; DB 1; Length 621; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
THYMUS-SPECIFIC SERINE PROTEASE.
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                        -----AAAPPPMPGWYGAAGAAPWHPGYGFPPPGLESQIMALAGA 411
                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                     53 SYLRNFLAAPPPQ----RAAMAA------QLQAVPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Thymus-specific serine protease precursor (EC 3.4.-.-).
PRSS16 OR TSSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dpc, with maximal expression at 16 dpc.
-!- SIMILARITY: Belongs to peptidase family S28.
                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6; TISSUE=Embryonic thymus; MEDLINE=20093985; PubMed=10630289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; S28.003; -.
MGD; MGI:1859181; Prss16.
InterPro; IPR008758; Peptidase_S28.
InterPro; IPR00379; Ser_estrs.
Pfam; PF05577; Peptidase_S28; I.
Hydrolase; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenetics 50:255-270(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ131775; CAB66137.1; -.
                                                                                                                                                                  Query Match
Best Local Similarity 33.0%;
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                          68
136
155
621 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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TSSP_MOUSE
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                                                                                                                                                                                                                     7 VGAGVASADPVDAVINTTCNYGQVVA-ALNATDPG-----AAAQ-----FNASPV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=74-0R23-1A / FGSC 987;

KOh-Luar S.I., Parish J.H., Bleasby A.J., Pappin D.J.C., Ainley K.,
Johansen F.E., Radford A.;

"Exported proteins of Neutrospora crassa: 1-glucoamylase.";

Enzyme Microb. Technol. 11:692-695(1989).

-!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
with release of beta-D-glucose.

-!- SIMILARITY: Belongs to family 15 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=74-OR23-1A / FGSC 987;
MEDINE=94031144; BubMed=822128;
Stone P.J., Makoff A.J., Parish J.H., Radford A.;
"Cloning and sequence analysis of the glucosmylase gene of Neurospora
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          P14804; Q9P5U5;
01-ARR-1990 (Rel. 14, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glucoamylase precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
(1,4-alpha-D-glucan glucohydrolase).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                            25;
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MEDILNE=22545210; PubMed=12655011;
Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "What's in the genome of a filamentous fungus? Analysis of the
                                                                                                                          15.3%; Score 73.5; DB 1; Length 509; 29.2%; Pred. No. 3.4; tive 13; Mismatches 37; Indels 25
                                                                                                                                                                                                                                                                                        260 AQAVLREBLGA------CGSLDLTEDQAELLGALGALVGGTVQY 297
                                                                                                                                                                                                                                                                    51 AQSYLRNFLAAPPPQRAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
                                                                      N-LINKED (GLCNAC. . .) (PC
CD8425F3F71EE43C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurospora genome sequence.";
Nucleic Acids Res. 31:1944-1954(2003).
   446
471
69 N-
171 N-
320 N-
54523 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Curr. Genet. 24:205-211(1993).
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                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                       69
171
320
369 AA;
                                                                                                                                             Similarity
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Local Sim.
31;
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MEDINE=22206494, PubMed=12218036, Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Colonay J.F., Nelson W.C., Umayan L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and Jaboratory strains."; SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh; g ઠે S SPECIES=M.tuberculosis, STRAIN=H37Rv;
MEDLINE=9825987, PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeiler K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLen J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998). POTENTIAL.
POTENTIAL.
POTENTIAL.
PUCCAMILAS.
SUBSTRATE (BY SIMILARITY).
CATALYTIC BASE (BY SIMILARITY).
INTERACT WITH SUBSTRATE (BY SIMILARITY).
INTERACT WITH SUBSTRATE (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-SING (IN REF. 1).
N-SESBDDBATABA19 CRC64; 4 SLTVGAGVASADPVDAVINTTCNYG----QVVAALNATDPGAAAQF---NASPVAQSYL-R HSSP; P04064; 1GAI.

R HSSP; P04064; 1GAI.

R InterPro; IPR002044; CBD_4.

R InterPro; IPR002044; CBD_4.

R InterPro; IPR00165; Glyco_hydro_15.

R InterPro; IPR00165; Glyco_hydro_15.

R Pfan; PF00666; CBM_20; I.

R Pfan; PF00666; CBM_20; I.

R Pfan; PF00723; Glyco_hydro_15; 1.

R PRSF; PIRSF001031; Glu-a-glcsd_SBD; 1.

R PRINF; PR001766; CBD_4; I.

R PRODOM; P0001568; CBD_4; I.

R PROSITE; PS00820; GLUCOAMYLASE; 1.

R Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein; Gaps Query Match
Best Local Similarity 26.9%; Pred. No. 4.8;
Best Local Similarity 26.9%; Pred. No. 4.8;
Matches 29; Conservative 19; Mismatches 34; Indels 26; Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium. NCBI_TaxID=1773, 1765; 56 ---RNFLAA-----PPPQRAAMAAQLQAVPGAAQYIGLVESVAGS 92 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical protein Rv1333/MT1375/Mb1368.
RV1333 OR MT1375 OR MTCY130.18 OR MB1368.
Mycobacterium tuberculosis, and
Mycobacterium boyis. PRT; 344 AA 66474 MW; STANDARD; SEQUENCE FROM N.A. RESULT 4
YD33 MYCTU

AC Q10644;
DT Q1-OCT-1996
DT Q1-OCT-2003
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[2] SEQUENCE FROM N.A.

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P19726; P03117;
21-JUL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
M1-FEB-1991 (Rel. 17, Last annotation update)
10. 206 LR----APPAEQIAALAQLSSPLGA 226 55 LENFLAAPPORAAMAAQLQAVPGA 79 EMBL; Z73902; CAA98097.1; -EMBL; AZ07011; AAK45639.1; -EMBL; EX248338; CAD94229.1; -PIR; A70771; A70771. 15.0%; ilarity 34.1%; Conservative 7 Query Match Best Local Similarity Matches 29; Conservat RESULT 5 VCAA_BPT7 GERRAR

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24; Gaps

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                                                                                                                                                                                                                                                                                               8 GAGVASADPVDAVINTICNYG-----QVVAALNATDPGAAAQFNASPVAQSYLRN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANBOUS: The active site is a redox-active disulfide bond.
-!- SIMILARITY: Belongs to class-I pyridine nucleotide-disulfide oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucifora G., Chu L., Silver S., Misra T.K.;
"Mercury operon regulation by the merR gene of the organomercurial resistance system of plasmid plasmid 1958.";
Eacteriol. 1711:4241-4247(1889).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Mercuric reductase (EC 1.16.1.1) (Hg(II) reductase) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 398;
                                                                                                                                                                                                Indels
                                                                       398 AA; 41830 MW; 97919FE8D4FE317A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        207 FYCDPDSYSAILAA---LMPNAANYAALIDPEKGSIRN 241
                                                                                                                                                                                                35,
                                                                                                                                                                                                                                                                                                                                                                              58 FLAAPPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNN
                                                                                                                                  DB 1;
                                                                                                                            15.0%; Score 72; DB 1
ilarity 31.6%; Pred. No. 3.8;
Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 HMA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, Q04656, 1AWO.
INTERPRO, IPRO01327, FAD_pyr_redox.
INTERPRO, IPRO06121; HeavyMe_transpt.
INTERPRO, IPRO06151, HG_reductase.
INTERPRO, IPRO06191, McEal_bind.
INTERPRO, IPRO01100; Pyr_redox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-342 FROM N.A.
MEDLINE=89327136; PubMed=2666393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae, Serratia.
NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 343-460 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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         PIR, B04344; VBBPA7.
Coat protein.
SEQUENCE 398 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A29010; A29010.
                                                                                                                                                            Local Similarity
ses 31; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POS662.
                                                                                                                                                                                                                                                                                                                      158
                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 GLGTAT-----VIETTQNKAALTDQVALGKEIIAAL--TKARAALTKNYVPAAD---RV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 GAGVASADPVDAVINTTCNYG------QVVAALNATDPGAAAQFNASPVAQSYLRN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol. Biol. 166:477-535(1983).
-!- MISCELLANBOUS: The minor capsid protein 10B is due to a translational shift to the -1 frame.
-!- SIMILARITY: TO THE T3 MINOR CAPSID PROTEIN 10B, EXCEPT IN THE C-TERMINAL EXTENSIONS.
Bacteriophage T7.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
T7-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses, dsDNA viruses, no RNA stage, Caudovirales, Podoviridae, T7-like viruses.
                                                                                                                                                                                                                       Dunn J.J., Studier F.W.;
"Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 genetic elements.";
J. Mol. Biol. 166477-538(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 genetic elements."; J. Mol. Biol. 166:477-535(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 AA; 36545 MW; 0CB7973954FE69F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: TO THE T3 MAJOR CAPSID PROTEIN 10A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 FLAAPPPORAAMAQLQAVPGAAQYIGLVESVAGSCNN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-707-7; P03717; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7; 21-707-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 15.0%; Score 72; DB 1
11 Similarity 31.6%; Pred. No. 3.3;
31; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                MEDLINE=83241725; PubMed=6864790;
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MEDLINE=83241725; PubMed=6864790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V01146; CAA24427.1; -. PIR; A04344; VABPA7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=10760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10760;
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VCAB_BPT7 RESULT 6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rhodovulum sulfidophilum photosynthetic regulatory genes.";
Submitted (AN-1998) to the ENEL/Geneback/Dabd databases.
-!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM REGE/REGA.
INVOLVED IN TRANSACTIVATING ANAEROBIC EXPRESSION OF THE PHOTOSYNTHETIC PAPARATUS. IT IS A TRANSKRIPTIONAL REGULATOR THAT IS RESPONSIBLE FOR ACTIVATING EXPRESSION OF THE PUF, PUH, AND PUC, OPPRONS IN RESPONSE TO A DECREASE IN OXYGEN TENSION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9. AGVASADPVDAVINTICNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLAAPPPQRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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Rhodobacteraceae, Rhodovulum.
                                                                                                                                            PROSITE; PSDUBBBB REDOX 1; 1.
PROSITE; PSDUO76; PYRĪDINE REDOX 1; 1.
Mercuric resistance; Oxidoreductase; Flavoprotein; FAD; NADP;
Mercury; Redox-active center; Metal-binding; Plasmid.
                                                                                                                                                                                                                                                                           (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 1; Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; Indels
                                                                                                                                                                                                                                                                                                                                                          MERCURY (POTENTIAL)
MERCURY (POTENTIAL)
628466EF3F653F05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains i response regulatory domain.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                        REDOX-ACTIVE
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PIRSF; PIRSF036385; Res_reg_RegA; 1.
ProDom; PD000039; Response_reg; 1.
                                                                            ProDom; PD000139; FAD PYF redox; 1. PROSITE; PS01047; HMA_1; 1. PROSITE; PS50846; HMA_2; 1.
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InterPro; IPR002197; HTH Fis.
InterPro; IPR008329; Res_reg_RegA.
InterPro; IPR01789; Response reg.
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HSSP; P10958; 1DBW.
                                                                                                                                                                                                                                                                                                                                                                                                                  48587 MW;
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32.6%;
                             HGRDTASE.
PNDRDTASEI
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  FADPNR
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30-MAY-2000 (Rel. 39,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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                                                       PR00411;
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136
342
457
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NP BIND
DISULFID
PRINTS;
PRINTS;
PRINTS;
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Best Local 9
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                                                                                                                                                                                                                                                         -----VDAVINTTCNYGQVVAAL 34
                                                                                                                                                                                                                                                                                           40 MAETVAAGKAIASARPPAYAVVDLRLEDGTGLDVVETLREKRPDAKIVVLTGYGAIATAV 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITINE=93049354; PubMed=1425703; Lane B.G., Cuming A.C., Fregeau J., Carpita N.C., Hurkman W.J., Lane B.G., Cuming A.C., Fregeau J., Carpita N.C., Hurkman W.J., Lane B.G., Cuming A.C., Fregeau J., Rennedy T.D.; Rendogermin is a uniquely thermostable water-soluble oligomeric Pseudogermin is a uniquely thermostable water-soluble oligomeric protein in ungerminated embryos and like germin in germinated embryos, it is incorporated into cell walls."; Eur. J. Blochem. 209:961-969(1992).

-!- SUBCELLULAR LOCATION: Cell wall.
-!- DEVELOPMENTL STAGE: Accumulates specifically during spherulation.
-!- MISCELLANBOUS: Spherulin is a major encystment-specific protein.
-!- SIMILARITY: Belongs to the germin family.
                                                                                                                                                                                                                  32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-ocr-2003 (Rel. 42, Last annotation update)
Spherulm lA precursor.
Physarum polycephalum (Slime mold).
Eukaryota, Mycetozoa, Myxogastria; Myxogastromycetidae, Physariida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-88137962; PubMed=2830170;
Bernier F., Lemieux G., Pallotta D.;
"Gene families encode the major encystment-specific proteins of Physarum polycephalum plasmodia.";
Gene 59:265-277(1987).

        MOD RES
        62
        62
        PHOSPHORYLATION (BY SIMILARITY)

        SEQUENCE
        183 AA;
        20219 MW;
        394DB79D39AAB23F CRC64;

                                                                                                                                                                          14.1%; Score 68; DB 1; Length 183; 27.7%; Pred. No. 4.3; ive 9; Mismatches 32; Indels
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PROSITE; PS00725; GERMIN; 1.
Cell wall; Signal; Glycoprotein; Manganese; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                               100 AAVKVGAIDYLSKPADANDVIAALLSNGEALPPPFENPMSA 140
                                                                                                                                                                                                                                                                                                                                        71
                                                                                                                                                                                                                                                                                                                                          35 NATDPGA----AAQFNASPVAQSYLRNFLAAPPPQRAAMAA
                                                                                             RESPONSE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01.MAR-1989 (Rel. 10, Created)
01.MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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InterPro; IPR007113; Cupin sup.
InterPro; IPR001929; Germin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M18428; AAA29982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE OF 20-34.
                                                                                                                                                                                                                                                           3 MSLTVGAG--VASADP-
                                                                                                                                                                                                 Similarity 27.7
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD:
                                                     Sensory transduction DNA-binding; Activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00190; Cupin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell wall; Signal Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRIA PHYPO
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                                                                                                                                                                            Query Match
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SRIA PHYPO
RANATTS
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SMART; SM00448; REC; 1. TIGREADS, TIGHT fis; 1. PROSITE; PSS0110; RESPONSE REGULATORY; 1. Sensory transduction; Phosphorylation; Transcription regulation;

FT FT FT FT SO

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FlyBase, FBgn0010218; Cpn.
GO; GO:0005509; F:calcium ion binding; IDA.
Calcium-binding.
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721
865 AA;
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                                                                                                                                                                                                                                                                                            155 TLEAGMATVFPQGAIHFEINWNCEPAMFVAAFNNEDPGVQTTASSFFGLPADVVGVSLNI 214
                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calcium and contains a leucine zipper.";

Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).

-!- FUNCTION: Might function as a calcium-sequestering "sponge" to regulate the amount of free cytoplasmic calcium. It binds 0.3 mole of Calcat) per mole of protein.

-!- SUBUNIT: Homodimer (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Canton-S;
MEDLINE=93165729; PubMed=8094559;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
                                                                                                                                                                                                                                                        6 TVGAGVASADPVDAV---INTTCNYGQVVAALNATDPG---AAAQFNASP-----V
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ballinger D.G., Xue N., Harshman K.D.;
"A Drosophila photoreceptor cell-specific protein, calphotin, binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Cytoplasmic; hypodense compartment.
                                                                                                                       .) (POTENTIAL)
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NCBL_TaxID=7227;
                                                                                                                                                                             Score 67.5; DB 1; Length 246;
                      SPHERULIN 1A.
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
                                                                                                                                                                                                                  34; Indels
                                                                                                                       -LINKED (GLCNAC. . .) (PC A06360A64A1B8BD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      865 AA.
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                                                                                                                       N-LINKED
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                                                                                                                                                                                                                                                                                                                                                         215 SSIOTVEDLGKHLPONPAVAMO 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                   51 AQSYLRNFLAAPPPQRAAMAAQ 72
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MEDLINE=93165730; PubMed=8434015;
                                                                                                                                             26138 MW;
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30.5%;
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PIR; A47283; A47283
                                                                                                                                           246 AA;
                                                                                                                                                                                                 Local Similarity
es 25; Conserv
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Q02910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 PVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLAAPPPQRAAMAAQLQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 PVSAPVAPSAVAAPVTPSAVAAPVQVVSPAAVAPAPAAPIAVTPV----APPPTLASVQPATVT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FXD1 HUMAN STANDARD; PRT; 465 AA.
016676; 012949;
01-00V-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
related transcription [FCHLB] (Forkhead-related protein FKHLB) (Forkhead-Flated transcription factor 4) (FREAC-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ernstsson S., Pierrou S., Hulander M., Cederberg A., Hellqvist M., Carlsson P., Enerback S., Carlsson P., Enerback S., Carlsson P., Enerpack S., Carlston D., Energiation of the human forkhead gene FREAC-4. Evidence for requiation by Wilms' tunor suppressor gene (WT-1) and p53."; J. Biol. Chem. 271:21094-21099(1996).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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VQ -> PP (IN REF. 2).
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
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STRAIN=S288C / AB972;

MEDLINE=97313268; PubMed=9169872;

MEDLINE=97313268; PubMed=9169872;

MEDLINE=97313268; PubMed=9169872;

Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,

Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.

Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII.";

Nature 387:90-93(1997).
                                                                                                                                                                                      R Genew; Haurissour,

R GO (00:00370); Fitzanscription factor activity; TAS.

R GO; OC:0003700; Fitzanscription factor activity; TAS.

R PRINTS; PRO00520; Fork_head.

R PRINTS; PRO00520; FORK_head; 1.

R PRODOM; PRO00425; TF Fork_head; 1.

R SMART; SM00339; FORK_HEAD.

R PROSITE; PS00668; FORK_HEAD.

DR PROSITE; PS00668; FORK_HEAD.

ET DOMAIN 26 34 POLY-GLU.

FT DOMAIN 39 43 POLY-GLU.

FT DOMAIN 69 72 POLY-GLU.

FT DOMAIN 69 72 POLY-GLU.

FT DOMAIN 73 76 POLY-GLU.

FT DOMAIN 73 76 POLY-GLU.

FT DOMAIN 73 FORK-HEAD.

FT DOMAIN 52 26 POLY-AAS.

FT DOMAIN 259 266 POLY-AAA.

FT DOMAIN 259 266 POLY-AAA.

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FT DOMAIN 259 266 POLY-PRO.

FT DOMAIN 293 303 POLY-AAA.
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D3E7854909CCBFAE CRC64;
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EMBL, U59831; AAC50660.1;
EMBL, U13222; AAA92039.1;
PIR, G02738; G02738.
PIR; S51627; S51627.
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Best Local Similarity 29.0*
                                                                                                                   HSSP; Q63245; 2HFH.
TRANSFAC; T02472; -.
Genew; HGNC:3802; FOXDI.
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STRAIN=SEY6210;
MEDLINE=9842453; PubMed=9748433;
Cappellaro C., Mrsa V., Tanner W.;
"New potential cell wall glucanases of Saccharomyces cerevisiae and their involvement in mating."
"Jew potential cell wall glucanases of Saccharomyces cerevisiae and their involvement in mating."
"Jew potential cell wall glucanases possibly play a role in cell expansion during growth, in cell-cell fusion during mating, and in spore release during sporulation (By similarity).
-- SUBCELLULAR LOCATION: Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROBABLE FAMILY 17 GLUCOSIDASE SCW10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSSP_HUMAN STANDARD; PRT; 514 AA.

10-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2003 (Rel. 41, Last annotation update)
Thymus-specific serine protease precursor (BC 3.4.-.-).
PRSS16 OR TSSP.
PRD SABJERS (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SER-RICH.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
AQ -> QE (IN REF. 2).
AQ -> QE (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: Glycosylated.-!- SIMILARITY: Belongs to family 17 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Thymus;
MEDLINE=99458809; PubMed=10527559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 27.4 nes 31; Conservative
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EMBL; M64495; AAA62785.1; -.
EMBL; AE000172; AAC73787.1; -.
EMBL; D90708; BAA35349.1; -.
PTR; A40839; A40839.
HSSP; P43099; 1C4K.
ECCGene; EG10964; SDPF.
INCEPPO; IPR000310; Decarbxylsel.
INCEPPO; IPR008286; Decarbxylsel.
INCEPPO; IPR008286; Decarbxylsel.
DREPPO; IPR008286; ORP D. INCEPPO; IPR005086; ORP D. INCEPPO; IPR005308; OKR D. INCEPPO; IPR005308; OKR D. INCEPPO; IPR005308; OKR D. INCEPPO; IPR005308; OKR D. INCEPPO; IPR005308; OKR D. INCEPPO; IPR005308; OKR D. INCEPPO; IPR005308; OKR D. INCEPPO; IPR005308; OKR D. INCEPPO; IPR005308; OKR D. INCEPPO; IPR005308; OKR D. INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; INCEPPO; 
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                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
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                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its word non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------PVAQ
DOWLUS C.L., Ahn J., Chu T., Gruen J.R.; "Cloning of a novel MHC-encoded serine peptidase highly expressed by cortical epithelial cells of the thymus."; Cell. Immunol. 196:80-86(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Gaps
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POTENTIAL.
THYMUS-SPECIFIC SERINE PROTEASE.
THYMUS-SPECIFIC SERINE PROTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                           Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Protease that may play a role in T-cell development.
-!- SUBCELLULAR LOCATION: Vesicular, either lysosomal or endosomal.
-!- TISSUE SPECIFICITY: Expressed predominantly in cortical thymic epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Kashiwagi K., Suzuki T., Suzuki F., Furuchi T., Kobayashi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match
Local Similarity 31.6%; Pred. No. 19;
les 31; Conservative 14; Mismatches 30; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AGVASADPVDAVINTTCNYGQVVA-ALNATDPGAAAQFNAS-----
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EF39BC06C560709A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM, 607169; -.
GO; GO:0008236; F:serine-type peptidase activity; NAS.
GO; GO:0030163; P:protein catabolism; NAS.
InterPro: IPR008758; Peptidase S28.
Ffam; PF05577; Peptidase Z28; I.
Hydrolase; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 AALKTELSACGPLGRAENQAELLGALQALVGGVVQYDG 300
                                                                                                                                                                                                                                                                                                                                                   -!- DEVELOPMENTAL STAGE: Expressed in fetal thymus. -!- SIMILARITY: Belongs to peptidase family S28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 SYLRNFLAAPPP-----QRAAMAAQLQA-VPGAAQYIG 84
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01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
0rnithine decarboxylase, inducible (EC 4.1.1.17).
SPEF OR B0693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            732 AA.
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EMBL; AL021808; CAB94769.1; ALT_SEQ.
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Genew; HGNC:9480; PRSS16.
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70
172
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514 AA;
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DCOS_ECOLI
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DNA Res. 3:137-155(1996).

-! CATALYTIC ACTIVITY: Lornithine = putrescine + CO(2).
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                                                                                                                                                                                                                                                                                        MEDLINE=97426617; PubMed=9278503; Blattner F.R., Punkett G. III, Bloch C.A., Perna N.T., Burland V., Blatener F.R., Punkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; science 277:1453-1474(1997).
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"Coexistence of the genes for putrescine transport protein and ornithine decarboxylase at 16 min on Bscherichia coli chromosome."; J. Biol. Chem. 266:20922-20927(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- PATHWAY: Biographesis of spermidine from arginine; third step. -i- INDUCTION: By low environmental pH. -i- SIMILARITY: Belongs to the Orn/Lys/Arg decarboxylase class-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRIDOXAL PHOSPHATE (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82415 MW; C2C030BEAB9D23F6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Meyer A.L., Petrovskis E.A., Duffus W.P.N., Thomsen D.R.,
Meyer A.L.,
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: GH AND GL FORM A COMPLEX THAT INDUCES NEUTRALIZING AND
SYNCYTIA INHIBITING ANTIBODIES (BY SIMILARITY):
-!- SIMILARITY: Belongs to the herpesviruses glycoprotein H family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R EMBL; X58867; CAA41677.1; -.
R EMBL; Z78205; CAB01604.1; -.
R EMBL; Z78205; CAB01604.1; -.
R EMBL; Z78205; CAB01604.1; -.
R EMBL; AJ004801; CAA06112.1; -.
R DIR; S18462; S18462.
T Glycoprotein; Transmembrane; Signal.
T CARBOHYD 1 2 6 842 GLYCOPROTEIN H.
CARBOHYD 12 112 N-LINKED (GLCNAC. .) (POTENTIAL).
T CARBOHYD 617 617 N-LINKED (GLCNAC. .) (POTENTIAL).
T CARBOHYD 666 666 N-LINKED (GLCNAC. .) (POTENTIAL).
T CARBOHYD 760 760 N-LINKED (GLCNAC. .) (POTENTIAL).
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13.8%; Score 66.5; DB 1; Length 8:
Best Local Similarity 28.4%; Pred. No. 31;
Matches 25; Conservative 11; Mismatches 43; Indels
                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last annotation update)
Glycoprotein H precursor.
GH OR UL22.
Viruses, dsDNA viruses, no RNA stage; Herpesviridae,
Alphaherpesvirinae; Varicellovirus.
NCBL TaxID=10323;
                                                                                                                                                    842 AA.
                                                                                PRT;
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P27599;
RESULT 15
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Gencore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 22, 2004, 16:55:54; Search time 7.84949 Seconds

(without alignments)
3858.816 Million cell updates/sec

Title: US-09-886-349A-22
Perfect score: 481
Sequence: 1 VAMSITYGAGVASADPVDAV......PGAAQYIGLVESVAGSCNNY 96
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_fungi:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mham:*
10: sp_mhage:*
10: sp_phage:*
11: sp_rodent:*
11: sp_rodent:*
11: sp_vortus:*
12: sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O50430 mycobacteri	Q7u0g8 mycobacteri	Q9w6t6 brachydanio	Q8s2d6 oryza sativ	Q8rz79 oryza sativ	Q98he8 rhizobium l	Q8nty7 corynebacte	Q81n25 oryza sativ	Q84x68 chlamydomon	Q8vpa4 pseudomonas	Q8dwe7 streptococc	Q8u9p5 agrobacteri	Q84jp1 arabidopsis	Q9s9p9 arabidopsis	Q8p938 xanthomonas	
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* Query Match 1	100.0	100.0	16.4	16.2	16.0	15.7	15.6	15.4	15.4	15.3	15.3	15.3	15.1	15.1	15.1	
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PRELIMINARY;	(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.	Hypothetical protein Rv1174c. Rv1174C OR MTV005.10C OR MT1211.	Mycobacterium tuberculosis. Bacteria: Actinobacteria: Actinobacteridae; Actinomycetales	Corynebacterineae, Mycobacteriaceae, Mycobacterium	۲۶,	N.A.	1 . 1 8 6	Cole S.T., Brosch R., Parkhill J.,	Gordon S.V., Eiglmeier K., Gas	Basham D.,	Davies R., Devlin K., Feltwell T.,	T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,	Seeger K.,	Sulston J.E., Taylor K.,	"Deciphering the biology	complete genome sequence.	7-544	2	SEKOBNCE FROM N.A.	Fleischmann R.D., Alland D., Eisen J.A.,	Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.	Nelsa	elcher A., Utterback T., Weidman J., Khourl H., Gill		"Whole genome comparison of Mycobacterium tuberculosis	laboratory strains."; Submitted (APR-2001) to
Pi		cal r	erium Acti	teri	/T=01	FROM	37RV;	, Bro		ζ., Β <u>ζ</u>	., Der	ا: ا بى	., Os)	S., Se	П.	ring	geno	93:53	700	ַבְּיֵלְ בְּיֵלְ	ann R	٦,٠	J.F.,	₽., G	•	enone	d (AP
30	01-JUN-1998 01-JUN-1998 01-JUN-1998 01-JUN-2003	Hypothetical RV1174C OR MT	bacte	mebac	NCBI_TAXID=1773; [1]	SEQUENCE FROM N.A	STRAIN=H37RV; MEDIINE=98295	E O	lon S	Badcock K.,	les R	Hornsby	rer S	Rutter S	ston	ciphe	plete	ire 3	[2]		ischm	erson	onay .	cher	Bishai W.;	ole g	orato mitte
JLT 1 130 050430	01-40N- 01-70N- 01-70N-	Hypo RV11	Mycc	000	ΞE	SEO	STR	Cole	Gord	Bado	Dav:	Hori	0111	Rutt	Sul	"De	COM	Nati	7 2 6	N D	E E	Pet	Ko1	Del	Bis	ď.	Subi
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Matches

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925 DGIINPNAFY-IYLSAWVSNDPVAYAASQANIRPHPPEWLHDRTDSIPASRLNIPAAEPI 983
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
clone:P0400G10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
1-07T-2003 (TrEMBLrel. 25, Last annotation update)
1-07T-2003 (TrEMBLrel. 25, Last annotation update)
1-0401G10.4 protein (Similar to RNA-binding protein).
1-0401G10.4 OR 0J1294 F06.21.
1-072a sativa (Sponica cultivar-group).
1-072a sativa (Sponica cultivar-group).
1-072a sativa (Sponica cultivar-group).
1-072a sativa (Sponica cultivar-group).
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1-072a sativar-group).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.4%; Score 79; DB 13; Length 1243; 29.3%; Pred. No. 49;
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16.2%; Score 78; DB 10; Length 280;
Best Local Similarity 34.2%; Pred. No. 12;
Matches 27; Conservative 6; Mismatches 42; Indels
                                                                                                                              Lewis K.E., Concordet J.P., Ingham P.W.;

"Characterisation of the second ptc gene in zebrafish.";

Submitted (1942-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ007742; CAB39726.1;

ZFIN; ZDB-GENE-980526-196; ptc2.

ZO, GO:001621; C:integral to membrane; IEA.

GO; GO:001621; C:integral to membrane; IEA.

InterPro; IPR004339; Patched.

InterPro; IPR004766; Patched.

InterPro; IPR004766; Patched.

InterPro; IPR00731; SSD_SIW.
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G0: 00154F; F:nucleic acid binding; IEA.
InterPro; IRR00504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
PROSTITE; PS00102; RRM; 1.
PROSTIE; PS001030; RRM; 1.
SEQUENCE 280 AA; 28689 WW; 852687706D3DBCSF CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Created)
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TGRRPAM; TIGRO018; 2A060602; I.
PROSITE; PS50156; SSD; I.
SEQUENCE 1243 AA; 138548 MW; I
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EMBL; AP004326; BAB92880.1;
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                                                                                                         FROM N.A.
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Best Local Simi
Matches 27;
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STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
"The Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                      0; Gaps
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
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                                                                                                                                                                                                                                                                    Length 110;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                 0309DDB489150061 CRC64;
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Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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1 Similarity 100.0%; Pred. No. 3.1e-39;
96; Conservative 0; Mismatches 0;
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Hypothetical protein; Complete proteome.
SEQUENCE 110 AA; 10881 MW; 0309DDB48
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EMBL, BX248337; CAD94068.1; -.
Complete proteome.
SEQUENCE 110 AA; 10881 MW;
EMBL; AL010186; CAA15851.1; -. EMBL; AE006998; AAK45468.1; -. PIR; F70875; F70875.
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                                                                                           TIGR; MT1211; -.
Tuberculist; Rv1174c;
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PTC2 OR PTC1.
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                           AGVASADPV-DAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLAAPPPQRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN 2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL; AP003791; BAB90534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SATAIN=C.v. Nipponbare; Sasaki T., Mateumoto T., Yamamoto K.; Sasaki T., Mateumoto T., Yamamoto K.; Carony asativa (japonica cultivar-group) genomic DNA, chromosome 1, clorg:Bl065G12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MAFF303099;
MEDLINE-21082390; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eppermatophyta; Nagnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 77; DB 10; Length 410;
; Pred. No. 22;
12; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Phyllobacteriaceae, Mesorhizobium.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Flagellar motor switch protein, FliG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TremBlrel. 21, Created)
(TremBlrel. 21, Last sequence update)
(TremBlrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 FLAAPPP----ORAAMAAQLQAVPGAAQYIGLVESVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR GO; GO: 0016787; EAB90534.1; -. GERBO.

OF GO; GO: 0016787; F: hydrolase activity; IEA.

ThterPro; IPR002018; CarbesteraseB.

R InterPro; IPR002018; CarbesteraseB.

R Pfam; PF00135; COesterase; 1.

Hydrolase.

SEQUENCE 410.
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28.3%;
                                                                                                                                                              68 AMAAQLQAVPGAAQYIGLV
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Best Local Similarity 28...
Local Similarity 28...
Loca 28; Conservative
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B1065G12.16.
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01-JUN-2002
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Q8RZ79;
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Q8RZ79
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Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takacuchi C., Yamada M., Tabata S.;
Tomplete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
DR Resorhizobium loti.";
RE DRA Res. 73131-338(2000).
RG GO:0002288; Cifadellum (sensu Bacteria); IEA.
DR GO; GO:0005622; Ciintracellular; IEA.
DR GO; GO:0005622; Ciintracellular; IEA.
DR GO; GO:0005374; F:motor activity; IEA.
DR GO; GO:0005375; F:structural constituent of ribosome; IEA.
DR GO; GO:0006315; P:chemotor activity; IEA.
DR GO; GO:0001539; P:chemotaxis; IEA.
DR GO; GO:0001539; P:chemotaxis; IEA.
DR GO; GO:0001539; P:chemotaxis; IEA.
DR GO; GO:0001539; P:chemotaxis; IEA.
DR GO; GO:000372; P:Chemotaxis; IEA.
DR GO; GO:000332; P:Chemotaxis; IEA.
DR GO; GO:000332; P:Chemotaxis; IEA.
DR PROSITE; PS00732; RIBOSOWAL_SI6; 1.
KW Complete protecome.
SEQUENCE 336 AA; 35986 MW; 90FCFAGED7B0FEDB CRC64;
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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005274; BAB97557.1;
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR00683; GFO_IDH_MOCA.
InterPro; IPR004104; GFO_IDH_MOCA.
Pfam; PF01408; GFO_IDH_MOCA.
Oxidoreductase; GFO_IDH_MOCA.
Science 337 AA; 36431 MW; F5EF6EAFA65924A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 TEGAGLIDSADRMDTIINESLSPEEMSAIMGNKKPEAAPEGPPPIWPDLEKLEPSRLGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 TVGAGVA-SADPVDAVINTTCNYGQVVAALNATDPGAAAQF-----NASPVAQSYLRNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Predicted dehydrogenases and related proteins (EC 1.1.1.18).
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37.3%; Pred. No. 28;
ive 11; Mismatches 26;
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.7%; Score 75.5; D 30.6%; Pred. No. 25; ive 13; Mismatches
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Best Local Similarity 37.3<sup>3</sup>
Matches 28; Conservative
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Best Local Similarity
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PRELIMINARY;
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                              Q84X68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M., Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B., Jin S.S., Koo H., Zismann V., Haidao J., Blunt S., Vanaken S.S., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Sub B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M., "Oryza sariva chromosome 10 BAC OSJNa0055023 genomic sequence."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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transcription, DNA-dependent; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Nipponbare;
The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Nipponbare;
Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC092389; AAM88627.1; -.
EMBL; AE017115; AAPS4799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 586 AA; 62859 MW; 659D0B54197B6301 CRC64;
                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.4%; Score 74; DB 10; 31.9%; Pred. No. 65;
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                                                                                                                                                                   586 AA.
                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
SMART; SM00574; POX; 1.
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InterPro; IPR006563; POX.
                                                                                                                                                                                                                                                                                 Putative homeodomain protein.
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----AVDAVLIAVPG 77
  78
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  64 PORAAMAAQLQAVPG
                                                                                                                                                                   PRELIMINARY;
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STRAIN=cv. Nipponbare;
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                                                                                                                                                           OSJNBA0053C23.7
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RESULT 9 Q84X68

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AAAQFNASPVAOSYLRNFLAAPPPQRAAMAAQLQA------VPGAAQYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VAMSLTVGAGVASADPVDAVINTT----CNYGQVVA------ALNATDPG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Gaps
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Bloodgood R.A., Spano A.J.;
Cloning and Characterization of Chlamydomonas reinhardtii Flagella
Membrane Glycoproteins.''
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY208914; AAO25118.1; -.
                                                                                                                                                                                             Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=PA.03-22;
Caballero A.R., Thibodeaux B.A., Marquart M.E., Traidej M.,
Caballero A.R., Thibodeaux B.A., Marquart M.E., Traidej M.,
Caballaghan R.J. Sr.;
"Pseudomonas protesses IV: gene identification, sequence, and
distribution.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AYO62882; AAA45683.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
INSEPTO: IPR009003; Cys_Ser_trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2213 AA; 220120 MW; 6F087758734FC0CA CRC64;
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                                                01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update). 01-JUN-2003 (TrEMBLrel. 24, Last annotation update). Flagella membrane glycoprotein 1B (Fragment). Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Protease IV (EC 3.4.21.50).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.4%; Score 74; DB 10; 27.5%; Pred. No. 2.9e+02;
PRT; 2213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 AAPPPORAAMAAQLQAVPGAAQYIGL 85
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                                                                                                                                                                                                                         Chlamydomonadaceae; Chlamydomonas
NCBI_TaxID=3055;
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Best Local Similarity 31.4'
Matches 27; Conservative
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Kutyavin T., Levy R., Ii M.-J., McClelland B., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W., "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
SEQUENCE 1489 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogen.";

Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).

EMBL, AE014863; AANS7895.1;

EMBL, AE014863; AANS7895.1;

GO; GO:0016020; C:membrane; IEA.

GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. .; IEA.

GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. .; IEA.

InterPro; IPR003352; Ptrans EliC.

InterPro; IPR003353; Ptrans EliC.

InterPro; IPR003353; Ptrans IIB fruc.

Pfam; PF02379; PTS_IIIE fruct.

Pfam; PF02379; PTS_IIIE fruct.

TIGRPAMS; TIGR00829; FRU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAINE-10159 / Arcc 700610 / Serotype C;
STRAINE-2295063; PubMed=12397166;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Prineaux C., Tian R., Kentron S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAMSLTVGAGVASADPVDAVINTTCNYGQVVAALNATDPGAAAQFNASPVAQSYLRNFLA
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
POLYKetide synthetase.
ATU3681 OR AGR L 2313.
ARU3681 OR AGR L 2313.
Bachedria, Proteobacteria, Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobian/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.3%; Score 73.5; DB 16; Length 26.0%; Pred. No. 56; ative 16; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                     Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 25, Last annotation update)
putative PTS system, fructose-specific IIBC component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 KRPGFVAGFVGGMMAVNGGSGFLGGI--IAGFAAGY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 APPPORAAMAAQLQAVPGAAQYIGLVESVAGSCNNY 96
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                                                                                                                                       466 AA
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Best Local Similarity 26.0%
Marches 25, Conservative
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                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                         Streptococcus.
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                                                                                                                                            Q8DWE7
                                                                                          RESULT 11
Q8DWE7
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373 İDTAAĞIA-----GFİKTVLCLKHGRIPASİHFRQANAKIDFPASFFAVNTVLRDWTAL 426
ANDLINE-2160851; PubMed=11743194;

MEDLINE-21608551; PubMed=11743194;

MEDLINE-21608551; PubMed=11743194;

MEDLINE-21608551; PubMed=11743194;

A Gondner B., Gattung S., Miller N., Blanchard M.,

A Gordner B., Goldman B., Cao Y., Askenazi M., Halling C., Mullin L.,

A Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

A Holman C., Crowell C., Gurson J., Lomo C., Sara C., Strub G.,

A Holman C., Allinger M., Doughty D., Scott C., Strub G.,

A Holman C., Allinger M., Doughty D., Scott C., Strub G.,

A Holman C., Allinger M., Doughty D., Scott C., Strub G.,

A Holman C., Allinger M., Doughty D., Scott C., Strub G.,

A Holman C., Allinger M., Doughty D., Scott C., Strub G.,

A Holman C., Allinger M., Doughty D., Scott C., Strub G.,

A Holman C., Allinger M., Doughty D., Scott C., Strub G.,

A Holman C., Allinger M., Doughty D., Scott C., Strub G.,

A Holman C., Allinger M., Doughty D., Scott C., Strub G.,

A Holman C., Allinger M., Doughty D., Scott C., Strub G.,

B Holman Profosology Adjourne S.,

B Holman Profosology Retoacyl synth.

B Ham, Profosology Retoacyl synth.

B RAMI, PROFOSO B, RETOACYL SYNTHASE, I.

B ROSITE; PSSOO75; ACP DOWAIN; I.

B ROSITE; PSSOO75; ACP DOWAIN; I.

B ROSITE; PSSOO75; ACP DOWAIN; I.

B ROSITE; PSSOO75; ACP DOWAIN; I.

B ROSITE; PSSOO75; ACP DOWAIN; I.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
ATIG30500.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 73.5; DB 16; Length 1489; 28.6%; Pred. No. 2.1e+02; ive 18; Mismatches 36; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1489 AA; 159121 MW; SBF4FF9FAEC90009 CRC64;
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Best Local Similarity
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EMBL; AC009917; AAF19754.1;

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SEQUENCE FROM N.A.
STRANS-C. Columbia.
STRANS-C. Columbia.
STRANS-C. Columbia.
Toriumi M., Calumbia.
Toriumi M., Chin C., Chiou J., Choi B., Chung M., Gonzalez A.,
Howng B., Koo T., Li J., Liu A., Vaysberg M., Altafi H., Brooks S.,
Bluehler E., Chao Q., Chomy A., Hansen N., Johnson-Hopson C.,
Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome I BAC PS6016 sequence.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases."; Arabidopsis thaliana (Mouse-ear cress). Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBI_TaxID=3702; STRAIN=cv. Columbia; Theologis A.; Sibmitted (BPC-1949) to the EMBI/Cenbank/hnb1 Astaban 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) PRT; 197 AA. F26G16.12 protein. F26G16.12. SEQUENCE FROM N.A , 64686Q Q9S9P9 RESULT 14 Q9S9P9

RC STRAINB-22022145; PubMed=12024217;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
A duaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
Ranatotte G., Cannavan F., Cardozo J., Chambergo F., Ciaplina L.P.,
RA Cicarelli R.M.B., Coutlinho L.L., Cursino-Santos J.R., Ellorry H.,
RA Eria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Tringladan A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
Anatins E.C., Machadus M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
Martins E.C., Machadus J.M., Manck C.F.M., Myaki C.Y., Moon D.H.,
Moreira L.M., Novo M.T.M., Okura V.R., Oliveira M.C., Ge Souza R.F.,
Ratidade dos Santos M., Truffi D., Tsai S.M., White F.F.,
Setubal J.C., Kitajima J.P.,
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
Comparison of the genomes of two Xanthomonas pathogens with differing
REL, REDISSOB, AM413171, ...
REL, REDISSOB, AM413171, ...
REL, RELL, RE ., 26 NYGQVVAALNATDPG-----AAAQFNASPVAQSYLRNFLAAPPPQ------RAAMAAQLQ 74 1 NYESIVTSLVYSDPGTINSMAPGQY---PYPDPYYRS-IFAPPPQPYTGVHLQLMGVQQQ 96 27; Gaps factor activity; IEA. transcription, DNA-dependent; IEA. Xanthomonas campestris (pv. campestris). Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas. DB 10; Length 197; 23; Indels 22127 MW; EB67C5050BE0F874 CRC64; 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein XCC2028. Score 72.5; DE Pred. No. 27; 8; Mismatches 654 AA. 97 GVPLPSDAVEEPVFVNAKQYHGIL 120 75 AVP------8AAQYIGLV 86 PRT; PIR; A86430; A66430.

GO; GO:0005534; Cinucleus; IEA-6
GO; GO:0005534; Cinucleus; IEA-6
GO; GO:0005355; P:regulation of tr Interpro; IPRO01289; TF CBRB.
PFG. PF0.005; CBFB. NFYA; 1.
PRINTS; PR00616; CCAATSUBUNTB.
PRODM; PR003860; TF CBFB; 1.
SNART; SM00521; CBF; 1.
SEQUENCE 197 AA; 22127 MW; EB6 15.1%; 31.0%; Query Match Best Local Similarity 31.00 Matches 26; Conservative PRELIMINARY; SEQUENCE FROM N.A. NCBI TaxID=340; Q8P938; Q8P938 RESULT 15 à 엄 ò

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27; Gaps

15; Gaps Query Match
Best Local Similarity 29.9%; Pred. No. 1e+02;
Matches 20; Conservative 11; Mismatches 21; Indels 15; GO; GO:0004563; F:beta-N-acetylhexosaminidase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR001540; G1yco_hydro_20.
Pfam; PF02838; G1yco_hydro_20; I.
Hypothetical protein; Complete proteome.
SEQUENCE 654 AA; 69164 MW; 9A96E86E1302P410 CRC64;

90 AGSCNNY 96 | ::: 633 DGVLDSF 639

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Search completed: June 22, 2004, 17:22:57 Job time: 10.8495 secs

RA . Protein e Protein e Mycobacte Mycobacte

Mycobacte tuberc Mycobacte

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This sequence represents an immunogenic portion of a Mycobacterium tuberculosis antigen of the invention. The polypeptides are useful for immunotherapy to treat or prevent uncuculosis (especially in humans), e.g. they can be included with an acceptable carrier in pharmaceutical compositions or included in vaccines, and administered to induce protective immunity in a patient against M. tuberculosis. Tuberculosis a chronic, infectious disease generally caused by M. tuberculosis is infection, and if left untreated typically results in serious complications and death. Fusion proceins containing the antigen, or DNA molecules can similarly be included with an acceptable carrier in pharmaceutical compositions or in vaccines and administered as above. The
                                                          Aay38991 M. tuberc
Aay39118 M. tuberc
Aae17911 Mycobacte
Aaw64339 Mycobacte
Aaw84339 Mycobacte
Aaw31705 M. tuberc
Aay38993 M. tuberc
Aay39899 M. tuberc
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Aay39136 M. tuberc
Aay39998 M. tuberc
Aab30969 Mycobacte
Abg30969 Mycobacte
Abg30969 Mycobacte
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                                   Aaw64321 |
Aaw81747 |
Aay32097 |
                         Aaw32444
                                                                                                                                                                                                                                                                                                      M. tuberculosis antigen clone Tb472 protein sequence.
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        ABU34018
AAW32376
AAW64321
AAW61747
AAY32097
AAY39118
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AAX39118
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AAY38993
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ABG30969
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98US-00073009
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WPI; 1999-045315/04.
N-PSDB; AAX01132.
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        20-MAY-1998;
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                 1586107 segs, 282547505 residues
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                                            - protein search, using sw model
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polypeptides are also useful for diagnosis of tuberculosis, by contacting dermal cells with at least one polypeptide and detecting an immune response (especially induration) on the patient's skin. Inhibiting the spread of tuberculosis requires vaccination and accurate diagnosis, since antibiotic therapy may not be effective due to the existence of an asymptomatic but contagious stage and to patient non-compliance. The polypeptides overcome concerns of safety and efficacy of current vaccination with live bacteria (usually Bacillus Calmette-Guerin) and lack of sensitivity and specificity of existing diagnostic techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents an immunogenic portion of a Mycobacterium tuberculosis antigen of the invention. The polypoptides are useful for immunotherapy to treat or prevent tuberculosis (especially in humans), e.g. they can be included with an acceptable carrier in pharmaceutical compositions or included in vaccines, and administered to induce a protective immunity in a patient against M. tuberculosis. Tuberculosis a chronic, infectious disease generally caused by M. tuberculosis in infections and death. Fusion proteins containing the antigen, or DNA molecules can similarly be included with an acceptable carrier in pharmaceutical compositions or in vaccines and administered as above. The polypeptides are also useful for diagnosis of tuberculosis, by contacting
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100.0%; Pred. No. 2.3e-48;
ative 0; Mismatches 0;
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AAW73759
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dermal cells with at least one polypeptide and detecting an immune response (especially induration) on the patient's skin. Inhibiting the spread of tuberculosis requires vaccination and accurate diagnosis, since antibiotic therapy may not be effective due to the existence of an asymptomatic but contagious stage and to patient non-compliance. The polypeptides overcome concerns of safety and efficacy of current vaccination with live bacteria (usually Bacillus Calmette-Guerin) and lack of sensitivity and specificity of existing diagnostic techniques
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                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                  1 MSLLIDAHIPOLVASOSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide comprising immunogenic Mycobacterium tuberculosis antigen useful for immunisation against M. tuberculosis infection to treat or prevent tuberculosis, and in diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                           1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
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                                                                                                                                                                                                               / Match 100.0%; Score 468; DB 2; Local Similarity 100.0%; Pred. No. 2.3e-48; les 97; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW73763 standard; protein; 97 AA
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98US-00073010.
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N-PSDB; AAX01166.
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                                                                                                                                                                               Sequence 97 AA;
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dermal cells with at least one polypeptide and detecting an immune response (especially induration) on the patient's skin. Inhibiting the spread of tuberculosis requires vaccination and accurate diagnosis, since antibiotic therapy may not be effective due to the existence of an asymptomatic but contagious stage and to patient non-compliance. The polypeptides overcome concerns of safety and efficiacy of current vaccination with live bacteria (usually Bacillus Calmette-decrin and lack of sensitivity and specificity of existing diagnostic techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents an immunogenic portion of a Mycobacterium tuberculosis antigen of the invention. The polypeptides are useful for e.g. tuberculosis (especially in humans), e.g. they can be included with an acceptable carrier in pharmaceutical compositions or included in vaccines, and administered to induce protective immunity in a patient against M. tuberculosis. Tuberculosis a chronic, infectious disease generally caused by M. tuberculosis is infection, and if left untreated typically results in sertious complications and death. Fusion proteins containing the antigen, or DNA molecules can similarly be included with an acceptable carrier in pharmaceutical compositions or in vaccines and administered as above. The polypeptides are also useful for diagnosis of tuberculosis, by contacting dermal cells with at least one polypeptide and detecting an immune
                                                                                                                                                                                                                                                                                                                          MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
                                                                                                                                                                                                                                                                                               1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
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                                                                                                                                                                                                               100.0%; Score 468; DB 2;
100.0%; Pred. No. 2.3e-48;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       AAAKUNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M. tuberculosis antigen cloneb protein #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW73869 standard; peptide; 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-00859381,
98US-00073010,
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                                                                                                                                                                                                                                                        97; Conservative
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                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                            Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium
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response (especially induration) on the patient's skin. Inhibiting the spread of tuberculosis requires vaccination and accurate diagnosis, since antibiotic therapy may not be effective due to the existence of an asymptomatic but contagious stage and to patient non-compliance. The polypeptides overcome connerns of safety and efficacy of current vaccination with live bacteria (usually Bacillus Calmette-Guerin and lack of sensitivity and specificity of existing diagnostic techniques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculosis, TB; vaccine; esat-6 gene family; Rv0287; Rv1036c; Rv1037c; Rv2346c; Rv2346c; Rv248c; Rv3653c; Rv2654c; Rv3020c; Rv3444c; Rv3445c; Rv3890c; Rv3891c; Rv3904c; Rv3905c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences for members of the esat-6 gene family from Mycobacterium tuberculosis. Thes proteins include Rv10287, Rv10366, Rv10376, Rv2346c, Rv2348c, Rv2543c, Rv2653c, Rv2664c, Rv3020c, Rv3444c, Rv3444c, Rv3445c, Rv3890c, Rv3891c, Rv3891c, and fragnosis. These can be used to produce vaccines against, and in the diagnosis of, tuberculosis (TB) infection. The present sequence is one the proteins of the invention
                                                                                                                                                                                                                                                                          1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
                                                                                                                                                                                                                                         1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
                                                                                                                                                                                                         Gaps
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                                                                                                                                                                       th 100.0%; Score 468; DB 2; Similarity 100.0%; Pred. No. 2.3e-48; 97; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.3e-48;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                            61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAB35221 standard; protein; 97
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99US-0144011P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
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N-PSDB; AAF24411.
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es 97; Conserv
                                                                                                                                        Sequence 97 AA;
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                                                                                                                                                                         Query Match
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                              1 MSILDAHIPQIVASQSAFAAKAGIMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An isolated polypeptide comprising a Mycobacterium antigen, e.g., from Mycobacterium tuberculosis, useful in a vaccine for enhancing an immune response to and inhibiting development of a Mycobacterium infection.
              MSLLDAHI PQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                    Tuberculosis; Mycobacterium infection; gene therapy; anti bacterial;
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                                                                                  61 AAAKVNTLLDVAQANLGEAAGTXVAADAAAASTYTGF 97
                                                                                                                                                                                                                            Mycobacterium tuberculosis polypeptide for MTb98.
                                                              61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97
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100.0%; Score 468; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 97; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovendale P,
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                                                                                                                                                    AAU08229 standard; protein; 97 AA
                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001; 2001WO-US005992
                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2000; 2000US-0185037P, 08-AUG-2000; 2000US-0223828P.
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                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                   immunostimulant; MTb98
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The present invention relates to the isolation of Mycobacterium tuberculosis antigen polypeptides (e.g. Tb224) and the nucleic acids encoding them. The invention describes compounds and methods for the diagnosis of tuberculosis or for inducing protective immunity against tuberculosis. The compounds comprise at least one immunogenic portion of one or more Mycobacterium proteins and nucleic acid molecules encoding such polypeptides. The Mycobacterium proteins and nucleic acid molecules encoding them can be used in diagnostic kits for the detection of Mycobacterium infection in patients and biological samples. The compounds of the invention and antibodies directed against the Mycobacterium proteins may be used in vaccines for immunisation against Mycobacterium infections. The nucleic acids encoding the Mycobacterium proteins may be used in persent sequence represents M. tuberculosis antigen Tb472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An isolated polypeptide comprising a Mycobacterium antigen, e.g., from Mycobacterium tuberculosis, useful in a vaccine for enhancing an immune response to and inhibiting development of a Mycobacterium infection.
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100.0%; Pred. No. 2.3e-48;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jen
                                                                                                                                                                   Mycobacterium tuberculosis antigen Tb472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 145-146; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovendale P,
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Encoded by G"
                                                                                                                                                                                                                                                                                                                                                                  Key Location/Qualifiers Misc-difference 89. .97
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                                                                                                                                                                                                                                                     immunostimulant; antigen Tb472.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-2000; 2000US-0185037P.
08-AUG-2000; 2000US-0223828P.
AAU08209 standard; protein;
                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campos-Neto A, Skeiky Y,
                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200162893-A2
                                                                                                             17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2001
                                                         AAU08209;
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1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA

1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA

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61 AAAKUNTLLDVAQANLGBAAGTYVAADAAAASTYTGF 97

heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, ADS.

Sequence 97 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccinating against Mycobacteria infections in mammals using proteins comprising combinations of heterologous antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dillon DC,
                                                                                  tuberculosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                  label= Mtb9.8_derived_peptide_158..97
                                                                                                                                                                                                                                                                                                Mtb9.8_derived_peptide_10
                                                                                                                                                                                                                                                                                                         51. .65
/label= Mtb9.8_derived_peptide_11
                                                                                                                                                                                                                                                                                                                                 label= Mtb9.8_derived_peptide_12
                                                                                                                                                                                                                                                                                                                                         %1. .75
/label= Mtb9.8_derived_peptide_13
                                                                                                                                                                                                                                                                                                                                                         66. .80
/label= Mtb9.8_derived_peptide_14
                                                                                                                                                                                                                                                                       11. .55
|label= Mtb9.8_derived_peptide_9
                                                                                                                                      .. .15
/label= Mtb9.8_derived_peptide_1
                                                                                                                                                     'label= Mtb9.8_derived_peptide_2
                                                                                                                                                                    4. .30
|abel= Mtb9.8_derived_peptide_4
                                                                                                                                                                                                     11 .35 Tabel= Mtb9.8_derived_peptide_5
                                                                                                                                                                                                                     26. .40
/label= Mtb9.8_derived_peptide_6
                                                                                                                                                                                                                                               Mtb9.8_derived_peptide_7
                                                                                                                                                                                                                                                        6. .50
|abel= Mtb9.8_derived_peptide_8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcneill PD,
                                                                  M. tuberculosis partial antigen Mtb9.8 (MSL)
                                                                                                                                                                                                                                                                                                                                                                                                    "Encoded by GCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 145; 168pp; English.
                                                                                                                           Location/Qualifiers
                AAU01893 standard; protein; 97 AA.
                                                                                 Mtb9.8; MSL; antigen; vaccine; tw
acquired immunodeficiency disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2000; 2000WO-US028095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0158338P.
                                                                                                           tuberculosis
                                                                                                                                                                                                                                                                                       46. .60
/label= 1
                                                                                                                                                                                                                                      31. .45
'label= :
                                                                                                                                                                                                                                                                                                                                                                            89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS03784
                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200124820-A1
                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1999;
07-OCT-1999;
                                                29-AUG-2001
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                                AAU01893
                                                                                                                            Key
Peptide
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                         Jaccine; immunity; diagnostic agent; gene therapy; MSL antigen; MTB9.8.
                                                                                        1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
                                                                    1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
                                      Gaps
                                      0
      Length 97;
                                    Indels
                                                                                                                                  97
                                                                                                                                                               97
      ; Score 468; DB 4;
; Pred. No. 2.3e-48;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis MSL antigenic protein.
                                                                                                                                    61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
                                                                                                                                                     AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      88. .97
/note= "Encoded by GCTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 101; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guderian J;
                                                                                                                                                                                                                                             Ą
                                                                                                                                                                                                                                             AAE29712 standard; protein; 97
      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2001; 2001US-0275837P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002WO-US008223
                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                           (first entry)
Ouery Match
Best Local Similarity 100.0
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brannon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200272792-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2002;
                                                                                                                                                                                                                                                                                                          27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky Y,
                                                                                                                                                                                                                                                                             AAE29712;
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The sequence represents Mycobacterium tuberculosis Mtb9.8 (also known MSb), an M. tuberculosis antigen. Compositions comprising at least 2

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Matches
                                                                                                                                                                                                                                                                               RESULT 11
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in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis MSL antigenic protein. MSL is also referred to as MTB9.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to fusion proteins containing at least two mycobacterium species antigens, nuclectides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnosit coll in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humaral antibodies or cell-mediated immunity against M. tuberculosis, for the
                                                                                                                      9
                                                                                                                                         1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising MTB39 antigen and MTB32A antigen from um species, useful for eliciting immune response in a subject
                                                                                                                      1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                      Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB9.8; MSL protein.
                                                                                                .
0
                                                                        97;
                                                                                              Indels
                                                                        Length
                                                                                                                                                                      97
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                                                                                                .
0
                                                                      100.0%; Score 468; DB 5;
100.0%; Pred. No. 2.3e-48;
iive 0, Mismatches 0;
                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis MTB9.8 (MSL) protein.
                                                                                                                                                                       61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
                                                                                                                                                                                      AAAKVNTLLDVAQANLGEAAGTYVAADAAASTYTGF
                                                                                                                                                                                                                                                                                                                                                                                                                             88. .97
/note= "Encoded by GCTG"
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 117; 136pp; English.
                                                                                                                                                                                                                                                        AAE17576 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-2001; 2001WO-US019959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis
                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium species,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-147798/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP
                                                                      Query Match
Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky Y, Reed S,
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                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200198460-A2
                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition
                                                                                                                                                                                                                                                                                                        22-APR-2002
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                                                                                                                                                                                                                                                                                 AAE17576;
                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                            AAE17576
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diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is M. tuberculosis MTB9.8
                                                                                                                                                                                                                                                                                                                              1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a recombinant Mycobacterium tuberculosis tri-
antigen fusion protein; termed Mtb31f, composed of the antigens DPV, MTI
and MSL. The fusion protein is expressed in host cells using a vector
carrying a polynucleotide (see AAZ20202) comprising the coding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen; fusion protein; Mtb31f; DPV; MTI; MSL; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                             1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion proteins useful for diagnosis, prevention and treatment of
                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                    Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen fusion protein Mtb31f.
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                  100.0%; Score 468; DB 5;
100.0%; Pred. No. 2.3e-48;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          61 AAAKWNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy; vaccine; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY32067 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9. .90
/note=
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                                                                                                                                                                                                                                                             Local Similarity
les 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ20202
                                                                                                                                                                                          Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuberculosis;
                                                                                                                                             (MSL) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-APR-1998;
30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9951748-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tuberculosis
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                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous bolynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion
                                                                                                                                                                                                                                                                                                   New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MI5 or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
for the 3 antigens. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymuclectides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis antibod are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine, immunity, diagnostic agent, gene therapy, DPV-MII-MSL-MICC#2, MTb71F; MTB8.4, MTB9.9A, MTB9.8, MTB41, fusion protein.
                                                                                                                                                                                                                                                                              1 MSLLDAHIPOLVASOSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
                                                                                                                                                                                                       Length 299;
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium sp. DPV-MTI-MSL-MTCC#2 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                       AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 285
                                                                                                                                                                                                                                                                                                                                                    AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97
                                                                                                                                                                                                   100.0%; Score 468; DB 2;
100.0%; Pred. No. 9.6e-48;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 114-115; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE29723 standard; protein; 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2002; 2002WO-US008223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-2001; 2001US-0275837P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium sp.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD47100
                                                                                                                                                                    Sequence 299 AA;
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                                                                                                                                 components
                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE29723;
                                                                                                                                                                                                                                                                                                                                                                                       249
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polypeptides are used for enhancing the expression of polynucleotides, as in twive diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is MTb71F fusion protein. This fusion protein comprises DPV (MTB8.4)-MTI (MTB9.48) MSI (MTB9.8) protein sequences from M. tuberculosis and MTCC#2 (MTB41) protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                              189 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are immunised with BGC. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnosit cools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject
                                                                                                                                                                                                                                                                          1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTb71F; DPV-MTI-MSL-MTCGR2 protein.
                                                                                                                                                                                                                                       0
                                                                                                                                                                                                Length 299;
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                                                                                                                                                                                              100.0%; Score 468; DB 5;
100.0%; Pred. No. 9.6e-48;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                       61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium species MTb71F fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE17587 standard; protein; 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alderson M;
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01-FEB-2001; 2001US-0265737P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Lac 97; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD28358
                                                                                                                                                           Sequence 299 AA;
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Length 299;

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Fusion protein; tuberculosis; Mycobacterium tuberculosis; tuberculostatic; immunogen; vaccine; DPV-MTI-MSL; Mtb31f. Antigenic fusion protein DPV-MTI-MSL (Mtb31f) Location/Qualifiers 300 Ą. AAU74596 standard; protein; 306 99US-00287849 RESULT 14 AAU74596

/label= OTHER // Xaa. Xaa= In frame stop codon"

97US-00818112. 97US-00942578. 98US-00025197. 98US-00056556. 98US-00223040. 01-OCT-1997; 18-FEB-1998; 07-APR-1998; 30-DEC-1998;

REED S G. SKEIKY Y A. DILLON D C. ALDERSON M. (DILL/) (ALDE/) (REED/)

CAMPOS-NETO A.

(CAMP/)

Campos-Neto A; Alderson M, Dillon DC, Skeiky YA, WPI; 2002-171134/22. N-PSDB; ABK14136. Reed SG,

Claim 1; Fig 9; 62pp; English

WPI; 1999-601610/51 N-PSDB; AAZ20200 New fusion proteins of Mycobacterium tuberculosis antigens, useful for diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.

The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein of the invention. (Updated on 29-AUG-2003 to standardise OS field) ö 189 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 248 1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60 Gaps Tuberculosis, antigen; fusion protein; Mtb46f; ERD14; DPV; MTI; MSL; diagnosis; therapy; vaccine; immunogen. .. Length 306; Indels Mycobacterium tuberculosis antigen fusion protein Mtb46f. 97 .. 0 100.0%; Score 468; DB 5; 100.0%; Pred. No. 9.9e-48; AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 0; Mismatches l. .8 /note= "Met/His tag" Location/Qualifiers AAY32065 standard; protein; 433 AA /note= "ERD14" 155. .236 'note= "DPV" Mycobacterium tuberculosis. (first entry) Conservative .152 al Similarity 97; Conserva Sequence 306 AA; 17-JAN-2000 Query Match Local Peptide Protein Protein Protein Matches g ò 염

99WO-US007717 239. .332 /note= "MTI" 98US-00056556 98US-00223040 /note= "MSL" .433 (CORI-) CORIXA CORP. WO9951748-A2 07-APR-1999; 07-APR-1998; 30-DEC-1998; 14-OCT-1999 Protein

Campos-Neto Alderson M, Skeiky YAW, treatment of New fusion proteins useful for diagnosis, prevention and tuberculosis. us-09-886-349a-24.rag

Claim 1; Fig 7A-B; 83pp; English

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This sequence represents a recombinant Mycobacterium tuberculosis tetra-
antigen fusion protein, termed Mtb46f, composed of the antigens BRD14,
DPV, MTI and MSL. The fusion protein is expressed in host cells using a
vector carrying a polynuclectie (see AAZ2020) comprising the coding
sequences for the 4 antigens. The invention provides fusion proteins
sequences for the 4 antigens. The invention provides fusion proteins
fusion proteins and polynuclectides encoding them are useful as vaccines
for preventing tuberculosis (claimed), for diagnosis (via in vitro assays
or intradermal skin tests for detection of anti-M. tuberculosis
antibodies), monitoring of disease progression, and treatment of
tuberculosis. They are more effective immunogens than mixtures of the
individual protein components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 97; Conservative 0; Mismatches 0; Indels 0
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1 MSLLDAHIPQLVASQSAFAA......BAAGTYVAADAAASTYTGF
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US-09-056-556-88
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equence 1	equence 117,	Ņ	equence 117,	equence 124,	equence 124,	Ap	equence 5390,	equence 126,	Sequence 126, App	quence 118,			Sequence 13565, A	114	114	Sequence 4, Appli	4,
-08-818-111-11	09-056-556-11	ı	00	-09-073	-09-073-	US-09-344-529-2	US-09-543-681A-5390	N	-09-073-010-1	US-09-073-009-118	-60	US-09-489-039A-12707	US-09-489-039A-13565	US-09-073-009-114	-60-	US-08-433-854-4	US-08-174-745A-4
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Best Local Similarity 100.0%; Pred. No. 8.7e-53;
Matches 97; Conservative 0; Mismatches 0; Indels
us-oy-073-009-109

Sequence 109 Application US/09073009

Patent No. 6555653

Patent No. 6555653

APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos.Nato, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: Gastle
STATE: Washington
COUNTRY: Seatile
STATE: Washington
COUNTRY: US
ZIP: Mashington
COUNTRY: US
ZIP: Path NORM: PC-COMPAINE
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: OS-MAY-1998
FILING DATE: OS-MAY-1998
FILING DATE: OS-MAY-1998
FILING DATE: OS-MAY-1998
FILING DATE: OS-MAY-1998
FILING DATE: OS-MAY-1998
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FILING DATE: OS-MAY-
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; MOLECULE TYPE: protein
US-09-073-009-109
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STRANDEDNESS: sir
TOPOLOGY: linear
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APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS AND
NUMBER OF SEQUENCES: 144
ADDRESSEE: SEED and BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
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                                                                                                          COUNTRY: ...
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,010
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/ACENT INFORMATION:
NAME: Naki, David J.
REGISTRATION NUMBER: 31,392
REPERBNOS/DOCKET NUMBER: 210121.440C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
INFORMATION POR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
ISRUGTH: 97 amino acids
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ZIP: 98104
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,010
FILING DATE: OS-MAY-1998
CURRENTON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 468; DB 4;
Best Local Similarity 100.0%; Pred. No. 8.7e-53;
Matches 97; Conservative 0; Mismatches 0;
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Coumbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SEED and BERRY 6300 Coumbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 143, Application US/09073010 Patent No. 6613881 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-073-010-109
                                                                        CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6300 Coumb
CITY: Seattle
STATE: Washington
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Patent No. 6613881
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: Compounds FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS AND NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
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8.7e-53;
hes 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTONREY/AGENT INFORMATION:
NAME: MAKI, DAVIG J. 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.441C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 206-622-4900
                                                                                                                                                                                     Sequence 143, Application US/09073009
Patent No. 6555653
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Billon, Davin C.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
CORRESPONDENCES: 144
ADDRESSEE: SEED and BBRRY
ADDRESSEE: SEED and BBRRY
STREET: CORP.
                            61 AAAKUNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97
                                                              AAAKVNTLLDVAQANLGEAAGTYVAADAAASTYTGF 97
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100.0%; Pred. No. 8.7
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORMATION FOR SEQ ID NO: 143: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
TELEFAX: 2:
INFORMATION FOR
                                                                                                                                                                   JS-09-073-009-143
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Relative A.W.
APPLICANT: Dillow, Davin C.
APPLICANT: Dillow, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: 1999-04-07
TITLE OF INVENTION NUMBER: US 08/818,112
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PLING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,566
PRIOR APPLICATION NUMBER: US 09/025,23,040
PRIOR APPLICATION NUMBER: US 09/026,566
PRIOR APPLICATION NUMBER: US 09/026,566
PRIOR APPLICATION NUMBER: US 09/026,566
PRIOR APPLICATION NUMBER: US 09/026,566
PRIOR APPLICATION NUMBER: US 09/026,566
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PRIOR APPLICATION NUMBER: US 09/026,566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
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US-09-287-849-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 46%; DB 4;
Best Local Similarity 100.0%; Pred. No. 8.7e-53;
Matches 97; Conservative 0; Mismatches 0;
                                                                                           10121.440C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09287849
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEPAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                        LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-073-010-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-287-849-19
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61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97

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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Steven G.
APPLICANT: Steven G.
APPLICANT: Steven G.
APPLICANT: Steven G.
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: and Their Uses
FILE OF INVENTION: And Their Uses
FILE REPERENCE: 0.04058-00902003
FILE OF INVENTION: AND THE USES
FILE REPERENCE: 0.04058-00902003
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT APPLICATION NUMBER: US/08/112
PRIOR FILING DATE: 1999-04-07
PRIOR PELLING DATE: 1999-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PELLING DATE: 1998-02-18
PRIOR PELLING DATE: 1998-02-18
PRIOR PELLING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 14
FENDER DATE: PATENTIN VET: 2.1
SEQ ID NO 14
FENDER DATE: PATENTIN VET: 2.1
FENDER DATE: PATENTIN VET: 2.1
FENDER DATE: PATENTIN VET: 2.1
FENDER DATE: PATENTIN VET: 2.1
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corization
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens;
TITLE OF INVENTION: And Their Uses
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-005020US
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/912,578
PRIOR PILING DATE: 1997-10-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion
US-09-287-849-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
249 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 AAAKVNTLIDVAQANIGEAAGTYVAADAAAASTYTGF 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 468; DB 4; Best Local Similarity 100.0%; Pred. No. 6.2e-52; Matches 97; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09287849
Patent No. 6627198
GENERAL INFORMATION:
                                                                                                                                                                                    US-09-287-849-14
; Sequence 14, Application US/09287849
; Patent No. 6627198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-287-849-16
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US 09/025,197

PRIOR APPLICATION NUMBER:

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US-08-818-112-88
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US-08-818-112-88
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US-08-818-111-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion US-09-287-849-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT

ORGANISM: Artificial Sequence

FATURE:
OTHER HFORMATION: Description of Artificial Sequence:penta-fusion
US-09-287-849-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 100.0%; Score 468; DB 4; Length 710; Local Similarity 100.0%; Pred. No. 1.2e-51; nes 97; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.5e-51;
Matches 97; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 285
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
LENGTH: 710
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Matches
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18 FAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLDVAQANLG 77
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                                                                                                                                                                                                                                                                                             APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.7%; Score 87.5; DB 3; Length 95; 34.9%; Pred. No. 0.00071; cive 8; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPTARE: BATENTIN FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/818,112
FILLING DATE: 13-MAR-1997
                                  395 AAAKVNTLLDVAQANLGEAAGTYVAADAAASTYTGF 431
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADUKESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington
61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY, AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                         Sequence 88, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 89, Application US/08818111;
Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 EAAGTYVAAD---AAAASTYTGF
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
                                                                                                                                                                                                                             Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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Best Local Similarity 34.9%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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us-09-886-349a-24.rai

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18 FAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLDVAQANLG 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Campos. Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Danniel R.
APPLICANT: Twardzik, Danniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                18.7%; Score 87.5; DB 4; 34.9%; Pred. No. 0.00071; tive 8; Mismatches 43;
                        CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
MAME: Maki, David J.
REGITRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 anino acids
TYBE: amino acids
TYBE: amino acids
TYBE: amino acids
TYBE: amino acids
TYBE: alinear
US-09-056-556-88
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STREET: 6300 Columbia Center, 701 Fi
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIF: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EIBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 EAAGTYVAAD---AAAASTYTGF 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 89, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reidy, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPRAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 899:
          07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 34.95
Matches 29; Conservative
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LENGTH: 95 amino acids
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APPLICANT:
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                                                                                  TUBERCULOSIS
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US-09-056-556-88
; Sequence 88, Application US/09056556
; Fatent No. 6356456
; Patent No. 6356456
; GENERAL INPORMATION:
; APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND MYNBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
18.7%; Score 87.5; DB 4; Length 95;
Best Local Similarity 34.9%; Pred. No. 0.00071;
Matches 29; Conservative 8; Mismatches 43; Indels
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CITY: Machington
COUNTRY: Washington
COMPUTER MACHINGTON
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk-
COMPUTER: IBM PC compatible
OFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 62-4900
TELEPAX: (206) 62-6031
INFORMATION FOR SEQ ID NO: 89:
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linear
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78 EAAGTYVAAD --- AAAASTYTGF 97
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Best Local Similarity 34.9%
Matches 29; Conservative
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TITLE OF INVENTION: COMP
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BE
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US-08-818-112-115
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                                                                                                      Gaps
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                                                                  18.7%; Score 87.5; DB 4; Length 95; 34.9%; Pred. No. 0.00071; ive 8; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 34.9%; Pred. No. 0.00071;
Matches 29; Conservative 8; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US(09/072,967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELEPHONE: (206) 622-4000
                                                                                                                                                                                                                                                                                                                                                    LINCERMATION:
JICANT: Reed, Steven G.
JICANT: Reed, Steven G.
JICANT: Dillon, Davin C.
JICANT: Campos-Neto, Antonio
JICANT: Houghton, Raymond
JICANT: Houghton, Raymond
JICANT: Wedvick, Thomas S.
JICANT: Twardzik, Daniel R.
JICANT: Hendrickson, Ronald C.
JICANT: Hendrickson, Ronald C.
B OF INVENTION: COMPOUNDS AND ME
                                                                                                                                                                                                                                      73 QAGVQYSRADEEQQQALSSQMGF 95
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Patent No. 6592877
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TELERAX: (206) 682-6031
INPORMATION FOR SEQ ID NO. 88:
SEQUENCE CHARACTERISTICS:
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                                                    Query Match
Rest Local Similarity 34.5,
79: Conservative
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ADDRESSEE: SEED and
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STREET: 6300
CITY: Seattle
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                   linear
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STRANDEDNESS: si
; STRANDEDNESS:
; TOPOLOGY: lin
US-09-072-596-89
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JS-09-072-967-88
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18 FAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLDVAQANLG 77
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                                                                                                                                                                                                                                                        Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Camoos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
VVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
VVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.7%; Score 87.5; DB 3; Length 100; 34.9%; Pred. No. 0.00076; ive 8; Mismatches 43; Indels
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FILOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
ATTONEY/AGENI INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C6
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHAN: (206) 622-4900
TELEPHAN: (206) 622-4900
TELEPHAN: (206) 622-4900
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US-08-818-111-110
; Sequence 110, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yaeir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 OAGVQYSRADEEQQQALSSQMGF 100
73 OAGVOYSRADEEQQQALSSQMGF 95
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                                                                                                RESULT 14
US-08-818-112-115
; Sequence 115, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
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us-09-886-349a-24.rai
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TUBERCULOSIS
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomsel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUNDEBRE OF SEQUENCES: 148
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS;
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: Mashington
COUNTRY: Washington
ZIP: 98104-7092
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Best Local Similarity 34.9%; Pred. No. 0.00076;
Matches 29; Conservative 8; Mismatches 43; Indels
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Search completed: June 23, 2004, 17:10:43 Job time : 38 secs

78 EAAGTYVAAD---AAAASTYTGF 97

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June 23, 2004, 17:12:36 ; Search time 43 Seconds (without alignments) 636.847 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                              Copyright
                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description		Sequence 109,	Sequence 143,	Seguence 10	Sequence 143	Sequence 24,	Seguence	Seguence 19	Sequence 47,	Seguence 19,	Sequence 47	Sequence 14,	Seguence 14	Sequence 16,	Sequence 49	Sequence 16
SUMMERTES		ID		US-09-073-009-109	US-09-073-009-143	US-09-793-306-109	US-09-793-306-143	US-09-886-349A-24	US-10-098-732A-24	US-09-287-849-19	US-09-886-349A-47	US-10-359-460-19	US-10-098-732A-47	US-09-287-849-14	US-10-359-460-14	US-09-287-849-16	US-09-886-349A-49	US-10-359-460-16
		DB	-	σ	σ	σ	6	12	14	σ	12	14	14	σ	14	თ	12	14
		Length	1 1 1	97	97	97	97	97	97	299	299	299	299	433	433	710	710	710
	æ	Query Match	1 1 1 1 1	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score		468	468	468	468	468	468	468	468	468	468	468	468	468	468	468
	·	Result No.			7	m	4	ເກ	ø	7	80	σ	10	11	12	13	14	15

INFORMATION FOR SEQ ID NO: 109: SEQUENCE CHARACTERISTICS: LENGTH: 97 amino acids TYPE: amino acid

Sequence 49, Appl Sequence 12, Appl Sequence 12, Appl Sequence 30, Appl Sequence 37, Appl Sequence 37, Appl Sequence 31, Appl Sequence 35, Appl Sequence 110, Appl Sequence 110, Appl Sequence 10, Appl Sequence 214, Appl Sequence 214, Appl Sequence 214, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 114, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 118, Appl Seq	
4 US-10-098-732A-49 US-09-287-849-12 US-10-289-460-12 US-10-393-449-37 US-10-393-449-37 US-10-393-449-37 US-10-393-449-37 US-10-282-122A-62027 US-10-282-122A-62027 US-10-282-122A-62027 US-10-282-122A-62027 US-10-282-123A-35-440-88 US-10-282-849-8 US-10-282-849-8 US-10-282-849-8 US-10-282-849-8 US-10-287-849-8 US-10-287-849-8 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-10 US-10-287-849-11 US-10-287-849-11 US-10-287-849-11 US-10-287-849-11 US-10-287-849-11 US-10-287-849-11 US-10-287-849-117 US-10-287-849-117 US-10-287-849-117	7-751-675-01-50-7
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RESULT 1
US-09-073-009-109
US-09-073-009-109
Sequence 109, Application US/09073009
Sequence 109, Application US/09073009
Sequence 109, Application US/09073009
Sequence 109, Application
Second Mark
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Gampos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: GA300 Counbia Center, 701 Fifth Ave.
CITY: Seatile
SITATE: Washington
COUNTRY: Seatile
SITATE: Washington
COUNTRY: Balogy disk
COMPUTER: IEM PC compatible
SITATE: Pachalle FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Beachin Release #1.0, Version #1.30
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0,
CURERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Davin UNBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Wast, David J.
REBERENCE-DOCKET NUMBER: 210121.441C1
TELECOMMUNICATION INFORMATION:
TELEPAN: 206-621-4900
TELEPAN: 206-62-4900

TUBERCULOSIS AND MET

ALIGNMENTS

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GENERAL INPORMATION:
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Ovendale, Pamela
APPLICANT: Ovendale, Pamela
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
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APPLICANT: Lodes, Michael
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APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: US 4004793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
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APPLICANT: Jen, Shyian
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
TITLE OF INVENTION: of Tuberculosis
FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US 409793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR PLICATION NUMBER: US 60/185,037
PRIOR PLING DATE: 2000-02-28
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOUTHARE PARENTE 2000-08-08
NUMBER OF SEQ ID NOS: 164
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100.0%; Score 468; DB 9;
Best Local Similarity 100.0%; Pred. No. 4.4e-47;
Matches 97; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                            Sequence 109, Application US/09793306 Patent No. US20020098200A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 143, Application US/09793306
Patent No. US20020098200A1
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GENERAL INFORMATION:
APPLICANT: Campos-Netc, Antonio
APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Tb472 (MSL) US-09-793-306-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
COTHER INFORMATION: Mtb9.8
US-09-793-306-143
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US-09-793-306-143
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                                                                                                                                                    Query Match 100.0%; Score 468; DB 9; Length 97; Best Local Similarity 100.0%; Pred. No. 4.4e-47; Matches 97; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTONENYAGENT INFORMATION:
NAME: MAKI, DAVIG J. 31,392
REGISTRATION NUMBER: 210121.441C1
TELEPROMONICATION INFORMATION:
TELEPROMONICATION INFORMATION:
TELEPROMONICATION INFORMATION:
TELEPROMONICATION INFORMATION:
TELEPROMONICATION INFORMATION:
TELEPROMONICATION INFORMATION:
TELEPROMONICATION INFORMATION:
TELEPROMONICATION INFORMATION:
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100.0%; Score 468; DB 9;
Best Local Similarity 100.0%; Pred. No. 4.4e-47;
Matches 97; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
ITILE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S: SEED and BERRY 6300 Coumbia Center, 701 Fifth Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 143, Application US/09073009 Patent No. US20010012888A1
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-073-009-109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
US
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STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 CC CITY: Seattle STATE: Washingt COUNTRY: US
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RESULT 8
US-09-886-349A-47
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US-10-08-732A-24

US-10-08-732A-24

Sequence 24, Application US/10098732A

Publication No. US20330175294A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Vasir

APPLICANT: Brannon, Mark

APPLICANT: Guderian, Jeffrey

APPLICANT: Grachian, Jeffrey

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a

TITLE OF INVENTION: Leishmania Antigen

FILE REFERENCE: 014058-01201008

CURRENT APPLICATION NUMBER: US/10/098,732A

CURRENT APPLICATION NUMBER: US 60/275,837

PRIOR PILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SEQ ID NO 24
                                                                                                        1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
                                                                                                                                                        1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
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| Sequence 24, Application US/09886349A |
| Publication No. US20040086523A1 |
| GENERAL INFORMATION: |
| APPLICANT: Skeiky, Yasir |
| APPLICANT: Skeiky, Yasir |
| APPLICANT: Corixa Corporation |
| APPLICANT: Corixa Corporation |
| APPLICANT: Corixa Corporation |
| APPLICANT: Corixa Corporation |
| TILLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis |
| FILE REFERENCE: US/09/086,349A |
| CURRENT FILING DATE: 2001-06-20 |
| PRIOR FILING DATE: 2001-06-20 |
| PRIOR FILING DATE: 2001-06-20 |
| PRIOR FILING DATE: 2001-06-20 |
| PRIOR FILING DATE: 2001-06-20 |
| NUMBER OF SEQ ID NOS: 50 |
| SEQ ID NOS: 50 |
| SEQ ID NOS: 50 |
| SEQ ID NO 24 |
| LENGTH: 97
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                                                                                                                                                                                                                61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 468; DB 12; Best Local Similarity 100.0%; Pred. No. 4.4e-47; Matches 97; Conservative 0; Mismatches 0;
100.0%; Score 468; DB 9;
100.0%; Pred. No. 4.4e-47;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: MTB9.8 (MSL) US-09-886-349A-24
                                                     97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97; Conservative
     Query Match
Best Local Similarity
Matches 97; Conserv
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APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: 1014058-00902003
CURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 299
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                                                                                                                                                                                                       Length 97;
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100.0%; Score 468; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.7e-46;
Matches 97; Conservative 0; Mismatches 0;
                                                                                                                                                                                                 Query Match
100.0%; Score 468; DB 14;
Best Local Similarity 100.0%; Pred. No. 4.4e-47;
Matches 97; Conservative 0; Mismatches 0;
LENGTH: 97
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 47, Application US/09886349A; Publication No. US20040086523A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/09287849
Patent No. US20020009459A1
GENERAL INFORMATION:
                                                                                                                ; OTHER INFORMATION: MTB9.8 (MSL) US-10-098-732A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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: Skeiky, Yasir A.W.
: Dillon, Davin C.
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ORGANISM: Artificial Sequence FEATURE:
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                                                  Query Match
Best Local Similarity 100.0
Matches 97; Conservative
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US-10-098-732A-47
  US-10-359-460-19
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APPLICANT: Alderson, maix
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Bud Their Uses
TITLE OF INVENTION: and Their Uses
TITLE APPLICATION NUMBER: US/10/359,460
CURRENT APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR PELING DATE: 1999-04-07
PRIOR PELING DATE: 1999-04-07
PRIOR PELING DATE: 1999-04-07
PRIOR PELING DATE: 1999-04-01
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19

LENGTH: 299
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                APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Red, Steven
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERBNCE: 014058-009070US
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
NUMBER OF SEQ ID NOS: 50
IENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein DPV-MTI-MSL (designated MTb31F) cDNA
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
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100.0%; Score 468; DB 12; Length 299;
Best Local Similarity 100.0%; Pred. No. 1.7e-46;
Matches 97; Conservative 0; Mismatches 0; Indels 0.
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Publication No. US20030147911A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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SENERAL INFORMATION:
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APPLICANT: Skelky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-01210108
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR APPLICATION NUMBER: US 60/275,837
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 47
LENGTH: 299
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APPLICANT: Alderson, Mark
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
APPLICANT: Campos-Neco, Antonio
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
CURRENT FILE REFERENCE: 014058-00902003
CURRENT FILING DATE: 1990-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
                                                                                                                                                                                       189 MSLLDAHIPOLVASOSAFAAKAGLMRHTIGOAEQAAMSAQAFHOGESSAAFQAAHARFVA 248
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                                                                Gaps
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   Length 299;
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                                                                                                                                                                                                                                                           61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97
100.0%; Score 468; DB 14;
100.0%; Pred. No. 1.7e-46;
tive 0; Mismatches 0;
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Patent No. US20020009459A1
GENERAL INFORMATION:
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US-09-886-349A-49
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Sequence 14, Application No. US2030147911A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Red, Steven G.

APPLICANT: APPLICANT: And Antonio

APPLICANT: APPLICANT: Antonio

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

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APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

APPLICANT: Campos-Netc, Antonio

CORRENT FILING DATE: 1999-04-07

PRIOR PILING DATE: 1999-04-07

PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR FILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-04-07

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; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion
US-10-359-460-14
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COTHER INFORMATION: Description of Artificial Sequence:tetra-fusion
US-09-287-849-14
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Best Local Similarity 100.0%; Pred. No. 2.7e-46;
Matches 97; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 08/942,5,5
PRIOR FILING DATE: 1997-10-0.1
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-04-07
PRIOR PILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PATENTIN VET: 2.1
; SOFTWARE: PATENTIN VET: 2.1
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-359-460-14
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LENGTH: 433
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GAPRICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
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                                                                                           335 MSILIDAHIPQLVASQSAFAAKAGIMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 394
1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion
US-09-287-849-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 0.099/7000S
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT APPLICATION NUMBER: US 09/597,796
PRIOR APPLICANTON NUMBER: US 09/597,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 468; DB 9; Length 710; 100.0%; Pred. No. 4.9e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 285
                                                                                                                                                                                                                                                                         395 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 431
                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 49, Application US/09886349A Publication No. US20040086523A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09287849
Patent No. US20020009459A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 97; Conservative
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APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-00020US
CURRENT APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US/09/25,197
PRIOR APPLICATION NUMBER: US/09/25,197
PRIOR APPLICATION NUMBER: US/09/25,197
PRIOR APPLICATION NUMBER: US/09/25,197
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
LENGTH: 710
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion; OTHER INFORMATION: protein DPV-MII-MSL-MTCC#2 (designated MTb71F) US-09-886-349A-49
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                                                                                                                                                                                                                                                                                                                                                                                     Length 710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 AAAKVNTLLDVAQANLGEAAGTYVAADAAASTYTGF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97
                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 468; DB 12; Best Local Similarity 100.0%; Pred. No. 4.9e-46; Matches 97; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ 1D NOS: 50
SEPTWARE: PatentIn Ver. 2.1
SEQ 1D NO 49
LENGTH: 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/10359460
Publication No. US20030147911A1
GENERAL INFORMATION:
                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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ORGANISM: Artificial Sequence
FEATURE:
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1 MSLLDAHIPQLVASQSAFAARAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60

61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97

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Db 249 AAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 285
Search completed: June 23, 2004, 17:18:23
Job time: 48 secs
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OM protein - protein search, using sw model

Run on:

June 23, 2004, 17:09:52 ; Search time 21 Seconds (without alignments) 444.313 Million cell updates/sec

US-09-886-349A-24

468 1 MSLLDAHIPQLVASQSAFAA.......BAAGTYVAADAAAASTYTGF 97 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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hypothetical glyci hypothetical glyci	antifreeze protein	hypothetical prote	pyruvate dehydroge	probable PE protei	hypothetical glyci	hypothetical prote	cytochrome-like pr	probable multi-dom	probable prfA prot	hypothetical prote	hypothetical glyci	hypothetical glyci	hypothetical glyci	probable PPE prote
G70917 H70846	S02376	QXBP1L	C59237	C70836	E70756	T42296	B84185	T37056	G70773	T25795	F70824	E70835	D70835	E70808
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741	900	401	978	102	558	646	810	2082	357	805	801	837	957	987
15.9	15.8	15.8	15.8	15.7	15.7	15.7	15.7	15.7	15.6	15.6	15.5	15.5	15.5	15.5
74.5	. 47	74	74	73.5	73.5	73.5	73.5	73.5	73	73	72.5	72.5	72.5	72.5
30	3 t	33	34	35	36	37	38	33	40	41	42	43	44	4 4 13

ALIGNMENTS

RESULT 1 B70836 probable transcription regulator Rv02; C;Species: Mycobacterium tuberculosis C;Dace: 17-011-1998 #sequence_revision C;Accession: E70836 R;Cole, S.T.; Brosch, R.; Parkhill, J. R;Cole, S.T.; Brosch, R.; Parkhill, J. R;Anthors: Sqares, R.; Parkhill, W.; A;Attle: Deciphering the biology of M;Reference number: A70500; MUID:9829 A;Reference number: A70500; MUID:9829 A;Reterence number: 1908 A;Reference 1-97 **Cole A;Redidues: 1-97 **Cole A;Cross-references: GB:AL021930; GB:A A;Cross-references: GB:AL021930; GB:A A;Experimental source: strain H37Rv C;Genetics: Ry0287	RESULT I B70836 C) Decides. Mycobacterium tuberculosis (strain H37RV) C; Species: Mycobacterium tuberculosis C; Detes: Nycobacterium tuberculosis C; Detes: Nycobacterium tuberculosis C; Detes: Nycobacterium tuberculosis C; Detes: Nycobacterium tuberculosis C; Detes: Nycobacterium tuberculosis R; Collos, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seger, K.; Skelton, S.; Squres, S. Nature 393, 537-544, 1998 Rycobacterium tuberculosis from the complete genome & A; Reference number: A70500; NUID:98295987; PMID:9634230 A; Reference number: A70500; NUID:98295987; PMID:9634230 A; Rocession: E70836 A; Scatus: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; References: GB:AL021930; GB:AL123456; NID:93261524; PIDN:CAA17362.1; PID:e125247(A; Experimental source: strain H37RV C; Gentles: RV0287
Query Match Best Local Similarity 100. Batches 97; Conservative Qy MSLLDAHIPOLVASQS Db MSLLDAHIPOLVASQS Qy 61 AAAKVNTLLDVAQANI Db 61 AAAKVNTLLDVAQANI	ch 100.0%; Score 468; DB 2; Length 97; 1 Similarity 100.0%; Pred. No. 1.3e-38; 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 MSLLDAHIPOLVASOSAFAAKAGLMRHTIGOAEQAAMSAQAFHQGESSAAFQAAHARFVA 60

RESULT 2
G70857
G70857
C;Species: Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-011-1998 #sequence_revision 17-011-1998 #text_change 22-Oct-1999
C;Accession: G70857
C;Accession: G70857
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S., Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A,Reference number: A70500; MuID:98295987; PMID:9634230
A,Stetus: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-97 cCOL>

Query Match Best Local Matches

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RESULT 3

g 8

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hypothetical protein Rv3874 - Mycobacterium tuberculosis (strain H37RV)

CiSpecies: Mycobacterium tuberculosis
CiSpecies: Mycobacterium tuberculosis
CiDate: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 20-Jun-2000
CiAccession: H70802

RiCole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Anture 393, 537-544, 1998

A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Atther. Deciphering the biology of Mycobacterium tuberculosis from the complete genome shacession: H70802
A.Accession: H70802
A.Accession: H70802
A.Accession: Draininary; nucleic acid sequence not shown; translation not shown
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A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1999
A;Reference number: 221559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: T34852
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DPA
A, Residues: 1-1156 < OLI>A, Residues: 1-1156 < OLI>A, Ross-references: EMBL: AL035478; PIDN: CAB36606.1; GSPDB: GN00070; SCOEDB: SC2G5.19
A, Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                             59 LAGELSAAVAPSG-----AVLSWQA-----NAVAVNAAHARAGAAAAAVSARMR 102
                                                                                                                                                                                                               11 LVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LVASGSA--FRAKAGL-----MRHIIGQAEQAAMSAQAFHQCBSSAAF-QAAHARFVAAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 FAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLDVAQANLG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 FERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQBAANKQKQELDEISTNIR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable secreted protein - Streptomyces coelicolor
C,Species: Streptomyces coelicolor
C,Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C,Accession: T34852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 87.5; DB 2; Length 100; Pred. No. 0.095; 8; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
18.6%; Score 87; DB 2; Length 1156;
Best Local Similarity 37.6%; Pred. No. 1.3;
Matches 35; Conservative 12; Mismatches 34; Indels 1
                                               Length 135;
                                               Score 92; DB 2; Length 135
Pred. No. 0.047;
8; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 ATAAALGQAARRYAGQDTAAAA 124
                                                                                                                                                                                                                                                                                                                                                                               71 VAOANLGEAAGTYVAADAAAS 92
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                                                   19.7%;
ilarity 36.6%;
Conservative
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Best Local Similarity 34.9%;
Matches 29; Conservative
                                                   Query Match
Best Local Similarity
Matches 30; Conserva
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C;Species: Mycobacterium tuberculosis
C;Dates: Mycobacterium tuberculosis
C;Dates: 17-011-1998 #sequence_revision 17-011-1998 #text_change 22-Oct-1999
C;Accession: 370659
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Sajadream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70509, MUID:98295987; PMID:9634230
A;Reference number: A70509
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-135 <COL>
A;Reperimental source: strain H37RV
C;Genesics: DNA
A;Residues: 1-135 <COL>
A;Reperimental source: strain H37RV
C;Genesics: DNA
A;Residues: DNA
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A;Residues:
A,Cross-references: GB:AL021287; GB:AL123456; NID:g3261508; PIDN:CAA16105.1; PID:e123776
A,Experimental source: strain H37Rv
C;Genetics:
A,Gene: PE
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R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R;Cole, S.T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
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A; Residues: 1-98 <STO>
A; Cross-references: GB:AL450380; NID:g13093794; PIDN:CAC32063.1; GSPDB:GN00147
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSLLDAHIPQLIASHTAFAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQCAHARFVA 60
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C;Species: Mycobacterium leprae
C;Date: 20-Apr_2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
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                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                    Score 442; DB 2; Length 97
Pred. No. 4.3e-36;
5; Mismatches 3; Indels
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Pred. No. 9.2e-28;
7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYTGF 97
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1 Similarity 91.8%;
89; Conservative
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Best Local Similarity 77.9%;
Matches 74; Conservative
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A; Gene: ML2532

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Chacesion: H70820
RiCole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Role, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A.Authors: agares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A.Reference number: A70500; MUID:9829597; PMID:9634230
A.Accession: H70820
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C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Reference number: Z21570
A/Accession: T15781
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-1147 <SEE>
A/Cross-references: EMBL.AL031013; PIDN:CAA19786.1; GSPDB:GN00070; SCOEDB:SC8A6.14c
C/Genetics:
A/GRee: SCOEDB:SC8A6.14c
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                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SC8A6.14c SC8A6.14c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
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R; Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1998
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Best Local Similarity 35.1%; Pred. No. 2;
Matches 34; Conservative 11; Mismatches 36; Indels
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A,Gene: Rv0980c
C,Superfamily: Phaseolus glycine-rich cell wall protein 1.8
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                       VNTLLDVAQANLGEAAGTYVAADAAAAS 92
                                                                                                                              68 VAAYQQRFVLALSQAGSTYAVAEAASAT 95
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Residues: 1.461 <COL>
A;Residues: 1.461 <COL>
A;Residues: 1.461 <COL>
A;Cross-references: GB:Z95387; GB:AL123456; NID:g3261763; PIDN:CAB08627.1; PID:g2104298
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A,Residues: 1-331 <COL>
A,FORSE-references: GB.AL021999, GB.AL123456; NID:g3261538; PIDN:CAA17577.1; PID:e125399 C,Genetics: A,Gene: Rv0978c
                                                                                                                                                                                                                                                                                                                                                                RESULT 7
FF0820
hypothetical glycine-rich protein Rv0978c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobaceerium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Cotcession: F70820
C;Cotcession: F70820
C;Cotcosine: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Cotcosine: R;Davies, R;Parkhill, J;Garnier, T;Ghurcher, C;Harris, D;Gordon, S;Cotnor, R;Davies, R;Devlin, K.;Feltwell, T;Gentles, S;Hamlin, N;Holroyd, S;Authors: Sqares, R;Sulston, JE;Taylor, K.;Mhitchead, S;Squares, S.
Nature 339, 537-544, 1998
A;Authors: Sqares, R;Sulston, JE;Taylor, K;Mhitchead, S;Saresll, B.G.
A;Authors: Sqares, R;Sulston, JE;Taylor, K;Mhitchead, S;Saresll, B.G.
A;Authors: Sqares, R;Sulston, JE;Taylor, K;Mhitchead, S;Saresll, B.G.
A;Accession: F70820
A;Accession: F70820
A;Accession: F70820
A;Accession: F70820
A;Accession: translation not shown
A;Moslecule type: DMA
A;Residues: 1-31 < COL.
A;Accession: CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;Col. CD,A;
     395 laaaqtatqaaaaagisaaatardsaaaaqqaavaaqasgaaqseaavaraaaaadaqa 454
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18.4%; Score 86; DB 2; Length 331;
Best Local Similarity 33.0%; Pred. No. 0.45;
Matches 29; Conservative 14; Mismatches 41; Indels
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                                                                                                                                                                                                               455 ARATKAANRAQSLANTAASAAAAARKAADSAAA 487
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Best Local Similarity
Matches 29; Conserva'
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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C,Superfamily: galactokinase
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nes 24; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: VC1595
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Best Local &
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| Cross-references: GB:AL008967, GB:AL123456, NID:g3261491, PIDN:CAA15564.1, PID:e117389
| Experimental source: strain H37Rv
                                C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C; Accession: G70682
R; Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S.; Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Accession: G70682
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Reference DA
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Unl-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Unl-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Unl-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Unl-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
R;Cole, S.T. Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamin, N.; Holroyd, S. Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70800; Mulb: 98295987; PMID: 9634230
A;Accession: G70881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 POLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGE---SSAAFQAAHARFVAAAAKV 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 80.5; DB 2;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 1.7;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 VAAAAKVNTLLDVAQANLGEAAGTYVAADAAAAS
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Best Local Similarity 35.1%;
Matches 33; Conservative 11
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nes 33; Conserv
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galactokinase VC1595 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C; Species: Vibrio cholerae

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Cjacession: G70929
R; Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Davlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.S.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobaccerium tuberculosis from the complete genome shreference number: A70500; MUID:98295987; PMID:9634230
C;Accession: F82181
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mexlanons, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Coses: 1-405 - HEL>
A;Cross.references: GB:AE004236, GB:AE003852; NID:g9656095; PIDN:AAF94749.1; GSPDB:GN0012
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A;Residues: 1-393 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17711.1; PID:e1254600
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70504
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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A,Status: preliminary; nucleic acid sequence not shown; translation not
A,Molecule type: DNA
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, M.; Holroyd, S.; Matlandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70504
A;Accession: A70504
A;Mesidues: J.394 ccCu.>
A;Residues: J.394 ccCu.>
A;Cross-references: GB:Z98268; GB:AL123456; NID:93261839; PIDN:CAB10963.1; PID:e332790; C;Genetics: PPE
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16.6%; Score 77.5; DB 2; Length 394;
Best Local Similarity 32.7%; Pred. No. 3.6;
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OM protein - protein search, using sw model

June 23, 2004, 17:09:52 ; Search time 17 Seconds (without alignments) 297.106 Million cell updates/sec Run on:

US-09-886-349A-24 468 1 MSLLDAHIPQLVASQSAFAA......BAAGTYVAADAAASTYTGF 97

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sulston J.E., Taylor K., Whitchead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.", Nature 393:537-544(1998). [3] SEQUENCE FROM N.A. SPECIES=W. tuberculosis, STRAIN=CDC 1551 / Oshkosh; MEDLINE=22206494; PubMed=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Hafte D., Hickey E., Peterson J., Deloyer R., Dodson R., Gwinn M., Hafte D., Hickey E., Peterson J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A. Bilaiai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; Biblai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; Biblai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; Biblai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; J. Bacteriol. 184:5479-5490(2002). [4] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SERVINGE M. S., Sharma P.;	Æ	Rutter S., 5	Seeger K.	, Skeltor	s., Squ	ares	S., Squares R.,		
"Deciphering the biology of mycobacterium tubercurose from complete genome sequence."; Nature 393:537544(1998). Nature 393:537544(1998). Sature and an arrange and arrange and arrange and arrange and arrange and arrange and arrange and arrange and arrange and arrange and arrange and arrange and arrange and arrange and arrange and arrange and arrange arrange and arrange arrange arrange and arrange arran	R.	Sulston J.E	, Taylor	K., Whit	ehead S.	Ba	rrell B.G.;	4	
complete genome sequence; Cauture 393:537-544(1998). [3] SEQUENCE FROM N.A. [3] SECIES=M tuberculosis, STRAIN=CDC 1551 / Oshkosh; SECIES=M tuberculosis, STRAIN=CDC 1551 / Oshkosh; MEDLINE=22206494; PubMed=12218036; Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Esen J.A., Exmolaeva M., Salzberg S., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L. Estate A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A. Bishai W., Jacobs W.R. JT., Venter J.C., Fraser C.M.; Estatome comparison of Mycobacterium tuberculosis clinical and laboratory strains; [4] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEGUENCE FROM N.A. SEGUENCE A., Sharma P.;	E !	"Deciphering	g the blo	logy or r	1ycobacte	1	capercatosis rion	,	
Nature 379.75.75.75.75.75.75.75.75.75.75.75.75.75.	Z Z	Complete ge	nome sequ						
SEQUENCE FROM N.A. SEQUENCE FROM N.A. SPECIESA. tuberculosis, STRAIN-CDC 1551 / Oshkosh; SPECIESA. tuberculosis, STRAIN-CDC 1551 / Oshkosh; MEDLINE-222066494; Pubmde=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Ermolaeva M., Salzberg S.L. Peletrson J., Delson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L. Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A. Bislail W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical ann laboratory strains."; J. Bacteriol. 184:5479-5490(2002). [4] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE A. Sinch S., Sharma P.;	1 2	[3]							
SPECIES-W. tuberculosis; STRAIN=CDC 1551 / Oshkosh; MEDLINE=22206494; PubMed=12218036; STRAIN=CDC 1551 / Oshkosh; MEDLINE=22206494; PubMed=12218036; Stein J.A., Carpenter L., White O., Petstsohmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Petstson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hiskey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L Delcher J., Utterback T., Weidman J., Khouri H., Gill J., Mikula A. Bishai W., Jacobs W.R. Jr., Weidman J., C., Fraser C.M.; Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; Imboratory strains., "Whole-genome comparison of Mycobacterium tuberculosis clinical ann laboratory strains.", J. Bacteriol. 184:5479-5490(2002). [4] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Siddicni Z., Sharma P.; Sharma P.; Sinch S., Sharma P.;	R.P.	SEQUENCE FRO	OM N.A.			•	•		
MEDLINE-22206494; PubMed=12218036, Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Ermolacva M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolacva M., Salzberg S.L Kolonay J.F., Nelson W.C., Umayam L.A., Ermolacva M., Salzberg S.L Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical an laboratory strains."; [4] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE A. Sharma P.;	RC	SPECIES=M.t	uberculos	is; STRA.	N=CDC 15	51 /	Oshkosh;		
FleasConman K.D., Alland D., Bisell D., Carpentor D., Mickey B., Scionay J., DoBoy R., Gwinn M., Haft D., Hickey B., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L. Delother A., Utterback T., Weidhan J., Knouri H., Gill J., Mikula A Bishai W., Jacobe W.R. Jr., Wenter J.C., Fraser C.M., "Whole-genome comparison of Mycobacterium tuberculosis clinical an laboratory strains"; J. Bacteriol. 184:S479-5490(2002). [4] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEGUENCE A. Sharma P.;	RX	MEDLINE=222	06494; Pu	DMed=122	.8036;		white		
Peterson U., DeBoy K., Dodani K., Marin H., Marin M., Salzberg S.L. Kolonay U.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L. Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; Hwhole-ganome comparison of Mycobacterium tuberculosis clinical an laboratory strains."; Whole-ganome comparison of Mycobacterium tuberculosis clinical an Jescuror FROM N.A. SEQUENCE FROM N.A. Span S., Sharma P.; Spar Luberculosis, Spar Marma P.; Sharma P.; Sharma P.; Sharma P.;	2 :	Fieischmann	K.U., AL	land D.,		``````````````````````````````````````) Addrig	•	
Anglordy V. T., Marthan T., Meidhan J., Khouri H., Gill J., Mikula A. Belcher A., Uterback T., Weidhan J., Khouri H., Gill J., Mikula A. Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "whole-genome comparison of Mycobacterium tuberculosis clinical an laboratory strains."; J. Bacteriol. 184:5479-5490(2002). [4] SEQUENCE FROM N.A. SECISS. M. tuberculosis; Species. M. tuberculosis; Sparma P.; Sinch B. Siddimi Z., Sharma P.;	RA F	Peterson J.	, DeBoy R	Dodgood ':	1 K., Gwl		٠,	S.L	
Delgier M., Outching M. M., Tandan, J. Fraser C.M.; Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical an laboratory strains."; J. Bacteriol. 184:5479-5490(2002). [4] SEQUENCE FROM N.A. SPECIES M. tuberculosis; SPECIES M. tuberculosis; Sinch R. Siddimi Z., Sharma P.;	A G	Kolonay J. F	TITTOTADO	10 13 CT 15	The man	i 6		-α	
"Whole-genome comparison of Mycobacterium tuberculosis clinical laboratory strains."; J. Bacteriol. 184:5479-5490(2002). [4] SEQUENCE FROM N.A. SPECIESM tuberculosis; SPECIESM tuberculosis;	ξά A c	Delcher A.,	Jacobs W.	R. Jr.	Zenter J.		Fraser C.M.;		
	5 E	"Whole-geno	me compar	ison of	Aycobacte	rium			
J. Bacteriol. 184:5479-5490(2002). [4] SEQUENCE FROM N.A. SPECIES-M.tuberculosis; sinch R. Siddimi Z., Sharma P	RI	laboratory	strains."						
141 SEQUENCE FROM N.A. SEQUENCE PROM N.A. SPECIES=M.tuberculosis; Sinch R. Siddimi Z., Sharma P	RL	J. Bacterio	1. 184:54	79-5490 (2002).				
SPECIES=M.tuberculosis;	z Z U	SEOUENCE FR	OM N.A.						
	28.5	SPECIES=M.t	uberculos	is;	ď		•		

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'DNA sequence of both chromosomes of the cholera pathogen Vibrio
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                                                                                                                                                                                                                                                                                  HAMAP; MF_00246; .; 1.
InterPro; IPR000705; Galactokinase.
InterPro; IPR001074; Galkinase.
InterPro; IPR006204; GHMP_kinase.
InterPro; IPR006204; GHMP_kinase.
InterPro; IPR006205; MeMPKinase AIP.
InterPro; IPR006206; MeV_galkinase.
Pfam; PF00288; GHMP_kinases; 1.
PRINTS; PR00960; LMBPRPROTEIN.
PRINTS; PR00960; LMBPRPROTEIN.
                                                                                                                                                                                                                                                        EMBL; AE004236; AAF94749.1; -.
TIGR; VC1595; -.
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STRAIN=SB1003 / St Louis;
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STRAIRE I TOR NIS961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.A.
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.
                                                                      MEDLINE=22709107; PubMed=12788972;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglemeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglemeier K., Camus J.-C., Medina N., Mansoor H.,
Bryor M., Duthoy S., Gerodin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. US. A. 100:7877-7882(2003).
-: SUBCELLULAR LOCATION: Secreted.
-: SIMILARITY: Belongs to the ESAT-6 (esx) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
"Rv3874 (mtsa-10) gene of a clinical isolate of Mycobacterium tuberculosis from India."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.7%; Score 87.5; DB 1; Length 99; 34.9%; Pred. No. 0.049; Live 8; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 AA; 10663 MW; EBCAE6A996C5489D CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FB-2003 (Rel. 41, Last annotation update)
GALK OR VC1595.
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BMBL, ABC02212; CAAL7966.1; --
EMBL, AE007190; AAK4836.1; --
EMBL, AF419854; AAL14999.1; --
PMBL; BYZ48347; CAD96090.1; --
PIR, H70802; H70802.
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Antigen, Complete proteome.
INIT_MET 0 0
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SILDAHIPQLVASQSAF-AAKAGLMRHTIGQAEQAAMSAQAFHQGES---SAAFQAAHAR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Gaps
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Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
-!- FUNCTION: SbcCD cleaves DNA hairpin structures. These structures can inhibit num renlication and are intermediated in contain num
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97404404; PubMed=9256491;
Vlcek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.;
"Sequence of a 189-kb segment of the chromosome of Rhodobacter
                                                                         phosphate.
--- PATHAAX: Galactose metabolism; first step.
--- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
--- SIMILARITY: Belongs to the GHMP kinase family.
Nature 406:477-483(2000).
-!- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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PROSITE; PSO0106; GALACTÓKINASE; 1.
PROSITE; PSO0627; GHMP KINASES ATP; 1.
Transferase; Kinase; Galactose_metabolism; ATP-binding;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nuclease sbcCD subunit C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 17.1%; Score 80; DB 1; Local Similarity 27.3%; Pred. No. 0.93; les 24; Conservative 17; Mismatches
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MEDLINE=88174422; PubMed=2832701;
Morlon J., Chartier M., Bidaud M., Lazdunski C.;
"The complete nucleotide sequence of the colicinogenic plasmid ColA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJNE-84036205; PubMed-6313941;
Morlon J., Lloubes R., Varenne S., Chartier M., Lazdunski C.;
"Complete nucleotide sequence of the structural gene for colicin A,
gene translated at non-uniform rate.";
J. Mol. Biol. 170:271-285(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid ColA-CA31.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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                                                                                                                                                                                                           EMBL; X792591; CAA63335.1; -

REAL; X7942; CAA50744.1; -

REAL; X7942; CAA50744.1; -

REAL; X7942; CAA50744.1; -

REAL; D47746; D47746.

RESP; O6324; D4FF.

REANSPAC; T02442; -

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DB8A8EFD1E94AB10 CRC64;
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13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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37.1%;
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Local Similarity 3/...
Set Local Similarity 3/...
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428 AA;
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P04480;
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                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 KAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLDVAQANLGEAA 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                       EMEL, APOTION 1996.

R PIR; T03465; T03465.

R PIR; T03465; T03465.

R InterPro; IPR003439; ABC transporter.

Hydrolase, Nuclease; Exomuclease; Endonuclease; DNA replication;

M DNA recombination; ATP-binding; Coiled coil.

I DOMAIN 395 438 COILED COIL (POTENTIAL).

T DOMAIN 466 487 COILED COIL (POTENTIAL).

T DOMAIN 724 770 COILED COIL (POTENTIAL).

T DOMAIN 724 770 COILED COIL (POTENTIAL).

T DOMAIN 901 943 COILED COIL (POTENTIAL).

T DOMAIN 1019 1052 COILED COIL (POTENTIAL).

T DOMAIN 1019 1052 COILED COIL (POTENTIAL).

T SEQUENCE 1238 AA; 128046 MW, 2B6BCGCGSA8S9AEI CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse),
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
recombination reactions. The complex acts as a 3'->5' double strand exonuclease that can open hairpins. It also has a 5' single-strand endonuclease activity (By similarity). SUBDNIT: Heterodimer of sbcC and sbcD (By similarity). SIMILARITY: Belongs to the SMC family. SbcC subfamily.
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Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- DEVELOPMENTAL STAGE: Expressed during embryogenesis.
-!- SIMILARITY: Contains 1 fork-head domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Forkhead box protein B2 (Transcription factor FKH-4).
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31.6%;
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Q40237;
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                            19; Gaps
                                                                                Parker M.W., Postma J.P.M., Pattus F., Tucker A.D., Tsernoglou D., "Refined structure of the pore-forming domain of colicin A at 2.4-A
                                                                                                                                                                                                                                                                                                                                                                                            EMBL, X01008; CAA35503.1; -
R PIR; 140784; IKEBGA.
PDB; 1CCL; 15-JUL-9; Channel_colicin.
PFAMINTS; PR000293; Channel_colicin.
PFAMINTS; PR00260; CHANLCOLICIN.
PPODOM; PR00260; CHANLCOLICIN.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
PROSITE; PS00276; CHANNEL_COLICIN; 1.
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TRANSMEM 555 675 POTENTIAL.
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h extent of homology with ColE1.";
. Gen. Genet. 211:231-243(1988).
                                                                   MEDLINE=92235820; PubMed=1373773;
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MPSB_LOLPR

RESULT 6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 134:235-240(1993).
-!- SUBCELLULAR LOCATION: STARCH GRANULE (BY SIMILARITY).
-!- TISSUE SPECIFICITY: Pollen, starch granules (By similarity).
-!- ALLERGEN: Causes an allergic reaction in human. Causes grass pollen allergy.
-!- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.
                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAJOR POLLEN ALLERGEN LOL P 5B.
9 X 3 AA TANDEM REPEATS OF [PA]-A-[TA].
1-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 X 9 AA APPROXIMATE TANDEM REPEATS OF
T-A-T-A-T-P-A-A-A.
2-1 (INCOMPLETE).
2-2.
                                                                                                                                                                                                                                                                                                                                      TISSUE=Pollen;
MEDLINE=94085783; PubMed=8262382;
Ong E.K., Griffith I.J., Knox R.B., Singh M.B.;
Cloning of a cDNA encoding a group-V (group-IX) allergen isoform from rye-grass pollen that demonstrates specific antigenic immunoreactivity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 339;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Major pollen allergen Lol p 5b precursor (Lol p Vb).
Lolium perenne (Perennial ryegrass).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.0%; Score 75; DB 1; 35.2%; Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, JT0756; JT0756.
InterPro; IPR001778; POA_allergen_C.
InterPro; IPR002914; POA_allergenN.
Pfam; PF01620; Pollen_allergenN.
PRINTS; PR00833; POAALLERGEN.
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319
328
81
288
339 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=H37Rv;
MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
Gold S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares R.,
                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-MODD / Nigg.
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Elinher K., Weidman W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 QAIQNOVAMAPEIGNAIRTQANHQAAATELQAKOSLISGITNIVGFAVSVGGGILSASKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 --GESSAAF----QAAHARFVAAAAKVNTLLDVAQANLGEAAGTYVAADAAAAST 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 LGGLKSAAFTNETATAASSATSAAAKTAVNALDDV--ANVAATAGTKAASGAASAAS
                                                                                                                                                                                                                                                                                                                                                               "Genome sequences of Chlamydia trachomatis MoFn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
-!- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0808/CT579/TC0868 FAMILY.
                                                                                            Bacteria, Chlamydiae, Chlamydiales, Chlamydiaceae, Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 15.9%; Score 74.5; DB 1, Length 436; Local Similarity 28.2%; Pred. No. 3.6; Onservative 10; Mismatches 39; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 OLVASOSAFAAKAGLMRHTIGQAEQAAMSAQAFHQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     il protein, Complete proteome.
436 AA, 43891 MW, 43E21C9924CD7A48 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PE-FGRS family protein Rv1818c/MT1866,
RV1818C OR MT1866 OR MTCY1A11.25C.
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE002353; AAF39664.1; -.
PIR; G81655; G81655.
                                               Hypothetical protein TC0868.
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  16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Hypothetical pro
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ID YII8_MYCTU
AC Q50615;
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DVVLDIAVVKEGDANRLLQEIVAIREAVPSPVVLKFILETAVVSDEAIVTAVNALIAAGA 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakagawa S.;
"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
"Lomalited (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 2-decxy.D-ribose 5-phosphate = D-glyceraldehyde 3-phosphate + acetaldehyde.
-!- PATHWAY: Nucleotide and decxyribonucleotide catabolism.
-!- SUBCELULIAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELULIAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCERIULIAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Deoxyribose-phosphate aldelase (EC 4.1.2.4) (Phosphodeoxyriboaldolase)
(Deoxyriboaldolase) (DERA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AAGTYVAADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 21.7%; Pred. No. 1.9;
Matches 28; Conservative 18; Mismatches 34; Indels 49
                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
BY SIMILARITY.
563C3D6B6805DD08 CRC64;
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                                                                                                                                                                        222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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       AKVNTLLDVAQANLGEAAGTYVAADAAAST
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InterPro; IPR002915, DeoC.
InterPro; IPR003009; FMN_enzyme.
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Y868 CHLMU STANDARD; 1
AC 29963; DT 16-OCT-2001 (Rel. 40, Created)
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                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                             STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Elsen J.A., Eate D., Hickey E.,

Kolonay J.F., Delson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,

Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;

"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
-!- SUBFAMILY.
complete genome sequence."; Mycobacterium tuberculosis from the Nature 393:537-544 (1998).
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4F6F78F2482586BA CRC64;
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C70720; C70720.
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Pfam; PF00934; PE; 1
ProDon; PD001223; PE_region; 1.
Hypothetical protein; Transmemb IRANSMEM.
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nes 29; Conservative
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ANP_LIMFE P09031; 01-NOV-1988 01-NOV-1988

RESULT 10
ANP_LIMFE
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(Rel. 09, Created) (Rel. 09, Last sequence update)

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                                                                                                                                                                                                                                                                         MEDLINE=88029483; PubMed=3665937;
Scott G.K., Davies P.L., Shears M.A., Fletcher G.L.;
"Structural variations in the alanine-rich antifreeze proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 AAKAGIMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLDVAQANLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 ААКАА----РАВУАПРААВАВАУАПТАЅПАВ--АВАВАТАВАВК--ВАВПТАВАВКА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Gaps
01-AUG-1990 (Rel. 15, Last annotation update)
Autifreeze protein precursor (AFP).
Limanda ferruginea (Yellowtail flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Limanda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses, dsDNA viruses, no RNA stage, Caudovirales, Siphoviridae,
Lambda-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 168:629-633(1987).
-!- FUNCTION: Ahtlfreeze proteins lower the blood freezing point.
-!- SIMILARITY: BELONGS TO THE TYPE-! AFP FAMILY. TYPE 1 AFP ARE
- ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REMOVED BY A DIPEPTIDYLPEPTIDASE
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3; Mismatches 34; Indels
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62AD582DF8E459B6 CRC64;
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MEDLINE=83189071; PubMed=6221115;
MEDLINE=83189071; PubMed=6221115;
Sanger F., Coulson A.R., Hong G.F., Hill D.F., Peter Sanger F., Coulson A.R., Hong G.F., Hill D.F., Peter Suncleotide sequence of bacteriophage lambda DNA.";
J. Mol. Biol. 162:729-773(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STF LAMBD STANDARD; PRT; 774 AA. P03764; P03764; (Rel. 01, Created) [6-OCT-2010 (Rel. 40, Last sequence update)] 15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROBABLE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR, S02376, S02376.
InterPro, IPR000104, Antifreeze 1.
PRINTS, PR00308, ANTIFREEZEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL, TENTIFICATION AS STF. MEDLINE=92165720; PubMed=1531648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X06356; CAA29655.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 AADTAAAAAEAAAATARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 42.3 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Side taïl fiber protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 AA;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               pleuronectinae.";
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                                                                                                                                                                                               NCBI_TaxID=8258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
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                                                                                                                                                          MEDLINE-9306310; PubMed=1439823;
Hendrix R.W. Duda R.L.;
Hendrix R.W. Duda R.L.;
Hendrix R.W. Duda R.L.;
Hendrix R.W. Duda R.L.;
Hendrix R.W. Duda PaPa: not the mother of all lambda phages.";
Science 258:1145-1148(1992)

-!- MISCELLANEOUS: The common laboratory strain of bacteriophage
lambda; lambda PaPa; carries a frameshift mutation relative to Ur-
lambda, the original isolate: The Ur-lambda virions have thin,
jointed tail fibers (side tail fibers) that are absent from lambda
wild type. Relative to lambda PaPa, Ur-lambda has expanded
receptor specificity and adsorbs to E.coli cells more rapidly.
-!- SIMILARITY: Belongs to the tail fiber family.
-!- CAUTION: This is a conceptual translation; a frameshift was
corrected in position to 396 to recreate the original stf protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AHIPQLV--ASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAA
                                  evidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND CHARACTERIZATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Haggaard-Ljungquist E., Halling C., Calendar R.; "DNA sequences of the tail fiber genes of bacteriophage P2: for horizontal transfer of tail fiber genes among unrelated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.8%; Score 74; DB 1; Length 774; 32.2%; Pred. No. 6.8;
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024206; 046064; 09M575;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Broad-complex core-protein isoform 6.
BR OR BR-C OR EG:17A9.1 OR EG:25D2.1 OR EG:123F11.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESSKNAAATSAGAAKTSETNAAASOOSAAT 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; C43009; QXBP2L.
InterPro; IPR008969; CarboxypepD_reg.
InterPro; IPR005003; Phage fiber.
InterPro; IPR005008; Phage fiber.
Pfam; PF03335; Phage fiber, 6.
Pfam; PF03406; Phage_fiber_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J02459; AAA96555.1; ALT_FRAME.
EMBL; J02459; AAA96557.1; ALT_FRAME.
                                                                                               Bacteriol. 174:1462-1477(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Imaginal disks, and Larva; MEDLINE=96299417; PubMed=8660872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           774 AA; 77527 MW;
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                                                                            bacteriophages.
                                                                                                                   [3]
RECONSTRUCTION
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SEQUENCE 774
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Best Local Simil
Matches 29, (
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Burdon R.C., Rogers Y.-H.C., Blazel, R.G., Champe M., Pfelifer B.D.,

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Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
Dreano S., Gloux S., Lelaure V., Mottler S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                    pression is regulate
Drosophila imaginal
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-!- FUNCTION: BROAD-COMPLEX PROTEINS ARE REQUIRED FOR PUFFING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97384928; PubMed=9242423;
Bayer C.A., von Kalm L., Fristrom J.W.;
"Relationships between protein isoforms and genetic functions
demonstrate functional redundancy at the Broad-Complex during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "From sequence to chromosome: the tip of the X chromosome of
Bayer C.A., Holley B., Fristrom J.W.;
"A switch in broad-complex zinc-finger isoform expression
posttranscriptionally during the metamorphosis of Drosophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION OF ISOFORMS, AND MUTATIONAL ANALYSIS
                                                                                                                                                                                                                                                                                                                         STRAIN=Oregon-R;
MEDLINE=20196011; PubMed=10731137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanogaster.";
Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila metamorphosis.";
Dev. Biol. 187:267-282(1997)
                                                                                                                                                                                       Dev. Biol. 177:1-14(1996)
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lover D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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TRANSCRIPTION OF SALIVARY GLAND LATE GENES DURING METAMORPHOSIS.

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                                                                                                                 Name=3; Synonyms=BCORE-Q2-Z1; Isold=Q01255-3; Sequence=External; Name=4; Synonyms=BCORE-Z2; Isold=Q01295-3; Sequence=External; Name=4; Synonyms=BCORE-Z2; Isold=Q01295-5; Sequence=External; Name=5; Synonyms=BCORE-NS-Z3; Isold=Q01295-5; Sequence=External; Sequence=External; Obvertopymental, STAGE: ACCUMULATES TO A HIGH LEVEL AT THE BEGINNING OF THE ECDYSONE RESPONSE, DURING THE METAMORPHOSIS OF IMAGINAL DISKS IN PUFF STAGE 1, AND ABRUPTLY DISAPPEARS AFTER SEVERAL HOURS.
                                                                                                                                                                                                                                                 -!- INDUCTION: INDUCED AS A PRIMARY RESPONSE TO 20-HYDROXYECDYSONE IN THIRD INSTAR LARVAL IMAGINAL DISKS.

THIRD INSTAR LARVAL IMAGINAL DISKS.

-!- SIMILARITY: Contains 1 BTP POZ domain.

-!- SIMILARITY: Contains 2 C2H2-type zinc fingers.

-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 534

TO 619 AND 656 TO 694 DUE TO FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV -> L (IN REF. 1).
MISSING (IN REF. 1).
KL -> NV (IN REF. 1).
500C0A4A38663AAF CRC64;
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POLY-ALA.
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POLY-PRO.
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POLY-ALA.
POLY-ALA.
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POLY-CLN.
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POLY-CLN.
POLY-CLN.
POLY-CLN.
POLY-CLN.
POLY-CLN.
                                Event=Alternative splicing, Named isoforms=6;
Name=6; Synonyms=BCORE-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REF.
                                                         Isoid=024206-1; Sequence=Displayed;
Name=1; Synonyms=BCORE-TNT1-01-21;
Isoid=0201295-1; Sequence=External;
Name=2; Synonyms=BCORE-01-21;
Isoid=0201295-2; Sequence=External;
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C2H2-TYPE 2.
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AV -> L (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U51585; AAB09760.1; ALT_FRAME.
         -!- SUBCELLULAR LOCATION: Nuclear
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL009146; CAA15627.1; -. EMBL; AE003421; AAF45647.1; -.
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FlyBase; FBgn0000210; br.
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880 AA;
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                                            2
                                                                                                                   775 HGAG-VSQAGSPGSRLHQSLSSLS-----AAAAANNSVNVGGGSVGGAGGNAVAA 824
                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.Y., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Barry C.E., Hamin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Squares R., Squares R., Squares R., Squares R., Shiphering T., Taylor K., Whitehead S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                27 HTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLDVAQANLGEAAGTYVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22206494; PubMed=12218036; Risen Garpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Eisen J.A., Haft D., Hickey E., Kolonay J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M., "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 184:5479-5490(2002).
Score 74; DB 1; Length 880;
Pred, No. 7.7;
                                                                                                                                                                                                                                                                                                                                   01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
Hypothetical Rel. 44, Last annotation update)
Hypothetical PE-PGRS family protein Rv1983/MT2036.
RV1983 OR MT2036 OR MTCX39.36C.
                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuberculist, Rv1983; -.
InterPro. IPR000084; PE_region.
Pfam, PF00934; PE_1 1.
ProDom, PD001223; PE_region; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, Z74025; CAA98400.1; -.
EMBL, AA007056; AAK46311.1; -.
PIR; E70756; E70756
TIGR: MT2036; -.
              15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence.";
Nature 393:537-544(1998).
                                                  24; Conservative
                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                     825 AAAAA 830
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                                  Similarity
                                                                                                                                                                 87 DAAAAS 92
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                                                                                                                                                                                                                                                                                                YJ83 MYCTU
Q10873;
              Query Match
Best Local S
Matches 24
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YJ83 MYCTU
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-! FUNCTION: Peptide chain release factor I directs the termination of translation in response to the peptide chain termination codons UAG and UAA (8y similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-M. tuberculosis, STRAIN=H37Rv;
MEDLINE=9825987; Pubmdd=9644230;
MEDLINE=98259879; Pubmdd=9644230;
Gordon S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Gliver S., Geeger K., Skelton S., Squares R.,
Shiston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Mature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                   7 VPEFLTSAAADVENIGSTLRAANAAAASTTALAAAGADEVSAAVAALFARFGQEYQAVS
                                                                                                                                                                                                                                                                                                                                          8 IPQLVASQSAFAAKAGLMRHTIGQAEQAAMSA-QAFHQGESSAAFQAAHARF----VAAA
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                               Length 558;
                                                                                                                                                                                                                                                                      46; Indels
Transmembrane, Complete proteome.
                                                                                                                               17ECBE43778E021E CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Peptide chain release factor 1 (RR-1).
PRFA OR RV1299 OR MI1338 OR MICY373.19 OR MB1331.
                                                                                                                                                                                                   DB 1;
                                                                                                                                                                          15.7%; Scor.
30.0%; Pred. No. 5.0,
"ive 12; Mismatches
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                                                                   POTENTIAL. POTENTIAL.
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J. Bacteriol. 184:5479-5490(2002)
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                            53 AL
352 PO
380 PO
; 53738 MW;
                                                                                                                                                                                                                                                                      27; Conservative
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       protein;
                               27
332
360
358 AA;
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Hypothetical
DOMAIN
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Q10605;
                                                            TRANSMEM
TRANSMEM
SEQUENCE
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STRAINSCAIRON-S; TISSUE-Head;
MEDLINE-99097004; PubMed=9878744;
Ma E., Xu T., Haddad G.G.;
"Gene regulation by O.2 deprivation: an anoxia-regulated novel gene in Drosophila melanogaster.";
Brain Res. Mol. Brain Res. 63:217-224(1999).
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., in P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
LOCATION: Cytoplasmic.
Belongs to the prokaryotic/mitochondrial release
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Anoxia upuregulated protein.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bohydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;

Bohydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.6%; Score 73; DB 1; Length 357; 27.2%; Pred. No. 4.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGRO0019; prfA; 1.
PROSITE; PS00745; RP PROX 1; 1.
PROCHID: Diosynthesis; Complete proteome.
PROFING 357 AA; 39036 MW; P6DE97400EFC0663 CRC64;
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Tuberculist, Rv1299, -.
HAWAP: MF 00093; -; 1.
InterPro; IPR0005139, PCRF.
InterPro; IPR000352; Pep rel_factor_I.
InterPro; IPR004373; PrfA.
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EMBL; AE077008; AAK4560.1; -.
EMBL; BX248338; CAD94192.1; -.
PIR, G70773; G70773.
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Pfam; PF00472; RF-1; 1
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-!- INDUCTION: By anoxia.

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Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G., Ballaw R. Barila J.F., Agbayani A., An H.-J., Andews-Pfannkoch C., Baldwin D., Ballaw R.M., Basen A., Baxendale U., Bayraktaroglu L., Basaley E.M., Beeson K.Y., Bernos P.V., Bernan B.D., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Basaley E.M., Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Achery J.M., Cawley S., Dahler C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., R. Bourbin K.J., Cawley S., Dahler C., Davengort L.B., Downes P., Dongson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dorbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferras C., Ferras C., Ferras C., Ferras C., Ferras C., Ferras M., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Alarielian A.B., Garg M.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Alalin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Alashon E., Kodira C.D., Kraft C., Kavitz S., Mup D., Lai Z., Alasko D., Lei Y., Levitsky A.A., Li J.H., Muzhy D., Muzhy B., Muzhy L., Muzhy D., Nelson D.L., Alasko D.R., Nalson K.A., Nusskern D.R., Pollar C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shen H., Shier K., Shen H., Shier K., Shen H., Shier K., Shen H., Shier K., Sheng L., Shan K., Shier B., Shier E., Sprading A.C., Stapleton M., Skupski M.P., Smith H.O., R. Shong K.H., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S., Wang S.,
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-! FUNGTION: Plays an important role in the regulation of tissue responsiveness to oxygen deprivation.
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Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mista S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdalle R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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TISSUE SPECIFICITY: Concentrated in lamina neurons, first optic
lobe neurons and cortical neurons of central brain.
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"Annotation of the Drosophila melanogaster euchromatic genome: a systematic review ";
genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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Comment=Experimental confirmation may be lacking
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427 IAAEEALLAEAA------AQKAAEBAKALKAAEDAAQKAAEEARLAEEAAQKVAEEA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 VASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVAAAAKVNTLLDV 71
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/FILLG-USP (004049.
/FILG-USP 004049.
IHSSNEYURSSEN -> SINTESLEPTSLVII HLSMDYYYSFLLYITHCSITSITSSLERQIRLVISPHII
                                                                                                                                                                                                                                                                                                                                                     TYYSPSYLPSTYTSTYIPTSYTTY -> TPRLDLCTDRPGS
HRSRASSDYSYTSKSSVEKSSYDSSNPHSYRPERSTYTSTV
EKTSRSGPGGSYNYSTERTSTTGAGPGGYSYSSTTSGNLPG
                                                                                                                                                                                                                                                                                                          ALA/GLU-RICH.
YPSVEKVTRVYKSSYPIYSSYSVPRRVYGATRVVTSPIRVV
TSPARVVSRVIHSPSPVRVVRTTTRVISSPERTTYSYTTPS
                                                                                                                                                                                                                                                                                                                                                                                                GTKYRHESYHV (in isoform C).
/FTId=VSP 004046.
/FTId=VSP 004040.
/FTId=VSP 004047.
YPTID=VSP 004047.
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PYVSTRDKNRTRILGMVRQHIDTVBAGGNTAGRTFRDSLDA
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/FIId=VSP 004051.
Missing (in isoform E).
/FIId=VSP 004052.
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                                                                                                                                         EMBL, AF154418; AAD38397.1; --
EMBL, AE003688; AAF54549.2; --
EMBL, AE003688; AAF54550.1; --
EMBL, AE003688; AAF54551.1; --
EMBL, AE003688; AAF5455.1; --
EMBL, AV19569; AAM50223.1; --
EMBL, AY119569; AAM50223.1; --
EMBL, AY119569; PSGT0020439; Fau.
GO: 00005979; P: response to ox:
Alternative splicing.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	053692 mycobacteri	053267 mycobacteri	Ċ	Q8vj87 mycobacteri		P95012 mycobacteri		Q8vjg4 mycobacteri		Q9z5a4 streptomyce	O53891 mycobacteri	Q8vka6 mycobacteri	006199 mycobacteri	087848 streptomyce	Q7u0x7 mycobacteri
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PIR, G70857, G70857.
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Local Similarity 91.8%;
les 89; Conservative
                                                                                                                                                                                                                                                                                                97 AA; 9842 MW;
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ESXS OR MB3046C.
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                            SEQUENCE FROM N.A.
NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                    Length
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                                                       Tuberculist; Rv0287; -.
Hypothetical protein; Complete proteome.
SEQUENCE 97 AA; 9778 MW; 927527DA610A1637 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterineae, Mycobacteriaceae, Mycobacterium
                                                                                                                   ; Score 468; DB 16;
; Pred. No. 3.3e-37;
0; Mismatches 0;
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100.0%; Pred. No. 3.3e-37;
tive 0; Mismatches 0;
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01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                    Conserved hypothetical protein TB9.8
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                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE=22709107; PubMed=12788972;
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 EMBL, ALO21930; CAA17362.1; -. EMBL; AAC06397, AAC44524.1; -. PIR, E70836; E70836.
                                                                                                                      100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S./
EMBL; BX248335; CAD93159.1;
                                                                                                                                                  97; Conservative
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nes 97; Conservative
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                                                                                                                      Query Match
Best Local Similarity
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Nature 1993:537-544 [1980].
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STRAIN=AFRIZE(97)
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Medina C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Harris B., Atkin R., Doggett J., Gordon S.V., Hewinson R.G.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
"The complete genome sequence of Mycobacterium bovis.";
"The Acad. Sci. U.S.A. 100:7877-7882(2003).
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1765,
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Last annotation update)
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Complete proteome.
SEQUENCE 98 AA;
Leproma; ML2532;
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRANDE-CDC 1521 / Oshkosh;
STRANDE-CDC 1521 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.,
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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94.4%; Score 442; DB 16; Length 102;
Best Local Similarity 91.8%; Pred. No. 1e-34;
Matches 89; Conservative 5; Mismatches 3; Indels
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NCBI_TaxID=1773;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL AE0071129; AAK47434.1; -.
TIGR; MT3105; -.
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Last sequence update)
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                                                                                                102 AA
                                                                                                                                               Created)
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MEDLINE=21128732; PubMed=11234002;
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EMBL, AL583926, CAC32063.1; -.
PIR, A87226, A87226.
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01-UUN-2001 (TrEMBLrel. 17, C;
01-UUN-2001 (TrEMBLrel. 17, Ls
01-UUN-2003 (TrEMBLrel. 24, Ls
PE-family protein.
ML2532.
                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2003 (TrEMBLrel. 24, PE family protein.
                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
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                                                                                                  PRELIMINARY;
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Q8VJ87
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                                                                                                                                                                                1 MSLLDAHIPQLVASQSAFAAKAGLMRHTIGQAEQAAMSAQAFHQGESSAAFQAAHARFVA 60
                                                                                                                                                                                                                                       1 MSLLDVHIPQLVASESAFAAKAALMRSQINQAECEAISAQAFHQGESSAAFQSAHAQFVT 60
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                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-935987, bubMed=9634230; Garnier T., Churcher C., Harris I Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badoock K., Basham D., Brown D., Chillingworth T., Comor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulton J.E., Seeger K., Skelton S., Squares S., Squares R., Sulton J.E., Taylor K., Whitehead S., Barrall B.G.; Burcher S., Seejer K., Skelton S., Squares R., Squares S., Squares R., Shelton S., Squares S., Squares R., Squares S., Sagares S., Squares S., Sagares S., Squares S., Sagares S., Squares S., Sagares S., Stalton J.E., Taylor K., Whitehead S., Barrall B.G.; Mycobacterium tuberculosis from the Nature 393:537-544(1998).
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                             Length 98;
                                                                                                                   14; Indels
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Tuberculist; RV-2541; Complete proteome.
Hypotherical protein; Complete proteome.
SEQUENCE 135 AA; 13403 MW; EEDC03B2B270DBCC CRC64;
98 AA; 10223 MW; F35750D374499928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTYC5,
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical alanine rich protein.
MB2570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                             Score 356; DB 16;
Pred. No. 1.5e-26;
7; Mismatches 14;
                                                                                                                                                                                                                                                                                                       61 AAAKVNTLLDVAQANLGEAAGTYVAADAAAASTYT 95
                                                                                                                                                                                                                                                                                                                                              61 AAEKINALLDIAQQHLGEAAETYVATDATAASTYT
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                                                                   76.18;
77.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY 1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 101-JUN-2003 (TrEMBLrel. 24, 14) Phypothetical protein RV2541. RV2541 OR MTCY159.15C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
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                                                                                             Local Similarity 77.9
nes 74; Conservative
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es 30; Conserv
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FROM N.A.
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SEQUENCE 457 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=AF2122/97;
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1765;
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Best Local S
                                                                         Q7U0X5
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                                                Q7U0X5
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Obeson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Gaps
                                                                                                                    SEQUENCE FROM N.A.
STRAIN=AF2122/97;
MEDLINE=22703107;
Darbier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Paryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Paryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S. A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole genome comparison of Mycobacterium tuberculosis clinical and
                Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007097, AAK46926.1; -.
TIGR; MT2615; -.
                                                                                                                                                                                                                                                                                                                                                                                                           135 AA; 13403 MW; EEDC03B2B270DBCC CRC64;
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373 AA; 38923 MW; BFA80E4609F2E908 CRC64;
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Last annotation update)
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36.6%; Pred. No. 0.29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
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Mycobacterium bovis
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1773;
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Q8VJG4;
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Matches
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"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                            MEDLINE=22709107; PubMed=12788972; Medina N., Mansoor H., Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Arkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
                                                                                                                                                                       Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bactéria; Actinobacteria, Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.0%; Score 89; DB 16; Length 457; 33.0%; Pred. No. 2.3; ive 16; Mismatches 39; Indels
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Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oliver K., Harris D.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 AA; 42096 MW; 429E35E2F624BA56 CRC64;
                                                               Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                           Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                        Created)
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                                        01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Conservative
PRELIMINARY;
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                                                                                                   PE-PGRS family protein.
PE PGRS18 OR MB1006C.
MyCobacterium bovis.
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us-09-886-349a-24.rspt

Tuberculist; Rv0978c;

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STRAIN=H3TRV,
MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987, PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Gardon S.V. Eiglumeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamilin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
MEDLINE=21996410 bubMed=12000953;
MEDLINE=21996410 bubMed=12000953;
Thomson N.B., Janes K.P., Cerdeno-Tarraga A.-M., Challis G.L.,
Harpper D., Bateman A., Brown S., Ghandra G., Chen C.W., Collins M.,
Harpper D., Bateman A., Brown S., Hadago J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Marren T., Metzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coelicolor A3(2).";
Nature 417.141-147(2002).
Nature 417.111-147(2002).
-i- COFACTOR: ZINC (BY ZINLARITY).
-i- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete genome sequence of the model actinomycete Streptomyces
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ilarity 37.6%; Pred. No. 10;
Conservative 12; Mismatches 34; Indels 12
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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PROSITE; PS00059; ADH ZINC; 1.
Oxidorreac; Zinc; Complete proteome.
SEQUENCE 1156 AA; 116717 MW; 70463814FB9517F8 CRC64;
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EMBL; AL021999; CAA17577.1; -.
PIR; F70820; F70820.
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RV0978C OR MTV044.06C
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"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
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Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                 Length 331;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE006985; AAK45254.1; -.
TIGR: MT1006; -.
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                                                                                                                                                                                      331 AA; 31019 MW; A093EC12F1691CA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.4%; Score 86; DB 16;
33.0%; Pred. No. 3.1;
iive 14; Mismatches 41;
                                                                                                                                                                                                                                              18.4%; Score 86; DB 16;
ilarity 33.0%; Pred. No. 3;
Conservative 14; Mismatches 41;
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InterPro; IPR000084; PE_region.
Pfam; PF01436; NHL; 3.
Pfam; PF00934; PE, PE_region.
Prodom; P0001223; PE_region; 1.
SEQUENCE 335 AA; 31351 MW; C2
         InterPro; IPR001258; NHL.
InterPro; IPR000084; PE_region.
Pfam; PF01436; NHL; 3.
Pfam; PF00934; PE; 1.
Probom; PD001223; PE_region; 1.
Complate proteome.
SEQUENCE 331 AA; 31019 MW; A0
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Best Local Similarity 33.09
Matches 29; Conservative
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01-MAR-2002 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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MTI006.1.
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ses 29; Conserv
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006199
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                               Churcher C., Harris
                                                                                                                                                                                                                                                                                    Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Genrles S., Hamin N., Holroyd Hornsby T., Jagels K., Kroph A., Mclean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Sulston J., Sylor M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Conplete genome sequence."
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                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Z95387; CAB08627.1; ALT_INIT.
EMBL; AE007102; AAK47006.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (PE PGRS family protein).
RV2615C OR MT2690 OR MTCY01A10.19.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein SCO6593.
SCO6593 OR SC8A6.14C.
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Local Similarity 33.0%; Pred. No. 4.6;
les 29; Conservative 14; Mismatches
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83 VAAYQQRFVLALSQAGSTYAVAEAASAT 110
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                                                                                                                                                                                                                                              STRAIN=H37Rv;
MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002952; Eggshell.
InterPro; IPR000084; PE_region.
                                                                                               Mycobacterium tuberculosis.
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Tuberculist; Rv2615c; -.
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                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                     NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 VASOSAFAAKAGLMRHTIGQAEQAAMS-----AQAFHQGESSAAFQAAHARFVAAAAK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A sac of condered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Gaps
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MEDLINE=21996410; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of the model actinomycete Streptomyces
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18.2%; Score 85; DB 16; Length 1147;
Best Local Similarity 35.1%; Pred. No. 16;
Matches 34; Conservative 11; Mismatches 36; Indels 16
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                                                                                                                          to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                           Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
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